

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:31:09 ; Search time 104.941 Seconds
(without alignments)
39.037 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62DX
Gapop 10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_03 : *
1: uniprot|prot : *
2: uniprot|trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	9	2 Q28121	Q28121 bos taurus
2	23	100.0	9	2 Q8WGE6	Q8WGE6 procamburus
3	23	100.0	10	2 Q70F01	Q70F01 sus scrofa
4	23	100.0	10	2 Q75885	Q75885 anolis pate
5	23	100.0	10	2 Q79897	Q79897 hapiocercus
6	23	100.0	10	2 Q79903	Q79903 oplurus cuv
7	23	100.0	10	2 Q79906	Q79906 phrynosoma
8	23	100.0	10	2 P92707	P92707 platysaurus
9	23	100.0	10	2 Q8W7U4	Q8W7U4 anolis nite
10	23	100.0	10	2 Q8W8Q2	Q8W8Q2 anolis punc
11	23	100.0	10	2 Q8W8Q3	Q8W8Q3 anolis nite
12	23	100.0	10	2 Q8W8Q4	Q8W8Q4 anolis punc
13	23	100.0	10	2 Q8W969	Q8W969 anolis orto
14	23	100.0	10	2 Q8W970	Q8W970 anolis nite
15	23	100.0	10	2 Q8W971	Q8W971 anolis fusc
16	23	100.0	10	2 Q8WDG6	Q8WDG6 anolis trac
17	23	100.0	10	2 Q8WDH0	Q8WDH0 anolis limi
18	23	100.0	10	2 Q8WDH2	Q8WDH2 anolis lem
19	23	100.0	10	2 Q8WDH4	Q8WDH4 anolis carp
20	23	100.0	10	2 Q8WDH6	Q8WDH6 anolis wood
21	23	100.0	10	2 Q8WDH8	Q8WDH8 anolis mest
22	23	100.0	10	2 Q8WDI8	Q8WDI8 anolis tran
23	23	100.0	10	2 Q6UJL5	Q6UJL5 strophurus
24	23	100.0	10	2 Q6WBN7	Q6WBN7 scelopor
25	23	100.0	10	2 Q6WBR1	Q6WBR1 scelopor
26	23	100.0	10	2 Q6WBR4	Q6WBR4 scelopor
27	23	100.0	10	2 Q6WBS3	Q6WBS3 scelopor
28	23	100.0	10	2 Q6WBT8	Q6WBT8 scelopor
29	23	100.0	10	2 Q6WBU1	Q6WBU1 scelopor
30	23	100.0	10	2 Q6WBU4	Q6WBU4 scelopor
31	23	100.0	10	2 Q6WBW2	Q6WBW2 phrynosoma

32	23	100.0	10	2 Q6WBW5	Q6WBW5 phrynosoma
33	23	100.0	10	2 Q6WBW8	Q6WBW8 phrynosoma
34	23	100.0	10	2 Q6WBX1	Q6WBX1 phrynosoma
35	23	100.0	10	2 Q6WBX4	Q6WBX4 phrynosoma
36	23	100.0	10	2 Q6WZN6	Q6WZN6 anolis cybo
37	23	100.0	10	2 Q6X061	Q6X061 anolis haet
38	23	100.0	10	2 Q6X071	Q6X071 anolis shre
39	23	100.0	10	2 Q6X0C3	Q6X0C3 anolis whit
40	23	100.0	10	2 Q6X0D2	Q6X0D2 anolis armo
41	23	100.0	10	2 Q6X0D8	Q6X0D8 anolis long
42	23	100.0	10	2 Q6X0E7	Q6X0E7 anolis marc
43	23	100.0	10	2 Q71DR5	Q71DR5 leiocephalu
44	23	100.0	10	2 Q71DR8	Q71DR8 leiocephalu
45	23	100.0	10	2 Q71DS4	Q71DS4 tropidurus
46	23	100.0	10	2 Q71DS7	Q71DS7 tropidurus
47	23	100.0	10	2 Q71DT0	Q71DT0 uranosodon
48	23	100.0	10	2 Q71DT3	Q71DT3 tropidurus
49	23	100.0	10	2 Q71DT6	Q71DT6 uracentron
50	23	100.0	10	2 Q71DT9	Q71DT9 stenocercus
51	23	100.0	10	2 Q71DU2	Q71DU2 stenocercus
52	23	100.0	10	2 Q71DU5	Q71DU5 stenocercus
53	23	100.0	10	2 Q71DU8	Q71DU8 scelopor
54	23	100.0	10	2 Q71DW0	Q71DW0 phrynosoma
55	23	100.0	10	2 Q71DW3	Q71DW3 polychrus m
56	23	100.0	10	2 Q71DW6	Q71DW6 polychrus a
57	23	100.0	10	2 Q71DW9	Q71DW9 anisolepis
58	23	100.0	10	2 Q71DX5	Q71DX5 urostrophus
59	23	100.0	10	2 Q71DX8	Q71DX8 enallius le
60	23	100.0	10	2 Q71DY1	Q71DY1 pristidacty
61	23	100.0	10	2 Q71DY4	Q71DY4 leiosaurus
62	23	100.0	10	2 Q71DY7	Q71DY7 leiosaurus
63	23	100.0	10	2 Q71DZ0	Q71DZ0 diplolaemus
64	23	100.0	10	2 Q71DZ3	Q71DZ3 diplolaemus
65	23	100.0	10	2 Q71E08	Q71E08 anolis cybo
66	23	100.0	10	2 Q71E11	Q71E11 chalarodon
67	23	100.0	10	2 Q71E17	Q71E17 morunasauru
68	23	100.0	10	2 Q71E20	Q71E20 envalioides
69	23	100.0	10	2 Q71E23	Q71E23 corytophane
70	23	100.0	10	2 Q71E35	Q71E35 baelliscus
71	23	100.0	10	2 Q71SD0	Q71SD0 liolaemus w
72	23	100.0	10	2 Q9T8U8	Q9T8U8 liolaemus p
73	23	100.0	10	2 Q9T8X1	Q9T8X1 liolaemus a
74	23	100.0	10	2 Q9ZYT2	Q9ZYT2 stenocercus
75	23	100.0	10	2 Q9ZYT6	Q9ZYT6 leiocephalu
76	23	100.0	11	2 Q8WES0	Q8WES0 ceratophora
77	23	100.0	11	2 Q8ESN4	Q8ESN4 mantheyus p
78	23	100.0	11	2 Q9G365	Q9G365 calotes emm
79	23	100.0	11	2 Q9G368	Q9G368 draco blanf
80	23	100.0	11	2 Q9G5Y9	Q9G5Y9 pseudocalot
81	23	100.0	11	2 Q9G5Z2	Q9G5Z2 pseudocalot
82	23	100.0	11	2 Q9G601	Q9G601 bronchocela
83	23	100.0	11	2 Q9G625	Q9G625 calotes ver
84	23	100.0	11	2 Q9G628	Q9G628 calotes mys
85	23	100.0	11	2 Q9G631	Q9G631 calotes nig
86	23	100.0	11	2 Q9G634	Q9G634 calotes lio
87	23	100.0	11	2 Q9G640	Q9G640 calotes cey
88	23	100.0	11	2 Q9G643	Q9G643 calotes cal
89	23	100.0	11	2 Q9G646	Q9G646 sitana pont
90	23	100.0	11	2 Q9G649	Q9G649 otocryptis
91	23	100.0	12	2 Q6WR31	Q6WR31 mycteria am
92	23	100.0	12	2 Q6WR34	Q6WR34 phoenicopte
93	23	100.0	12	2 Q6WR37	Q6WR37 buteo jamai
94	23	100.0	12	2 Q6WR43	Q6WR43 scolopax mi
95	23	100.0	12	2 Q6WR52	Q6WR52 asio otus (
96	23	100.0	12	2 Q6WR55	Q6WR55 musophaga v
97	23	100.0	12	2 Q6WR58	Q6WR58 musophaga v
98	23	100.0	12	2 Q6WR67	Q6WR67 neomorphus
99	23	100.0	12	2 Q6WR73	Q6WR73 coccyzus er
100	23	100.0	12	2 Q6WR79	Q6WR79 cuculus can
101	23	100.0	12	2 Q6WR82	Q6WR82 urocolius m
102	23	100.0	12	2 Q6WR88	Q6WR88 coracias sp
103	23	100.0	12	2 Q6WR91	Q6WR91 trogon curu
104	23	100.0	12	2 Q6WR94	Q6WR94 tockus eryt

105	23	100.0	12	2	Q6WR97	Q6wr97 anseranas s	178	22	95.7	18	2	Q7S173	Q7s173 neurospora
106	23	100.0	12	2	Q6WRA0	Q6wra0 chauna torq	179	22	95.7	18	2	Q7IU72	Q7iu72 homo sapien
107	23	100.0	12	2	Q6WRA3	Q6wra3 megapodius	180	22	95.7	19	2	Q99722	Q99722 lamprocorni
108	23	100.0	12	2	Q6WRA6	Q6wra6 alectura la	181	22	95.7	20	2	Q673D5	Q673d5 dehalococco
109	23	100.0	12	2	Q6WRA9	Q6wra9 crax rubra	182	21	91.3	6	1	E101_LITRU	P82096 litoria rub
110	23	100.0	12	2	Q8HN63	Q8hn63 sayornis ph	183	21	91.3	9	1	AKH_HELZE	P67787 heliothis z
111	23	100.0	12	2	Q8HN66	Q8hn66 acryllium v	184	21	91.3	15	2	Q9UC22	Q9uc22 homo sapien
112	23	100.0	12	2	Q53579	Q53579 rhodobacter	185	21	91.3	20	1	GBB4_RAT	O33535 rattus norv
113	23	100.0	13	1	BML2_BOMVA	P84211 bombina var	186	20	87.0	8	1	AKHG_GRYBI	P67785 gryllus bim
114	23	100.0	13	1	YPNP_PHOLU	P41122 photorhabdu	187	20	87.0	8	1	AKH_LITBAU	P25418 libellula a
115	23	100.0	13	2	Q9XLI2	Q9xli2 bemisia tab	188	20	87.0	8	1	AKH_PROTE	P61856 protophorni
116	23	100.0	13	2	Q7M1F5	Q7mif5 freesia ref	189	20	87.0	8	1	AKH_ROMMI	P67786 romalea mic
117	23	100.0	13	2	Q6GNE7	Q6gne7 borelia bu	190	20	87.0	8	1	AKH_TABAT	P14595 tabanus atr
118	23	100.0	14	2	Q71H30	Q71h30 andrena bra	191	20	87.0	8	1	HTF1_PERAM	P04548 periphaneta
119	23	100.0	15	2	Q53580	Q53580 rhodobacter	192	20	87.0	8	1	HTF2_PERAM	P04549 periphaneta
120	23	100.0	15	2	Q9R5D6	Q9r5d6 chromatium	193	20	87.0	8	1	HTF_TENMO	P67789 tenebrio mo
121	23	100.0	16	2	Q76019	Q76019 aspergillus	194	20	87.0	8	1	HTF_ZOPRU	P67790 zophobas ru
122	23	100.0	16	2	Q79B06	Q79b06 helicobacte	195	20	87.0	8	1	RPCH_PANBO	P08939 pandalus bo
123	23	100.0	16	2	Q8OGA1	Q8oga1 brachydanio	196	20	87.0	8	2	Q7M4H6	Q7m4h6 ischnura se
124	23	100.0	17	2	O15276	O15276 homo sapien	197	20	87.0	8	2	Q7M4H7	Q7m4h7 pseudogrion
125	23	100.0	17	2	Q8MIG9	Q8mig9 cynopterus	198	20	87.0	9	2	Q9UCQ9	Q9ucq9 homo sapien
126	23	100.0	17	2	Q9OQU4	Q9quj4 mus sp. mep	199	20	87.0	9	2	Q7M3N6	Q7m3n6 gryllus bim
127	23	100.0	17	2	Q6QLL7	Q6qli7 influenza a	200	20	87.0	10	1	GON1_PETWA	P04378 petromyzon
128	23	100.0	17	2	Q6QLL9	Q6qli9 influenza a	201	20	87.0	10	2	Q6UJL2	Q6ujl2 strophurus
129	23	100.0	17	2	Q6QLM0	Q6qlm0 influenza a	202	20	87.0	10	2	Q6XOE4	Q6xoe4 anolis stra
130	23	100.0	17	2	Q6QLM1	Q6qlm1 influenza a	203	20	87.0	10	2	Q7J5U5	Q7j5u5 ovis aries
131	23	100.0	18	2	Q9ZYW4	Q9zyw4 habrobracon	204	20	87.0	10	2	Q9ZYU4	Q9zyu4 sceloporos
132	23	100.0	18	2	Q9ZYX7	Q9zyx7 perga conde	205	20	87.0	11	1	CA31_LITCI	P82089 litoria cit
133	23	100.0	19	2	Q7S645	Q7s645 neurospora	206	20	87.0	11	1	CA32_LITCI	P82090 litoria cit
134	23	100.0	19	2	P83003	P83003 entamoeba h	207	20	87.0	11	2	O6E5M8	Q6e5m8 pyctolaem
135	23	100.0	19	2	Q9N1W2	Q9niw2 equus cabal	208	20	87.0	11	2	Q9G359	Q9g359 japalura fl
136	23	100.0	19	2	Q9TU41	Q9tu41 loxodonta a	209	20	87.0	11	2	Q9G607	Q9g607 aphanicotis
137	23	100.0	19	2	Q9TU42	Q9tu42 mammuthos p	210	20	87.0	12	2	P92680	P92680 trimeresuru
138	23	100.0	19	2	Q9T2V5	Q9t2v5 crithidia f	211	20	87.0	13	2	Q9MQK0	Q9mqk0 cervus elap
139	23	100.0	19	2	Q9ZYW7	Q9zyw7 aphidius ro	212	20	87.0	13	2	Q9MQK6	Q9mqk6 rupicapra r
140	23	100.0	19	2	Q9ZYW8	Q9zyw8 ichneutes b	213	20	87.0	14	2	Q9TQZ1	Q9tqz1 bos taurus
141	23	100.0	19	2	O44506	O44506 anabaena va	214	20	87.0	15	2	Q6LCZ7	Q6lcz7 homo sapien
142	23	100.0	19	2	Q6QLM2	Q6qlm2 influenza a	215	20	87.0	15	2	Q99386	Q99386 sus scrofa
143	23	100.0	19	2	O91329	O91329 human immun	216	20	87.0	15	2	Q6LBS9	Q6lbs9 raja erinac
144	23	100.0	19	2	Q9WJBI	Q9wjb1 human immun	217	20	87.0	16	2	Q9N237	Q9n237 pan troglod
145	23	100.0	20	1	CRTX_THUOB	P80972 thunnus obe	218	20	87.0	16	2	Q9T2Q8	Q9t2q8 solanum tub
146	23	100.0	20	1	CRTC_SPIOL	P30806 spinacia ol	219	20	87.0	16	2	Q9R4F2	Q9r4f2 streptomyc
147	23	100.0	20	2	Q95MJ7	Q95mj7 tarsius syr	220	20	87.0	16	2	Q9QW76	Q9qw76 mus sp. hom
148	23	100.0	20	2	Q95MJ8	Q95mj8 galago mona	221	20	87.0	17	2	Q7RMS4	Q7rm54 plasmodium
149	23	100.0	20	2	Q95MJ9	Q95mj9 pan troglod	222	20	87.0	17	2	Q8MJ33	Q8mj33 sus scrofa
150	23	100.0	20	2	Q95MK0	Q95mk0 pongo pygma	223	20	87.0	17	2	Q72017	Q72017 human immun
151	23	100.0	20	2	Q95MK1	Q95mk1 colobus ang	224	20	87.0	18	2	Q8N0X8	Q8n0x8 homo sapien
152	23	100.0	20	2	Q95MK2	Q95mk2 papio cynoc	225	20	87.0	18	2	Q9ZYW6	Q9zyw6 aleiodes sp
153	23	100.0	20	2	Q95MK3	Q95mk3 atales belz	226	20	87.0	18	2	Q8RU82	Q8ru82 zea maya lm
154	23	100.0	20	2	Q95MK4	Q95mk4 cheirogaleu	227	20	87.0	18	2	Q8NVH2	Q8nvh2 staphylococ
155	23	100.0	20	2	Q95MK5	Q95mk5 varecia var	228	20	87.0	18	2	Q9QW51	Q9qw51 mus sp. . a
156	23	100.0	20	2	Q95MK6	Q95mk6 eulemur cor	229	20	87.0	19	2	Q7REE1	Q7ree1 plasmodium
157	23	100.0	20	2	Q9TRA4	Q9tra4 sus scrofa	230	20	87.0	20	2	Q8WYR5	Q8wyr5 homo sapien
158	23	100.0	20	2	Q9R5E8	Q9r5e8 bacillus sp	231	19	82.6	8	2	Q7GEM6	Q7gem6 branchiosco
159	23	100.0	20	2	O61D18	Q6ld18 mus musculu	232	19	82.6	9	2	Q7LEB9	Q7leb9 homo sapien
160	23	100.0	20	2	Q66548	Q66548 human herpe	233	19	82.6	11	1	CORZ_PERAM	P11496 periphaneta
161	23	100.0	20	2	Q90X92	Q90x92 gallus gall	234	19	82.6	11	2	Q6T302	Q6t302 chlamydomon
162	22	95.7	10	1	AKHG_LOCMI	P81626 locusta mig	235	19	82.6	18	2	Q47246	Q47246 escherichia
163	22	95.7	10	1	HTF1_ROMMI	P18110 romalea mic	236	19	82.6	20	2	Q9R4Y6	Q9r4y6 porphyromon
164	22	95.7	10	1	HTF2_CARMO	P62542 carausius m	237	18	78.3	10	1	GON2_ALLMT	P68073 alligator m
165	22	95.7	10	1	HTF2_EXTTI	P62543 extatosoma	238	18	78.3	10	1	GON2_CHICK	P68072 gallus gall
166	22	95.7	10	1	HTF_BLAG	P84220 blattella g	239	18	78.3	10	1	GON2_CLUPA	P68075 clupea pall
167	22	95.7	10	1	HTF_GROPO	P84221 gromphadori	240	18	78.3	10	1	GON2_HYDCC	P68076 hydrotagus
168	22	95.7	10	1	HTF_HELZE	P16353 heliothis z	241	18	78.3	10	1	GON2_SQUAC	P68074 squalus aca
169	22	95.7	10	1	HTF_LEUMA	P84219 leucophaea	242	18	78.3	10	1	GON3_ONCKE	P20367 oncorhynch
170	22	95.7	10	1	HTF_NAUCI	P84218 nauphoeta c	243	18	78.3	10	1	GON3_PETWA	P30948 petromyzon
171	22	95.7	10	1	HTF_TABAT	P14596 tabanus atr	244	18	78.3	10	1	GONL_SQUAC	P27429 squalus aca
172	22	95.7	10	2	Q7M465	Q7m465 platyleura	245	18	78.3	10	2	O79912	Q79912 chamaeleo f
173	22	95.7	15	2	Q6UCQ4	Q6jcs2 tetratleurod	246	18	78.3	10	2	Q8SH83	Q8sh83 brookesia t
174	22	95.7	15	2	Q6UCS2	Q6jcs2 aleuroplatu	247	18	78.3	10	2	Q8SH85	Q8sh85 brookesia t
175	22	95.7	16	2	Q697F2	Q697f2 bemisia sp.	248	18	78.3	10	2	Q8SH88	Q8sh88 brookesia t
176	22	95.7	16	2	Q9XNP6	Q9xnp6 boophilus m	249	18	78.3	10	2	Q8SH90	Q8sh90 brookesia s
177	22	95.7	17	2	Q7Y1X8	Q7y1x8 lilium long	250	18	78.3	10	2	Q8SH96	Q8sh96 brookesia p

251	18	78.3	10	2	Q8SH99	Q8sh99 brookesia n	324	17	73.9	8	2	Q94V82	Q94V82 varanus yuw
252	18	78.3	10	2	Q8SHA2	Q8sha2 brookesia b	325	17	73.9	8	2	Q94V88	Q94V88 varanus tri
253	18	78.3	10	2	Q8SHA5	Q8sha5 brookesia a	326	17	73.9	8	2	Q94V91	Q94V91 varanus tim
254	18	78.3	10	2	Q8SHB1	Q8shb1 rhampoleon	327	17	73.9	8	2	Q94VA7	Q94V87 varanus sal
255	18	78.3	10	2	Q8SHB4	Q8shb4 furcifer ve	328	17	73.9	8	2	Q94VB2	Q94VB2 varanus sal
256	18	78.3	10	2	Q8SHB7	Q8shb7 furcifer ou	329	17	73.9	8	2	Q94VB5	Q94VB5 varanus sal
257	18	78.3	10	2	Q8SHC0	Q8shc0 furcifer la	330	17	73.9	8	2	Q94VC1	Q94VC1 varanus rud
258	18	78.3	10	2	Q8SHC3	Q8shc3 furcifer la	331	17	73.9	8	2	Q94VE4	Q94VE4 varanus mel
259	18	78.3	10	2	Q8SHC6	Q8shc6 furcifer be	332	17	73.9	8	2	Q94VF6	Q94VF6 varanus job
260	18	78.3	10	2	Q8SHC9	Q8shc9 furcifer ba	333	17	73.9	8	2	Q94VF9	Q94VF9 varanus ind
261	18	78.3	10	2	Q8SHD2	Q8shd2 chanaeleo w	334	17	73.9	8	2	Q94VJ4	Q94VJ4 varanus ben
262	18	78.3	10	2	Q8SHD5	Q8shd5 chanaeleo s	335	17	73.9	8	2	Q70Y57	Q70Y57 fuerstia af
263	18	78.3	10	2	Q8SHD8	Q8shd8 chanaeleo r	336	17	73.9	8	2	Q715L5	Q715L5 varanus dum
264	18	78.3	10	2	Q8SHE1	Q8she1 chanaeleo q	337	17	73.9	8	2	Q85406	Q85406 coxiella bu
265	18	78.3	10	2	Q8SHE4	Q8she4 chanaeleo g	338	17	73.9	8	2	Q7M124	Q7M124 kluyvera ci
266	18	78.3	10	2	Q8SHE7	Q8she7 chanaeleo p	339	17	73.9	8	2	Q62721	Q62721 rattus norv
267	18	78.3	10	2	Q8SHF3	Q8shf3 chanaeleo m	340	17	73.9	8	2	F79940	F79940 xenopus lae
268	18	78.3	10	2	Q8SHF6	Q8shf6 chanaeleo f	341	17	73.9	8	2	Q7L227	Q7L227 naja oxiata
269	18	78.3	10	2	Q8SHF9	Q8shf9 chanaeleo j	342	17	73.9	8	2	CAER_PHYSA	Q712c4 phyllomedus
270	18	78.3	10	2	Q8SHG2	Q8shg2 chanaeleo h	343	17	73.9	9	1	COW_CONVE	P83047 conus ventr
271	18	78.3	10	2	Q8SHG5	Q8shg5 chanaeleo h	344	17	73.9	9	1	NEF_HV128	P12481 human immun
272	18	78.3	10	2	Q8SHG8	Q8shg8 chanaeleo g	345	17	73.9	9	2	Q9H326	Q9H326 homo sapien
273	18	78.3	10	2	Q8SHH1	Q8shh1 chanaeleo f	346	17	73.9	9	2	Q9UK44	Q9UK44 homo sapien
274	18	78.3	10	2	Q8SHH4	Q8shh4 chanaeleo f	347	17	73.9	9	2	Q9UNA0	Q9UNA0 homo sapien
275	18	78.3	10	2	Q8SHH7	Q8shh7 chanaeleo e	348	17	73.9	9	2	Q7M4D5	Q7M4D5 diadema set
276	18	78.3	10	2	Q8SHI0	Q8shio chanaeleo d	349	17	73.9	9	2	Q8SHF0	Q8shf0 chanaeleo n
277	18	78.3	10	2	Q8SHI3	Q8shi3 chanaeleo c	350	17	73.9	9	2	Q94NA9	Q94na9 daubentonia
278	18	78.3	10	2	Q8SHI6	Q8shie chanaeleo c	351	17	73.9	9	2	Q94NB0	Q94nb0 microcebus
279	18	78.3	10	2	Q8SHI9	Q8shih chanaeleo c	352	17	73.9	9	2	Q94NB1	Q94nb1 microcebus
280	18	78.3	10	2	Q8SHJ2	Q8shj2 chanaeleo a	353	17	73.9	9	2	Q94NB2	Q94nb2 microcebus
281	18	78.3	10	2	Q8SHJ5	Q8shj5 calumma par	354	17	73.9	9	2	Q94VC6	Q94vc6 varanus pil
282	18	78.3	10	2	Q8SHJ8	Q8shj8 calumma osh	355	17	73.9	9	2	Q94VD8	Q94vd8 varanus nil
283	18	78.3	10	2	Q8SHK1	Q8shk1 calumma nas	356	17	73.9	9	2	Q94VE1	Q94ve1 varanus mer
284	18	78.3	10	2	Q8SHK4	Q8shk4 calumma hil	357	17	73.9	9	2	Q94VG2	Q94vg2 varanus ind
285	18	78.3	10	2	Q8SHK7	Q8shk7 calumma glo	358	17	73.9	9	2	Q94VH4	Q94vh4 varanus gla
286	18	78.3	10	2	Q8SHL0	Q8shl0 calumma gas	359	17	73.9	9	2	Q94VI0	Q94vi0 varanus gig
287	18	78.3	10	2	Q8SHL3	Q8shl3 calumma fur	360	17	73.9	9	2	Q94VI8	Q94vi8 varanus ere
288	18	78.3	10	2	Q8SHL6	Q8shl6 calumma cuc	361	17	73.9	9	2	Q94VJ1	Q94vj1 varanus dor
289	18	78.3	10	2	Q8SHL9	Q8shl9 calumma bre	362	17	73.9	9	2	Q94XE6	Q94xe6 tectocoris
290	18	78.3	10	2	Q8SHM2	Q8shm2 calumma boe	363	17	73.9	9	2	Q691D6	Q691d6 anolis sagr
291	18	78.3	10	2	Q8SHM5	Q8shm5 bradypodion	364	17	73.9	9	2	Q71DX2	Q71dx2 urostrophus
292	18	78.3	10	2	Q8SHM8	Q8shm8 bradypodion	365	17	73.9	9	2	Q85DB0	Q85db0 lepitemur s
293	18	78.3	10	2	Q8SHN1	Q8shn1 bradypodion	366	17	73.9	9	2	Q85DB8	Q85db8 lepitemur e
294	18	78.3	10	2	Q8SHN4	Q8shn4 bradypodion	367	17	73.9	9	2	Q97688	Q97688 gecko gecko
295	18	78.3	10	2	Q8SHN7	Q8shn7 bradypodion	368	17	73.9	9	2	Q8366	Q8366 bacterioph
296	18	78.3	10	2	Q8SHN0	Q8shn0 bradypodion	369	17	73.9	9	2	Q62200	Q62200 silene rotu
297	18	78.3	10	2	Q9G597	Q9g597 chanaeleo d	370	17	73.9	9	2	Q6VCX0	Q6vcx0 streptomyc
298	18	78.3	11	2	Q6DW13	Q6dw13 bos taurus	371	17	73.9	9	2	Q9R5M1	Q9r5m1 staphylococ
299	18	78.3	11	2	Q77894	Q77894 oreochromis	372	17	73.9	9	2	Q6LAQ1	Q6laq1 rattus norv
300	18	78.3	11	2	Q77895	Q77895 oreochromis	373	17	73.9	9	2	Q80X07	Q80x07 mus sp. thr
301	18	78.3	11	2	Q77896	Q77896 oreochromis	374	17	73.9	9	2	Q89491	Q89491 murine minu
302	18	78.3	11	2	Q77898	Q77898 oreochromis	375	17	73.9	9	2	Q78DU2	Q78du2 gallus gall
303	18	78.3	12	2	Q77915	Q77915 oreochromis	376	17	73.9	9	2	Q9PRJ4	Q9prj4 lepisosteus
304	18	78.3	13	2	Q9THR8	Q9thr8 bryopsis sp	377	17	73.9	9	2	Q85723	Q85723 simian sarc
305	18	78.3	13	2	Q718T2	Q718t2 newcastie d	378	17	73.9	10	1	APE_CAGPI	P80474 capnocytoph
306	18	78.3	15	1	GLN2_P1NPS	P81107 pinus pinas	379	17	73.9	10	1	BRK_ONCMY	P83465 agrocycbe ae
307	18	78.3	15	2	Q7M110	Q7m110 bacillus ci	380	17	73.9	10	1	CAI2_LITCI	P80474 capnocytoph
308	18	78.3	16	2	Q8HUM0	Q8hum0 uncultured	381	17	73.9	10	1	CAI2_LITSP	P62541 litoria spl
309	18	78.3	16	2	Q8HUM1	Q8hum1 uncultured	382	17	73.9	10	1	CAER_LITXA	P56264 litoria xan
310	18	78.3	17	2	Q6R800	Q6r800 saccharomyc	383	17	73.9	10	1	GRP_RANRI	P23260 rana ridibu
311	18	78.3	17	2	Q9TR22	Q9tr22 bos taurus	384	17	73.9	10	1	LABA_JATMU	P13270 jatropha mu
312	18	78.3	20	2	Q9TR25	Q9tr25 plasmodium	385	17	73.9	10	1	MP2_MICOC	P81533 microplitis
313	17	73.9	7	1	TY51_LITRU	P82065 litoria rub	386	17	73.9	10	2	Q7M530	Q7m530 pyrococcus
314	17	73.9	7	2	Q95945	Q95945 saccharomyc	387	17	73.9	10	2	Q15342	Q15342 homo sapien
315	17	73.9	7	2	Q49223	Q49223 glycine max	388	17	73.9	10	2	Q8WTT4	Q8wt4 homo sapien
316	17	73.9	8	1	AKH_GEOST	P84241 geotrupes s	389	17	73.9	10	2	Q6LA62	Q6la62 homo sapien
317	17	73.9	8	1	AKH_MELML	P84240 melolontha	390	17	73.9	10	2	Q7M2Z8	Q7m2z8 bos taurus
318	17	73.9	8	1	AKH_PACWA	P84242 pachnoda ma	391	17	73.9	10	2	Q7M3E8	Q7m3e8 sus scrofa
319	17	73.9	8	1	CKN_DASVI	P68125 dasyurus vi	392	17	73.9	10	2	Q9TR47	Q9tr47 bos taurus
320	17	73.9	8	1	CCKN_MACEU	P68126 macropus eu	393	17	73.9	10	2	Q79888	Q79888 basiliscus
321	17	73.9	8	1	VAME_MOUSE	P83653 mus musculus	394	17	73.9	10	2	Q79891	Q79891 crotaphytus
322	17	73.9	8	1	Q9TRY3	Q9try3 sus sp. ins	395	17	73.9	10	2	Q79894	Q79894 gambelia wi
323	17	73.9	8	2	Q8WGD7	Q8wgd7 lomus hirta	396	17	73.9	10	2		

397	17	73.9	10	2	079900	079900 liolaemus p	470	17	73.9	10	2	Q6WBH7	Q6WBH7 liolaemus h
398	17	73.9	10	2	079909	079909 sauromalus	471	17	73.9	10	2	Q6WB10	Q6WB10 liolaemus s
399	17	73.9	10	2	079915	079915 leiolepis b	472	17	73.9	10	2	Q6WB13	Q6WB13 liolaemus p
400	17	73.9	10	2	079924	079924 elgaria pan	473	17	73.9	10	2	Q6WB16	Q6WB16 liolaemus k
401	17	73.9	10	2	079926	079926 aspidocelli	474	17	73.9	10	2	Q6WB19	Q6WB19 liolaemus h
402	17	73.9	10	2	079932	079932 eramias gra	475	17	73.9	10	2	Q6WB22	Q6WB22 liolaemus p
403	17	73.9	10	2	079948	079948 lialis jica	476	17	73.9	10	2	Q6WB25	Q6WB25 liolaemus g
404	17	73.9	10	2	079954	079954 euprepis au	477	17	73.9	10	2	Q6WB28	Q6WB28 liolaemus n
405	17	73.9	10	2	079973	079973 fejevaraya	478	17	73.9	10	2	Q6WB31	Q6WB31 sceloporur
406	17	73.9	10	2	079978	079978 teratosticinc	479	17	73.9	10	2	Q6WB34	Q6WB34 sceloporur
407	17	73.9	10	2	079976	079976 uromastix a	480	17	73.9	10	2	Q6WB37	Q6WB37 sceloporur
408	17	73.9	10	2	079976	079976 varanus gri	481	17	73.9	10	2	Q6WB40	Q6WB40 sceloporur
409	17	73.9	10	2	079977	079977 xenosaurus	482	17	73.9	10	2	Q6WB43	Q6WB43 sceloporur
410	17	73.9	10	2	079977	079977 xantusia vi	483	17	73.9	10	2	Q6WB46	Q6WB46 sceloporur
411	17	73.9	10	2	079983	079983 brookesia p	484	17	73.9	10	2	Q6WB49	Q6WB49 sceloporur
412	17	73.9	10	2	079988	079988 rhampoleon	485	17	73.9	10	2	Q6WB52	Q6WB52 sceloporur
413	17	73.9	10	2	079988	079988 xantusia ar	486	17	73.9	10	2	Q6WB55	Q6WB55 sceloporur
414	17	73.9	10	2	079988	079988 xantusia be	487	17	73.9	10	2	Q6WB58	Q6WB58 sceloporur
415	17	73.9	10	2	079988	079988 xantusia he	488	17	73.9	10	2	Q6WB61	Q6WB61 sceloporur
416	17	73.9	10	2	079988	079988 liolaemus m	489	17	73.9	10	2	Q6WB64	Q6WB64 sceloporur
417	17	73.9	10	2	079988	079988 anolis line	490	17	73.9	10	2	Q6WB67	Q6WB67 sceloporur
418	17	73.9	10	2	079988	079988 anolis sagr	491	17	73.9	10	2	Q6WB70	Q6WB70 sceloporur
419	17	73.9	10	2	079988	079988 rana muscos	492	17	73.9	10	2	Q6WB73	Q6WB73 sceloporur
420	17	73.9	10	2	079988	079988 rana muscos	493	17	73.9	10	2	Q6WB76	Q6WB76 sceloporur
421	17	73.9	10	2	079988	079988 varanus sca	494	17	73.9	10	2	Q6WB79	Q6WB79 sceloporur
422	17	73.9	10	2	079988	079988 varanus var	495	17	73.9	10	2	Q6WB82	Q6WB82 sceloporur
423	17	73.9	10	2	079988	079988 varanus spe	496	17	73.9	10	2	Q6WB85	Q6WB85 sceloporur
424	17	73.9	10	2	079988	079988 varanus pan	497	17	73.9	10	2	Q6WB88	Q6WB88 sceloporur
425	17	73.9	10	2	079988	079988 varanus oli	498	17	73.9	10	2	Q6WB91	Q6WB91 sceloporur
426	17	73.9	10	2	079988	079988 varanus kin	499	17	73.9	10	2	Q6WB94	Q6WB94 sceloporur
427	17	73.9	10	2	079988	079988 varanus gri	500	17	73.9	10	2	Q6WB97	Q6WB97 sceloporur
428	17	73.9	10	2	079988	079988 varanus gle	501	17	73.9	10	2	Q6WB100	Q6WB100 sceloporur
429	17	73.9	10	2	079988	079988 rana muscos	502	17	73.9	10	2	Q6WB103	Q6WB103 sceloporur
430	17	73.9	10	2	079988	079988 rana casc	503	17	73.9	10	2	Q6WB106	Q6WB106 sceloporur
431	17	73.9	10	2	079988	079988 rana aurora	504	17	73.9	10	2	Q6WB109	Q6WB109 sceloporur
432	17	73.9	10	2	079988	079988 rana pretio	505	17	73.9	10	2	Q6WB112	Q6WB112 sceloporur
433	17	73.9	10	2	079988	079988 rana boylii	506	17	73.9	10	2	Q6WB115	Q6WB115 sceloporur
434	17	73.9	10	2	079988	079988 rana tempor	507	17	73.9	10	2	Q6WB118	Q6WB118 sceloporur
435	17	73.9	10	2	079988	079988 rana sylvat	508	17	73.9	10	2	Q6WB121	Q6WB121 sceloporur
436	17	73.9	10	2	079988	079988 rana cateab	509	17	73.9	10	2	Q6WB124	Q6WB124 sceloporur
437	17	73.9	10	2	079988	079988 heteronotia	510	17	73.9	10	2	Q6WB127	Q6WB127 sceloporur
438	17	73.9	10	2	079988	079988 gehyra vari	511	17	73.9	10	2	Q6WB130	Q6WB130 sceloporur
439	17	73.9	10	2	079988	079988 lialis jica	512	17	73.9	10	2	Q6WB133	Q6WB133 sceloporur
440	17	73.9	10	2	079988	079988 pseudotheca	513	17	73.9	10	2	Q6WB136	Q6WB136 sceloporur
441	17	73.9	10	2	079988	079988 phyllurus c	514	17	73.9	10	2	Q6WB139	Q6WB139 sceloporur
442	17	73.9	10	2	079988	079988 nephurus m	515	17	73.9	10	2	Q6WB142	Q6WB142 sceloporur
443	17	73.9	10	2	079988	079988 nephurus w	516	17	73.9	10	2	Q6WB145	Q6WB145 sceloporur
444	17	73.9	10	2	079988	079988 nephurus l	517	17	73.9	10	2	Q6WB148	Q6WB148 sceloporur
445	17	73.9	10	2	079988	079988 nephurus v	518	17	73.9	10	2	Q6WB151	Q6WB151 sceloporur
446	17	73.9	10	2	079988	079988 nephurus l	519	17	73.9	10	2	Q6WB154	Q6WB154 sceloporur
447	17	73.9	10	2	079988	079988 carphodactyl	520	17	73.9	10	2	Q6WB157	Q6WB157 sceloporur
448	17	73.9	10	2	079988	079988 crenodactyl	521	17	73.9	10	2	Q6WB160	Q6WB160 sceloporur
449	17	73.9	10	2	079988	079988 oedura marm	522	17	73.9	10	2	Q6WB163	Q6WB163 sceloporur
450	17	73.9	10	2	079988	079988 rhynchoedur	523	17	73.9	10	2	Q6WB166	Q6WB166 sceloporur
451	17	73.9	10	2	079988	079988 dipodactyl	524	17	73.9	10	2	Q6WB169	Q6WB169 sceloporur
452	17	73.9	10	2	079988	079988 strophurus	525	17	73.9	10	2	Q6WB172	Q6WB172 sceloporur
453	17	73.9	10	2	079988	079988 strophurus	526	17	73.9	10	2	Q6WB175	Q6WB175 sceloporur
454	17	73.9	10	2	079988	079988 dipodactyl	527	17	73.9	10	2	Q6WB178	Q6WB178 sceloporur
455	17	73.9	10	2	079988	079988 strophurus	528	17	73.9	10	2	Q6WB181	Q6WB181 sceloporur
456	17	73.9	10	2	079988	079988 dipodactyl	529	17	73.9	10	2	Q6WB184	Q6WB184 sceloporur
457	17	73.9	10	2	079988	079988 dipodactyl	530	17	73.9	10	2	Q6WB187	Q6WB187 sceloporur
458	17	73.9	10	2	079988	079988 dipodactyl	531	17	73.9	10	2	Q6WB190	Q6WB190 sceloporur
459	17	73.9	10	2	079988	079988 dipodactyl	532	17	73.9	10	2	Q6WB193	Q6WB193 sceloporur
460	17	73.9	10	2	079988	079988 dipodactyl	533	17	73.9	10	2	Q6WB196	Q6WB196 sceloporur
461	17	73.9	10	2	079988	079988 dipodactyl	534	17	73.9	10	2	Q6WB199	Q6WB199 sceloporur
462	17	73.9	10	2	079988	079988 dipodactyl	535	17	73.9	10	2	Q6WB202	Q6WB202 sceloporur
463	17	73.9	10	2	079988	079988 dipodactyl	536	17	73.9	10	2	Q6WB205	Q6WB205 sceloporur
464	17	73.9	10	2	079988	079988 strophurus	537	17	73.9	10	2	Q6WB208	Q6WB208 sceloporur
465	17	73.9	10	2	079988	079988 strophurus	538	17	73.9	10	2	Q6WB211	Q6WB211 sceloporur
466	17	73.9	10	2	079988	079988 strophurus	539	17	73.9	10	2	Q6WB214	Q6WB214 sceloporur
467	17	73.9	10	2	079988	079988 liolaemus c	540	17	73.9	10	2	Q6WB217	Q6WB217 sceloporur
468	17	73.9	10	2	079988	079988 liolaemus x	541	17	73.9	10	2	Q6WB220	Q6WB220 sceloporur
469	17	73.9	10	2	079988	079988 liolaemus r	542	17	73.9	10	2	Q6WB223	Q6WB223 sceloporur

543	17	73.9	10	2	Q9B4W7	Q9b4w7 tylototrito	616	17	73.9	10	2	Q9TG53	Q9tg53 elgaria pau
544	17	73.9	10	2	Q9B4X0	Q9b4x0 notophthalm	617	17	73.9	10	2	Q9TG56	Q9tg56 elgaria kin
545	17	73.9	10	2	Q9G362	Q9g362 acanthosaur	618	17	73.9	10	2	Q9TG59	Q9tg59 elgaria coe
546	17	73.9	10	2	Q9G694	Q9g694 leioplepis g	619	17	73.9	10	2	Q9TG62	Q9tg62 messapis mo
547	17	73.9	10	2	Q9MJQ5	Q9mjqs podopora c	620	17	73.9	10	2	Q9TG65	Q9tg65 abronia oax
548	17	73.9	10	2	Q9T4P9	Q9t4p9 liolaemus d	621	17	73.9	10	2	Q9TG68	Q9tg68 gerthonotus
549	17	73.9	10	2	Q9T8F5	Q9t8f5 liolaemus b	622	17	73.9	10	2	Q9TG71	Q9tg71 barisia imb
550	17	73.9	10	2	Q9T8G0	Q9t8g0 liolaemus l	623	17	73.9	10	2	Q9TG74	Q9tg74 wetmorena h
551	17	73.9	10	2	Q9T8G5	Q9t8g5 liolaemus o	624	17	73.9	10	2	Q9TG77	Q9tg77 sauresia ag
552	17	73.9	10	2	Q9T8G8	Q9t8g8 liolaemus c	625	17	73.9	10	2	Q9TG80	Q9tg80 ophiodes st
553	17	73.9	10	2	Q9T8H1	Q9t8h1 liolaemus u	626	17	73.9	10	2	Q9TG83	Q9tg83 diploglossu
554	17	73.9	10	2	Q9T8H4	Q9t8h4 liolaemus i	627	17	73.9	10	2	Q9TG86	Q9tg86 diploglossu
555	17	73.9	10	2	Q9T8H7	Q9t8h7 liolaemus a	628	17	73.9	10	2	Q9TG89	Q9tg89 celestus en
556	17	73.9	10	2	Q9T8I0	Q9t8i0 liolaemus o	629	17	73.9	10	2	Q9TG92	Q9tg92 anniella pu
557	17	73.9	10	2	Q9T8I3	Q9t8i3 liolaemus q	630	17	73.9	10	2	Q9TG95	Q9tg95 anniella ge
558	17	73.9	10	2	Q9T8I6	Q9t8i6 liolaemus k	631	17	73.9	10	2	Q9TG98	Q9tg98 shinisaurus
559	17	73.9	10	2	Q9T8I9	Q9t8i9 liolaemus a	632	17	73.9	10	2	Q9TGA1	Q9tga1 heloderma s
560	17	73.9	10	2	Q9T8J2	Q9t8j2 liolaemus r	633	17	73.9	10	2	Q9TGS9	Q9tgs9 phymaturus
561	17	73.9	10	2	Q9T8J5	Q9t8j5 liolaemus m	634	17	73.9	10	2	Q9ZYT5	Q9zyt5 uta stansbu
562	17	73.9	10	2	Q9T8J8	Q9t8j8 liolaemus w	635	17	73.9	10	2	Q9ZYT8	Q9zyt8 urosaurus g
563	17	73.9	10	2	Q9T8K1	Q9t8k1 liolaemus s	636	17	73.9	10	2	Q9ZVU1	Q9zyu1 uma scopari
564	17	73.9	10	2	Q9T8K4	Q9t8k4 liolaemus s	637	17	73.9	10	2	Q9ZYU7	Q9zyu7 sator angus
565	17	73.9	10	2	Q9T8K7	Q9t8k7 liolaemus m	638	17	73.9	10	2	Q9ZIV0	Q9zyv0 petrosaurus
566	17	73.9	10	2	Q9T8L0	Q9t8l0 liolaemus o	639	17	73.9	10	2	Q9ZIV3	Q9zyv3 diposaurus
567	17	73.9	10	2	Q9T8L3	Q9t8l3 liolaemus l	640	17	73.9	10	2	Q9Z213	Q9z213 aegilops ta
568	17	73.9	10	2	Q9T8L6	Q9t8l6 liolaemus p	641	17	73.9	10	2	Q8KH9	Q8khn9 clostridium
569	17	73.9	10	2	Q9T8L9	Q9t8l9 liolaemus f	642	17	73.9	10	2	Q93T35	Q93t35 acinetobact
570	17	73.9	10	2	Q9T8M2	Q9t8m2 liolaemus c	643	17	73.9	10	2	Q6JL97	Q6jl97 neisseria g
571	17	73.9	10	2	Q9T8M5	Q9t8m5 liolaemus a	644	17	73.9	10	2	Q6R101	Q6r101 clostridium
572	17	73.9	10	2	Q9T8M8	Q9t8m8 liolaemus m	645	17	73.9	10	2	Q79AV7	Q79av7 klebsiella
573	17	73.9	10	2	Q9T8N1	Q9t8n1 liolaemus p	646	17	73.9	10	2	Q8G8W5	Q8g8w5 borrelia bu
574	17	73.9	10	2	Q9T8N4	Q9t8n4 liolaemus d	647	17	73.9	10	2	Q9F9H5	Q9f9h5 helicobacte
575	17	73.9	10	2	Q9T8N7	Q9t8n7 liolaemus o	648	17	73.9	10	2	Q9R5N2	Q9r5n2 clostridium
576	17	73.9	10	2	Q9T8P0	Q9t8p0 liolaemus f	649	17	73.9	10	2	Q70580	Q70580 mus musculu
577	17	73.9	10	2	Q9T8P3	Q9t8p3 liolaemus a	650	17	73.9	10	2	Q9ESU5	Q9esus mus musculu
578	17	73.9	10	2	Q9T8P6	Q9t8p6 liolaemus r	651	17	73.9	10	2	Q7LZC5	Q7lzc5 kassina mac
579	17	73.9	10	2	Q9T8P9	Q9t8p9 liolaemus m	652	17	73.9	10	2	Q8UT83	Q8ut83 human immun
580	17	73.9	10	2	Q9T8Q2	Q9t8q2 liolaemus s	653	17	73.9	10	1	CEP1_ACHFU	P05624 achatina fu
581	17	73.9	10	2	Q9T8Q5	Q9t8q5 liolaemus l	654	17	73.9	11	1	LPW_THETH	P05624 thermus the
582	17	73.9	10	2	Q9T8Q8	Q9t8q8 liolaemus e	655	17	73.9	11	1	MLG_THETS	P41989 theromyzon
583	17	73.9	10	2	Q9T8R1	Q9t8r1 liolaemus a	656	17	73.9	11	1	OAIF_SARBU	P83318 sarcophaga
584	17	73.9	10	2	Q9T8R4	Q9t8r4 liolaemus p	657	17	73.9	11	1	RANC_RANPI	P08951 rana pipien
585	17	73.9	10	2	Q9T8R7	Q9t8r7 liolaemus c	658	17	73.9	11	1	RR2_CONAM	P42341 conopholis
586	17	73.9	10	2	Q9T8R9	Q9t8r9 liolaemus b	659	17	73.9	11	1	Q9G1R7	Q9c1r7 saccharomyc
587	17	73.9	10	2	Q9T8S1	Q9t8s1 liolaemus l	660	17	73.9	11	2	Q8TDA8	Q8tda8 homo sapien
588	17	73.9	10	2	Q9T8S4	Q9t8s4 liolaemus c	661	17	73.9	11	2	Q9UCR1	Q9ucr1 homo sapien
589	17	73.9	10	2	Q9T8S7	Q9t8s7 liolaemus n	662	17	73.9	11	2	Q9UE69	Q9ue69 homo sapien
590	17	73.9	10	2	Q9T8T0	Q9t8t0 liolaemus f	663	17	73.9	11	2	Q9UEL0	Q9uel0 homo sapien
591	17	73.9	10	2	Q9T8T3	Q9t8t3 liolaemus n	664	17	73.9	11	2	Q6UZ55	Q6uz55 littorina s
592	17	73.9	10	2	Q9T8T6	Q9t8t6 liolaemus m	665	17	73.9	11	2	Q77908	Q77908 oreochromis
593	17	73.9	10	2	Q9T8T9	Q9t8t9 liolaemus l	666	17	73.9	11	2	Q77914	Q77914 oreochromis
594	17	73.9	10	2	Q9T8U2	Q9t8u2 liolaemus t	667	17	73.9	11	2	Q78118	Q78118 oreochromis
595	17	73.9	10	2	Q9T8U5	Q9t8u5 liolaemus z	668	17	73.9	11	2	Q78636	Q78636 laudakia hi
596	17	73.9	10	2	Q9T8V0	Q9t8v0 liolaemus c	669	17	73.9	11	2	Q79639	Q79639 laudakia le
597	17	73.9	10	2	Q9T8V3	Q9t8v3 liolaemus c	670	17	73.9	11	2	Q79642	Q79642 laudakia mi
598	17	73.9	10	2	Q9T8V6	Q9t8v6 liolaemus b	671	17	73.9	11	2	Q79918	Q79918 physignathu
599	17	73.9	10	2	Q9T8V9	Q9t8v9 liolaemus g	672	17	73.9	11	2	Q79921	Q79921 phrynoceph
600	17	73.9	10	2	Q9T8W2	Q9t8w2 liolaemus b	673	17	73.9	11	2	Q79985	Q79985 laudakia ca
601	17	73.9	10	2	Q9T8W5	Q9t8w5 liolaemus r	674	17	73.9	11	2	Q79986	Q79986 laudakia er
602	17	73.9	10	2	Q9T8W8	Q9t8w8 liolaemus b	675	17	73.9	11	2	Q8SKN0	Q8skn0 ctenophorus
603	17	73.9	10	2	Q9T8X4	Q9t8x4 liolaemus c	676	17	73.9	11	2	Q8SKN3	Q8skn3 ctenophorus
604	17	73.9	10	2	Q9T8X7	Q9t8x7 phymaturus	677	17	73.9	11	2	Q8SKN6	Q8skn6 ctenophorus
605	17	73.9	10	2	Q9T8Y6	Q9t8y6 teratoscinc	678	17	73.9	11	2	Q8SKN9	Q8skn9 ctenophorus
606	17	73.9	10	2	Q9T8Y9	Q9t8y9 teratoscinc	679	17	73.9	11	2	Q8SKP2	Q8skp2 ctenophorus
607	17	73.9	10	2	Q9T8V2	Q9t8v2 teratoscinc	680	17	73.9	11	2	Q8SKP5	Q8skp5 ctenophorus
608	17	73.9	10	2	Q9TFV5	Q9tfv5 eublepharis	681	17	73.9	11	2	Q8SKP8	Q8skp8 ctenophorus
609	17	73.9	10	2	Q9TG32	Q9tg32 ophisaurus	682	17	73.9	11	2	Q8SKQ1	Q8skq1 ctenophorus
610	17	73.9	10	2	Q9TG35	Q9tg35 ophisaurus	683	17	73.9	11	2	Q8SKQ4	Q8skq4 ctenophorus
611	17	73.9	10	2	Q9TG38	Q9tg38 ophisaurus	684	17	73.9	11	2	Q8SKQ7	Q8skq7 ctenophorus
612	17	73.9	10	2	Q9TG41	Q9tg41 ophisaurus	685	17	73.9	11	2	Q8SKR0	Q8skr0 rankinia di
613	17	73.9	10	2	Q9TG44	Q9tg44 anguis frag	686	17	73.9	11	2	Q8WCZ9	Q8wc29 ctenophorus
614	17	73.9	10	2	Q9TG47	Q9tg47 ophisaurus	687	17	73.9	11	2	Q8WD02	Q8wd02 ctenophorus
615	17	73.9	10	2	Q9TG50	Q9tg50 elgaria mul	688	17	73.9	11	2		

689	17	73.9	11	2	Q8WD05	Q8WD05 ctenophorus	762	17	73.9	11	2	Q9G5X7	Q9G5X7 trapelus ru
690	17	73.9	11	2	Q8WD08	Q8WD08 ctenophorus	763	17	73.9	11	2	Q9G5Y0	Q9G5Y0 pseudotraper
691	17	73.9	11	2	Q8WD11	Q8WD11 ctenophorus	764	17	73.9	11	2	Q9G5Y3	Q9G5Y3 agama impal
692	17	73.9	11	2	Q8WD14	Q8WD14 ctenophorus	765	17	73.9	11	2	Q9G5Y6	Q9G5Y6 agama agama
693	17	73.9	11	2	Q8WD17	Q8WD17 ctenophorus	766	17	73.9	11	2	Q9G5Z5	Q9G5Z5 japalura sp
694	17	73.9	11	2	Q8WD20	Q8WD20 ctenophorus	767	17	73.9	11	2	Q9G5Z8	Q9G5Z8 acanthosaur
695	17	73.9	11	2	Q8WD23	Q8WD23 ctenophorus	768	17	73.9	11	2	Q9G604	Q9G604 gonoccephalu
696	17	73.9	11	2	Q8WD26	Q8WD26 ctenophorus	769	17	73.9	11	2	Q9G610	Q9G610 lyriocephal
697	17	73.9	11	2	Q8WD29	Q8WD29 ctenophorus	770	17	73.9	11	2	Q9G613	Q9G613 cophotis ce
698	17	73.9	11	2	Q8WD50	Q8WD50 ceratophora	771	17	73.9	11	2	Q9G616	Q9G616 ceratophora
699	17	73.9	11	2	Q8WER4	Q8WER4 ceratophora	772	17	73.9	11	2	Q9G619	Q9G619 ceratophora
700	17	73.9	11	2	Q8WER7	Q8WER7 ceratophora	773	17	73.9	11	2	Q9G622	Q9G622 salea horsf
701	17	73.9	11	2	Q94V74	Q94V74 lanthanotus	774	17	73.9	11	2	Q9G637	Q9G637 caiotes lio
702	17	73.9	11	2	Q94V77	Q94V77 heloderma s	775	17	73.9	11	2	Q9G652	Q9G652 japalura va
703	17	73.9	11	2	Q94V94	Q94V94 varanus sto	776	17	73.9	11	2	Q9G655	Q9G655 japalura tr
704	17	73.9	11	2	Q94VB8	Q94VB8 varanus sal	777	17	73.9	11	2	Q9G658	Q9G658 hydrosaurus
705	17	73.9	11	2	Q94VE7	Q94VE7 varanus kom	778	17	73.9	11	2	Q9G661	Q9G661 typanocryp
706	17	73.9	11	2	Q94VG8	Q94VG8 varanus gou	779	17	73.9	11	2	Q9G664	Q9G664 diporiphora
707	17	73.9	11	2	Q94VH7	Q94VH7 varanus gil	780	17	73.9	11	2	Q9G667	Q9G667 calmanops a
708	17	73.9	11	2	Q94V15	Q94V15 varanus exa	781	17	73.9	11	2	Q9G670	Q9G670 rankinia ad
709	17	73.9	11	2	Q94VK1	Q94VK1 varanus aca	782	17	73.9	11	2	Q9G673	Q9G673 ctenophorus
710	17	73.9	11	2	Q6ESN1	Q6ESN1 ptyctolaemu	783	17	73.9	11	2	Q9G676	Q9G676 amphiboluru
711	17	73.9	11	2	Q6WR61	Q6WR61 nandayus ne	784	17	73.9	11	2	Q9G679	Q9G679 hypsilurus
712	17	73.9	11	2	Q6WR64	Q6WR64 neophena el	785	17	73.9	11	2	Q9G682	Q9G682 chelosania
713	17	73.9	11	2	Q7Y9B6	Q7Y9B6 amphiboluru	786	17	73.9	11	2	Q9G685	Q9G685 arua modest
714	17	73.9	11	2	Q7Y9B9	Q7Y9B9 typanocryp	787	17	73.9	11	2	Q9G688	Q9G688 physignathu
715	17	73.9	11	2	Q7Y9C2	Q7Y9C2 typanocryp	788	17	73.9	11	2	Q9G691	Q9G691 lophognathu
716	17	73.9	11	2	Q7Y9C5	Q7Y9C5 typanocryp	789	17	73.9	11	2	Q9GD68	Q9GD68 elaeis guin
717	17	73.9	11	2	Q7Y9C8	Q7Y9C8 typanocryp	790	17	73.9	11	2	Q7M1U2	Q7M1U2 oryza sativ
718	17	73.9	11	2	Q7Y9D1	Q7Y9D1 typanocryp	791	17	73.9	11	2	Q7M1W2	Q7M1W2 canavalia e
719	17	73.9	11	2	Q7Y9D4	Q7Y9D4 typanocryp	792	17	73.9	11	2	Q8GL19	Q8GL19 borrelia bu
720	17	73.9	11	2	Q7Y9D7	Q7Y9D7 pogona vitt	793	17	73.9	11	2	Q8GL24	Q8GL24 borrelia bu
721	17	73.9	11	2	Q7Y9E0	Q7Y9E0 pogona null	794	17	73.9	11	2	Q6LD68	Q6LD68 mus sp. acu
722	17	73.9	11	2	Q7Y9E3	Q7Y9E3 pogona mitc	795	17	73.9	11	2	Q9QVH3	Q9QVH3 rattus sp.
723	17	73.9	11	2	Q7Y9E6	Q7Y9E6 pogona mino	796	17	73.9	11	2	Q65CG7	Q65CG7 sinaloa tom
724	17	73.9	11	2	Q7Y9E9	Q7Y9E9 pogona mini	797	17	73.9	11	2	Q90735	Q90735 gallus gall
725	17	73.9	11	2	Q7Y9F2	Q7Y9F2 pogona henr	798	17	73.9	11	2	Q83410	Q83410 mouse mamma
726	17	73.9	11	2	Q7Y9F5	Q7Y9F5 pogona brev	799	17	73.9	11	2	Q8AD18	Q8AD18 human immun
727	17	73.9	11	2	Q7Y9F8	Q7Y9F8 lophognathu	800	17	73.9	12	1	LICA_BACSU	LICA_BACSU
728	17	73.9	11	2	Q7Y9G1	Q7Y9G1 hypsilurus	801	17	73.9	12	1	NO40_LOTUA	NO40_LOTUA
729	17	73.9	11	2	Q7Y9G4	Q7Y9G4 hypsilurus	802	17	73.9	12	1	NO40_SESRO	NO40_SESRO
730	17	73.9	11	2	Q7Y9G7	Q7Y9G7 hypsilurus	803	17	73.9	12	1	NO40_SOYBN	NO40_SOYBN
731	17	73.9	11	2	Q7Y9H0	Q7Y9H0 hypsilurus	804	17	73.9	12	1	RF1_CONSP	RF1_CONSP
732	17	73.9	11	2	Q7Y9H3	Q7Y9H3 hypsilurus	805	17	73.9	12	1	UR2A_CATCO	UR2A_CATCO
733	17	73.9	11	2	Q7Y9H6	Q7Y9H6 hypsilurus	806	17	73.9	12	1	UR2B_CATCO	UR2B_CATCO
734	17	73.9	11	2	Q7Y9H9	Q7Y9H9 diporiphora	807	17	73.9	12	1	UR2B_CYPCA	UR2B_CYPCA
735	17	73.9	11	2	Q7Y9I2	Q7Y9I2 diporiphora	808	17	73.9	12	1	UR2_GILMI	UR2_GILMI
736	17	73.9	11	2	Q7Y9I5	Q7Y9I5 diporiphora	809	17	73.9	12	1	UR2_POLSP	UR2_POLSP
737	17	73.9	11	2	Q7Y9I8	Q7Y9I8 diporiphora	810	17	73.9	12	1	UR2_SCVCA	UR2_SCVCA
738	17	73.9	11	2	Q7Y9J1	Q7Y9J1 diporiphora	811	17	73.9	12	2	Q8J0A7	Q8J0A7 saccharomyc
739	17	73.9	11	2	Q7Y9J4	Q7Y9J4 diporiphora	812	17	73.9	12	2	Q7RZZ4	Q7RZZ4 neurospora
740	17	73.9	11	2	Q7Y9J7	Q7Y9J7 diporiphora	813	17	73.9	12	2	Q16405	Q16405 homo sapien
741	17	73.9	11	2	Q7Y9K0	Q7Y9K0 diporiphora	814	17	73.9	12	2	Q6KEF1	Q6KEF1 homo sapien
742	17	73.9	11	2	Q7Y9K3	Q7Y9K3 diporiphora	815	17	73.9	12	2	Q6YBQ9	Q6YBQ9 homo sapien
743	17	73.9	11	2	Q7Y9K6	Q7Y9K6 diporiphora	816	17	73.9	12	2	Q9BZ49	Q9BZ49 homo sapien
744	17	73.9	11	2	Q7Y9K9	Q7Y9K9 amphiboluru	817	17	73.9	12	2	Q86CU1	Q86CU1 drosophila
745	17	73.9	11	2	Q7Y9L3	Q7Y9L3 amphiboluru	818	17	73.9	12	2	Q86FU4	Q86FU4 drosophila
746	17	73.9	11	2	Q7Y9L5	Q7Y9L5 amphiboluru	819	17	73.9	12	2	Q9BP48	Q9BP48 conus penna
747	17	73.9	11	2	Q9G2N4	Q9G2N4 chlamydomas	820	17	73.9	12	2	Q6X7V1	Q6X7V1 canis famil
748	17	73.9	11	2	Q9G350	Q9G350 laudakia sa	821	17	73.9	12	2	Q77889	Q77889 oreochromis
749	17	73.9	11	2	Q9G353	Q9G353 trapelus sa	822	17	73.9	12	2	Q77890	Q77890 oreochromis
750	17	73.9	11	2	Q9G356	Q9G356 agama atra	823	17	73.9	12	2	Q77891	Q77891 oreochromis
751	17	73.9	11	2	Q9G371	Q9G371 pogona barb	824	17	73.9	12	2	Q77919	Q77919 pseudotroph
752	17	73.9	11	2	Q9G374	Q9G374 molech horr	825	17	73.9	12	2	Q77920	Q77920 pseudotroph
753	17	73.9	11	2	Q9G5V0	Q9G5V0 laudakia st	826	17	73.9	12	2	Q6WR40	Q6WR40 burhinus se
754	17	73.9	11	2	Q9G5V3	Q9G5V3 phrynoceph	827	17	73.9	12	2	Q6WR46	Q6WR46 treron sieb
755	17	73.9	11	2	Q9G5V6	Q9G5V6 phrynoceph	828	17	73.9	12	2	Q6WR49	Q6WR49 columba leu
756	17	73.9	11	2	Q9G5V9	Q9G5V9 laudakia st	829	17	73.9	12	2	Q6WR70	Q6WR70 crotophaga
757	17	73.9	11	2	Q9G5W2	Q9G5W2 laudakia tu	830	17	73.9	12	2	Q6WR76	Q6WR76 centropus c
758	17	73.9	11	2	Q9G5W5	Q9G5W5 laudakia nu	831	17	73.9	12	2	Q6WR85	Q6WR85 colius stri
759	17	73.9	11	2	Q9G5W8	Q9G5W8 trapelus sa	832	17	73.9	12	2	Q6WRB2	Q6WRB2 eudromia el
760	17	73.9	11	2	Q9G5X1	Q9G5X1 trapelus pe	833	17	73.9	12	2	Q8LLC3	Q8LLC3 trifolium r
761	17	73.9	11	2	Q9G5X4	Q9G5X4 trapelus ag	834	17	73.9	12	2	Q93WB7	Q93WB7 lupinus lut

835	17	73.9	12	2	Q93WF2	Q93wf2	lupinus lut	908	17	73.9	13	2	Q9X514	Q9x514	enterococcu
836	17	73.9	12	2	Q7GCS7	Q7gcs7	oryza sativ	909	17	73.9	13	2	Q91XP1	Q91xp1	mus musculu
837	17	73.9	12	2	Q8GSB9	Q8gsb9	lolium pere	910	17	73.9	13	2	Q705X8	Q705x8	mus musculu
838	17	73.9	12	2	Q8H6E6	Q8h6e6	hordeum vul	911	17	73.9	13	2	Q7M059	Q7m059	mus musculu
839	17	73.9	12	2	Q9M433	Q9m433	lotus japon	912	17	73.9	13	2	Q7TMB4	Q7tmb4	mus musculu
840	17	73.9	12	2	Q9S8F0	Q9s8f0	zea mays (m	913	17	73.9	13	2	Q80Y03	Q80y03	rattus sp.
841	17	73.9	12	2	Q5ZMT6	Q5zmt6	oryza brach	914	17	73.9	13	2	Q9QW04	Q9qw04	mus sp. pl
842	17	73.9	12	2	O54226	O54226	saccharopol	915	17	73.9	13	2	Q9QW45	Q9qw45	rattus sp.
843	17	73.9	12	2	Q46747	Q46747	escherichia	916	17	73.9	13	2	Q9QCK3	Q9qck3	borna disea
844	17	73.9	12	2	O6V8J9	O6v8j9	salmonella	917	17	73.9	13	2	Q9QCK6	Q9qck6	borna disea
845	17	73.9	12	2	Q9S550	Q9s550	streptococc	918	17	73.9	13	2	Q9QCK9	Q9qck9	borna disea
846	17	73.9	12	2	Q63579	Q63579	rattus norv	919	17	73.9	13	2	Q9QCL2	Q9qcl2	borna disea
847	17	73.9	12	2	Q64313	Q64313	rattus norv	920	17	73.9	13	2	Q9QCL5	Q9qcl5	borna disea
848	17	73.9	12	2	O80XV4	O80xv4	rattus sp.	921	17	73.9	13	2	Q9QCL8	Q9qcl8	borna disea
849	17	73.9	12	2	O80Y04	O80y04	rattus sp.	922	17	73.9	13	2	Q9QCM1	Q9qcm1	borna disea
850	17	73.9	12	2	O8CFD7	O8cfd7	rattus sp.	923	17	73.9	13	2	Q9QCM4	Q9qcm4	borna disea
851	17	73.9	12	2	O8EQV3	O8eqv3	mus musculu	924	17	73.9	13	2	Q7LZ24	Q7l224	vipera aspi
852	17	73.9	12	2	Q90XT0	Q90xt0	grus canade	925	17	73.9	13	2	Q85645	Q85645	mouse mamma
853	17	73.9	12	2	Q90XT2	Q90xt2	larus glauc	926	17	73.9	14	1	ALYT_ALYOB	ALYT_alyob	alutys obst
854	17	73.9	12	2	O90XT5	O90xt5	puffinus gr	927	17	73.9	14	1	BOMB_BOMBO	BOMB_bombo	bombina bom
855	17	73.9	12	2	O90XU4	O90xu4	phalacrocor	928	17	73.9	14	1	CALI_CALGI	CALI_calgi	calotropis
856	17	73.9	12	2	O12036	O12036	caprine art	929	17	73.9	14	1	KARA_BROPL	KARA_bropl	bromelia pl
857	17	73.9	12	2	O41611	O41611	human immun	930	17	73.9	14	1	LPW_CITFR	LPW_citfr	citrobacter
858	17	73.9	12	2	O8QDY4	O8qdy4	human immun	931	17	73.9	14	1	LPW_ECOLI	LPW_ecoli	escherichia
859	17	73.9	12	2	O8QDY5	O8qdy5	human immun	932	17	73.9	14	1	LPW_RHIME	LPW_rhime	rhizobium m
860	17	73.9	12	2	O8QDY6	O8qdy6	human immun	933	17	73.9	14	1	LPW_SALTY	LPW_salty	salmonella
861	17	73.9	12	2	O8Q841	O8q841	human immun	934	17	73.9	14	1	MAST_VESBA	MAST_vesba	vespa basal
862	17	73.9	12	2	O8Q843	O8q843	human immun	935	17	73.9	14	1	NEJ2_FASHE	NEJ2_fashe	fasciola he
863	17	73.9	12	2	O8Q845	O8q845	human immun	936	17	73.9	14	1	PHE_STRMO	PHE_strmo	streptomyce
864	17	73.9	12	2	O8Q847	O8q847	human immun	937	17	73.9	14	1	PPK6_PERAM	PPK6_peram	periplaneta
865	17	73.9	12	2	Q98240	Q98240	human immun	938	17	73.9	14	1	SMS1_MYOSC	SMS1_myosc	myoxocephal
866	17	73.9	12	2	Q75729	Q75729	human immun	939	17	73.9	14	1	SMS_ALUMI	SMS_alumi	alligator m
867	17	73.9	12	2	BML1_BOMVA	B42121	bombina var	940	17	73.9	14	1	SMS_TRASC	SMS_trasc	trachemys s
868	17	73.9	13	1	BMPI_PSEGU	P42991	pseudophryn	941	17	73.9	14	2	Q7S023	Q7s023	neurospora
869	17	73.9	13	1	BMPI_BORJA	F01020	bothrops ja	942	17	73.9	14	2	Q7S6V5	Q7s6v5	neurospora
870	17	73.9	13	1	E121_LITRU	P82097	litoria rub	943	17	73.9	14	2	Q7SAY2	Q7say2	neurospora
871	17	73.9	13	1	E122_LITRU	P82098	litoria rub	944	17	73.9	14	2	Q13022	Q13022	homo sapien
872	17	73.9	13	1	MLA_ANOCA	P41589	anolis caro	945	17	73.9	14	2	O81VK4	O81vk4	homo sapien
873	17	73.9	13	1	MLA_CAMDR	P61281	camelus dro	946	17	73.9	14	2	O99902	O99902	homo sapien
874	17	73.9	13	1	MLA_HORSE	P61280	equus cabal	947	17	73.9	14	2	O86VF8	O86vf8	homo sapien
875	17	73.9	13	1	NO40_PEA	P55959	pisum sativ	948	17	73.9	14	2	O9BRY8	O9bry8	homo sapien
876	17	73.9	13	1	NO40_VICSA	P55961	vicia sativ	949	17	73.9	14	2	Q7RIM6	Q7rim6	plasmodium
877	17	73.9	13	1	TEML_RANTE	P57104	rana tempor	950	17	73.9	14	2	Q71M98	Q71m98	sus scrofa
878	17	73.9	13	1	TY13_PHYRO	P04096	phyllomedus	951	17	73.9	14	2	O863R0	O863r0	procyon lot
879	17	73.9	13	2	O16392	O10721	pseudallesc	952	17	73.9	14	2	O863R1	O863r1	basariscus
880	17	73.9	13	2	O16392	O16392	homo sapien	953	17	73.9	14	2	O863R2	O863r2	melogale mo
881	17	73.9	13	2	O16406	Q16406	homo sapien	954	17	73.9	14	2	O863R3	O863r3	arctonyx co
882	17	73.9	13	2	O6LAU9	O6lau9	homo sapien	955	17	73.9	14	2	O863R4	O863r4	taxidea tax
883	17	73.9	13	2	O6S860	O6se60	drosophila	956	17	73.9	14	2	O863R5	O863r5	meles meles
884	17	73.9	13	2	Q9U5J2	O9u5j2	trypanosoma	957	17	73.9	14	2	O863R6	O863r6	ictonyx str
885	17	73.9	13	2	O18890	O18890	ateles belz	958	17	73.9	14	2	O863R7	O863r7	galictia vi
886	17	73.9	13	2	O8WNS4	O8wns4	bos taurus	959	17	73.9	14	2	O863R8	O863r8	eira barbar
887	17	73.9	13	2	O99188	O99188	capivulus cau	960	17	73.9	14	2	O863R9	O863r9	gulo gulo (
888	17	73.9	13	2	O99783	O99783	caprimulgus	961	17	73.9	14	2	O863S0	O863s0	martes penn
889	17	73.9	13	2	P92460	P92460	taxus bacca	962	17	73.9	14	2	O863S1	O863s1	martes amer
890	17	73.9	13	2	O95808	O95808	gracilariop	963	17	73.9	14	2	O863S2	O863s2	mustela vis
891	17	73.9	13	2	O95925	O95925	porphyra pu	964	17	73.9	14	2	O863S3	O863s3	mustela fre
892	17	73.9	13	2	Q36622	Q36622	picea abies	965	17	73.9	14	2	O863S4	O863s4	mustela erm
893	17	73.9	13	2	Q85LH3	Q85lh3	plectura m	966	17	73.9	14	2	O863S5	O863s5	pteronura b
894	17	73.9	13	2	O9MQK3	O9mqk3	capra ibex	967	17	73.9	14	2	O863S6	O863s6	lutra macul
895	17	73.9	13	2	O8LFPV3	O8lpv3	deschampsia	968	17	73.9	14	2	O863S7	O863s7	lutra lutra
896	17	73.9	13	2	O6URV3	O6urv3	sorghum bic	969	17	73.9	14	2	O863S8	O863s8	lontra long
897	17	73.9	13	2	Q71N39	Q71n39	trifolium x	970	17	73.9	14	2	O863S9	O863s9	lontra fell
898	17	73.9	13	2	O8KHM6	O8khm6	streptococc	971	17	73.9	14	2	O863T0	O863t0	lontra cana
899	17	73.9	13	2	O8KRA4	O8kra4	streptococc	972	17	73.9	14	2	O863T1	O863t1	enhydra lut
900	17	73.9	13	2	O52920	O52920	rhizobium m	973	17	73.9	14	2	O863T2	O863t2	amblonyx ci
901	17	73.9	13	2	O53300	O53300	escherichia	974	17	73.9	14	2	O863T3	O863t3	aonyx capen
902	17	73.9	13	2	O6LAA7	O6laa7	shigella fl	975	17	73.9	14	2	O9TR83	O9tr83	sus scrofa
903	17	73.9	13	2	Q7M0L4	Q7m0l4	bacillus ce	976	17	73.9	14	2	Q617N3	Q617n3	haemaphysal
904	17	73.9	13	2	Q9L8K1	Q9l8k1	enterococcu	977	17	73.9	14	2	Q71H36	Q71h36	strongyloce
905	17	73.9	13	2	Q9R3R3	Q9r3r3	borrelia bu	978	17	73.9	14	2	O85C99	O85c99	strongyloce
906	17	73.9	13	2	Q9WW71	Q9ww71	enterococcu	979	17	73.9	14	2	O85CA0	O85ca0	strongyloce
907	17	73.9	13	2	Q9WW72	Q9ww72	enterococcu	980	17	73.9	14	2	O85CA1	O85ca1	strongyloce

881 17 73.9 14 2 Q85CA2
 882 17 73.9 14 2 Q85I00
 883 17 73.9 14 2 Q85I03
 884 17 73.9 14 2 Q85I10
 885 17 73.9 14 2 Q85I14
 886 17 73.9 14 2 Q85I17
 887 17 73.9 14 2 Q85I20
 888 17 73.9 14 2 Q85I26
 889 17 73.9 14 2 Q8HGT1
 890 17 73.9 14 2 Q9WJQ3
 891 17 73.9 14 2 Q9TEN1
 892 17 73.9 14 2 Q9TEN3
 893 17 73.9 14 2 Q94IT6
 894 17 73.9 14 2 Q7MIG6
 895 17 73.9 14 2 Q7MIG7
 896 17 73.9 14 2 Q7M261
 897 17 73.9 14 2 Q9SAP8
 898 17 73.9 14 2 Q6LDN2
 899 17 73.9 14 2 Q9R5I8
 1000 17 73.9 14 2 Q88400

ALIGNMENTS

RESULT 1
 ID Q28121 PRELIMINARY; PRT; 9 AA.
 AC Q28121;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Growth hormone receptor (Fragment).
 GN Name=GHR;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96043217; PubMed=7486254;
 RA Moody D.E., Pomp D., Barendse W., Womack J.E.;
 RT "Assignment of the growth hormone receptor gene to bovine chromosome
 RT 20 using linkage analysis and somatic cell mapping.";
 RL Anim. Genet. 26:341-343(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91146804; PubMed=2289631; DOI=10.1016/0303-7207(90)90143-V;
 RA Hauser S.D., McGrath M.F., Collier R.J., Krivi G.G.;
 RT "Cloning and in vivo expression of bovine growth hormone receptor
 RT mRNA.";
 RL Mol. Cell. Endocrinol. 72:187-200(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Moody D.M., Pomp D.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U24113; AAA91014.1; -.
 DR FIR; I46023; I46023.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1182 MW; D11E42C9D36769D6 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 9;
 Best Local Similarity 25.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXXWXXX 8
 |:::|:::
 Db 1 FQFPWFVI 8

RESULT 2
 ID Q8WGE6 PRELIMINARY; PRT; 9 AA.
 AC Q8WGE6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase subunit 1 (Fragment).
 OS Procamburus clarkii (Red swamp crayfish).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidea; Cambaridae; Procamburus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
 RA Cunningham C.W.;
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of
 RT the crab-like form.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).
 DR EMBL; AF436024; AAL31599.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1185 MW; 936BB9C733640321 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 9;
 Best Local Similarity 25.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXWXXX 8
 |:::|:::
 Db 1 FTKRWLFS 8

RESULT 3
 ID Q70F01 PRELIMINARY; PRT; 10 AA.
 AC Q70F01;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Calpastatin type 2 (Fragment).
 GN Name=CAST;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21531263; PubMed=11673859; DOI=10.1006/abbi.2001.2546;
 RA Parr T., Sensky P.L., Bardsley R.G., Buttery P.J.;
 RT "Calpastatin expression in porcine cardiac and skeletal muscle and
 RT partial gene structure.";
 RL Arch. Biochem. Biophys. 395:1-13(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Parr T.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ583410; CAEA7431.1; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXXWXXX 8
 |:::|:::
 Db 1 FQFPWFVI 8

Db 3 FASWYKT 10

RESULT 4

O79885 PRELIMINARY; PRT; 10 AA.
 AC O79885 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 GN Anolis paternus.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OC NCBI_TaxID=52189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT Mitochondrial genome among iguanian lizards."
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82679; AAC62284.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8

Db 2 FINRWFFS 9

RESULT 5

O79897 PRELIMINARY; PRT; 10 AA.
 AC O79897 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 GN Hoplocercus spinosus (Club-tail iguana).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
 OC Hoplocercus.
 OC NCBI_TaxID=52193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT Mitochondrial genome among iguanian lizards."
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82683; AAC62284.1; -.
 DR PIR; T17063; T17063.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8

Db 2 FISRWLFS 9

RESULT 6

O79903 PRELIMINARY; PRT; 10 AA.
 AC O79903 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 GN Oplurus cuvieri (Madagascan collared iguanid lizard).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Oplurinae; Oplurus.
 OC NCBI_TaxID=44151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT Mitochondrial genome among iguanian lizards."
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82685; AAC62293.1; -.
 DR PIR; T17066; T17066.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8

Db 2 FINRWFFS 9

RESULT 7

O79906 PRELIMINARY; PRT; 10 AA.
 AC O79906 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 GN Phrynosoma douglassii.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
 OC Phrynosoma.
 OC NCBI_TaxID=43611;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT Mitochondrial genome among iguanian lizards."
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82686; AAC62299.1; -.
 DR PIR; T17069; T17069.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FXXXWXXX 8
Db 2 FINRWFFS 9

RESULT 8
P92707 ID P92707 PRELIMINARY; PRT; 10 AA.
AC P92707;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Platyseurus capensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
OC Cordylidae; Platyseurus.
OX NCBI_TaxID=52175;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RT rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL; U71329; AAB48286.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1322 MW; 0A3480C9D36415B0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FISRWFFS 9

RESULT 9
Q8W704 ID Q8W704 PRELIMINARY; PRT; 10 AA.
AC Q8W704;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COI;
OS Anolis nitens.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174262;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337800; AAL72083.1; -.
DR EMBL; AF337801; AAL72085.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
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SQ SEQUENCE 10 AA; 1349 MW; C9348E29D3640449 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FPNRWFFS 9

RESULT 10
Q8W8Q2 ID Q8W8Q2 PRELIMINARY; PRT; 10 AA.
AC Q8W8Q2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit 1 (Cytochrome c oxidase subunit I)
DE (Fragment).
GN Name=COI; Synonym=COI;
OS Anolis punctatus (Amazon green anole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174263;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of iguanian
RT lizards.";
RL Herpetologica 59:399-419(2003).
RN [3]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337775; AAL72033.1; -.
DR EMBL; AF337776; AAL72035.1; -.
DR EMBL; AF337777; AAL72037.1; -.
DR EMBL; AF28726; AAQ09140.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FLNRWFFS 9

RESULT 11
Q8W8Q3 ID Q8W8Q3 PRELIMINARY; PRT; 10 AA.
AC Q8W8Q3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COI;
OS Anolis nitens.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174262;
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[1]
RN SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337793; AAL72069.1; -
DR EMBL; AF337794; AAL72071.1; -
DR EMBL; AF337795; AAL72073.1; -
DR EMBL; AF337796; AAL72075.1; -
DR EMBL; AF337797; AAL72077.1; -
DR EMBL; AF337798; AAL72079.1; -
DR EMBL; AF337799; AAL72081.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db |:::|:::
2 FLNRWFFS 9

RESULT 12
Q8W8Q4 PRELIMINARY; PRT; 10 AA.
AC Q8W8Q4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Names=COL;
OS Anolis punctatus (Amazon green anole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174263;
[1]
RN SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337771; AAL72025.1; -
DR EMBL; AF337772; AAL72027.1; -
DR EMBL; AF337773; AAL72029.1; -
DR EMBL; AF337774; AAL72031.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1315 MW; 4B3480C733640447 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db |:::|:::
2 FLNRWFLFS 9

RESULT 13
Q8W969 PRELIMINARY; PRT; 10 AA.
AC Q8W969;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment) (Fragment).
GN Names=COL;
OS Anolis orthonii (Bark anole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=44141;
[1]
RN SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337793; AAL72069.1; -
DR EMBL; AF337794; AAL72071.1; -
DR EMBL; AF337795; AAL72073.1; -
DR EMBL; AF337796; AAL72075.1; -
DR EMBL; AF337797; AAL72077.1; -
DR EMBL; AF337798; AAL72079.1; -
DR EMBL; AF337799; AAL72081.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db |:::|:::
2 FINRWFFS 9

RESULT 14
Q8W970 PRELIMINARY; PRT; 10 AA.
AC Q8W970;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment) (Fragment).
GN Names=COL;
OS Anolis nitens.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174262;
[1]
RN SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337805; AAL72093.1; -
DR EMBL; AF337806; AAL72095.1; -
DR EMBL; AF337807; AAL72097.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db |:::|:::
2 FINRWFFS 9

RESULT 15
Q8W971 PRELIMINARY; PRT; 10 AA.
AC Q8W971;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment) (Fragment).
GN Names=COL;
OS Anolis fuscoauratus (Slender anole).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=43584;
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[1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337786; AAL72055.1; -.
DR EMBL; AF337787; AAL72056.1; -.
DR EMBL; AF337788; AAL72057.1; -.
DR EMBL; AF337789; AAL72058.1; -.
DR EMBL; AF337790; AAL72059.1; -.
DR EMBL; AF337791; AAL72060.1; -.
DR EMBL; AF337792; AAL72061.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FINRWFFS 9

RESULT 16
Q8WDG6 PRELIMINARY; PRT; 10 AA.
AC Q8WDG6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COL;
OS Anolis trachyderma.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=141901;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337785; AAL72053.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FINRWFFS 9

RESULT 17
Q8WDH0 PRELIMINARY; PRT; 10 AA.
AC Q8WDH0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COL;
OS Anolis limifrons.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=38897;
RN [1]
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RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337783; AAL72049.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1315 MW; 0A3480C733640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FINRWLFS 9

RESULT 18
Q8WDH2 PRELIMINARY; PRT; 10 AA.
AC Q8WDH2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COL;
OS Anolis lemurinus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=141898;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337782; AAL72047.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 2 FINRWFFS 9

RESULT 19
Q8WDH4 PRELIMINARY; PRT; 10 AA.
AC Q8WDH4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COL;
OS Anolis carpenteri.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=141894;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337781; AAL72045.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
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SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8
|::|::|
Db 2 FINRWFFS 9

RESULT 20
Q8WDH6 PRELIMINARY; PRT; 10 AA.
AC Q8WDH6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COI;
OS Anolis transversalis (Banded tree anole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174261;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337780; AAL72043.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1315 MW; 0A3480C733640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8
|::|::|
Db 2 FINRWLFS 9

RESULT 21
Q8WDH8 PRELIMINARY; PRT; 10 AA.
AC Q8WDH8;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COI;
OS Anolis mestrei.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174261;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337779; AAL72041.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8
|::|::|
Db 2 FISRWLFS 9

RESULT 22
Q8WDI8 PRELIMINARY; PRT; 10 AA.
AC Q8WDI8;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN Name=COI;
OS Anolis transversalis (Banded tree anole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174264;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337769; AAL72021.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8
|::|::|
Db 2 FLNRWFFS 9

RESULT 23
Q6UJL5 PRELIMINARY; PRT; 10 AA.
AC Q6UJL5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Strophurus pulcher.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Strophurus.
OX NCBI_TaxID=255186;
RN [1]
RP SEQUENCE FROM N.A.
RA Melville J., Schulte J.A. II, Larson A.;
RT "A Molecular Study of Phylogenetic Relationships and Evolution of
RT Antipredator Strategies in Australian Diplodactylus Geckos, Subgenus
RT Strophurus.";
RT Biol. J. Linn. Soc. Lond. 82:123-138 (2004).
DR EMBL; AY369011; AAR18865.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C733641580 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8
|::|::|
Db 2 FISRWLFS 9
```

RESULT 24

Q6WB7 PRELIMINARY; PRT; 10 AA.
AC Q6WB7; 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COL;
OS Sceloporus woodi (Florida scrub lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297513; AAP84510.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:::|:::
Db 2 FINRWFFS 9

RESULT 25

Q6WB1 PRELIMINARY; PRT; 10 AA.
AC Q6WB1; 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COL;
OS Sceloporus teapensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=235404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297505; AAP84486.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:::|:::
Db 2 FINRWFFS 9

RESULT 26

Q6WB7 PRELIMINARY; PRT; 10 AA.
AC Q6WB7; 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COL;
OS Sceloporus woodi (Florida scrub lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297513; AAP84510.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:::|:::
Db 2 FINRWFFS 9

RESULT 27

Q6WB4 PRELIMINARY; PRT; 10 AA.
AC Q6WB4; 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COL;
OS Sceloporus jalapae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=57316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297504; AAP84483.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1315 MW; 0A3480C733640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:::|:::
Db 2 FINRWFFS 9

RESULT 27

Q6WB3 PRELIMINARY; PRT; 10 AA.
AC Q6WB3; 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COL;
OS Sceloporus maculosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297501; AAP84474.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:::|:::
Db 2 FINRWFFS 9

RESULT 28

Q6WB3 PRELIMINARY; PRT; 10 AA.
AC Q6WB3; 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COL;
OS Sceloporus maculosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297501; AAP84474.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:::|:::
Db 2 FINRWFFS 9

ID	Q6WBTS	PRELIMINARY;	PRT;	10 AA.
AC	Q6WBTS;			
DT	05-JUL-2004 (TReMBLrel. 27, Created)			
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE	Cytochrome oxidase subunit I (Fragment).			
GN	Name=COI;			
OS	Sceloporus carinatus.			
OG	Mitochondrion.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;			
OC	Sceloporus.			
OX	NCBI_TaxID=110853;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=42801591; PubMed=12920297; DOI=10.1126/science.1084786;			
RA	Harmon L.J., Schulte J.A., Larson A., Losos J.B.;			
RA	"Tempo and mode of evolutionary radiation in iguanian lizards.";			
RL	Science 301:961-964(2003).			
DR	EMBL; AY297495; AAP84459.1; -.			
DR	GO; GO:0005739; C:mitochondrion; IEA.			
KW	Mitochondrion.			
FT	NON TER 10 10			
SQ	SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;			
Query Match 100.0%; Score 23; DB 2; Length 10;				
Best Local Similarity 25.0%; Pred. No. 5.4e+03;				
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 FXXWXXX 8			
	:: :: ::			
Db	2 FINRWFFS 9			
RESULT 29				
Q6WBUI				
ID	Q6WBUI	PRELIMINARY;	PRT;	10 AA.
AC	Q6WBUI;			
DT	05-JUL-2004 (TReMBLrel. 27, Created)			
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE	Cytochrome oxidase subunit I (Fragment).			
GN	Name=COI;			
OS	Sceloporus squamosus.			
OG	Mitochondrion.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;			
OC	Sceloporus.			
OX	NCBI_TaxID=110857;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=42801591; PubMed=12920297; DOI=10.1126/science.1084786;			
RA	Harmon L.J., Schulte J.A., Larson A., Losos J.B.;			
RA	"Tempo and mode of evolutionary radiation in iguanian lizards.";			
RL	Science 301:961-964(2003).			
DR	EMBL; AY297495; AAP84456.1; -.			
DR	GO; GO:0005739; C:mitochondrion; IEA.			
KW	Mitochondrion.			
FT	NON TER 10 10			
SQ	SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;			
Query Match 100.0%; Score 23; DB 2; Length 10;				
Best Local Similarity 25.0%; Pred. No. 5.4e+03;				
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 FXXWXXX 8			
	:: :: ::			
Db	2 FINRWFFS 9			
RESULT 30				
Q6WBUI				
ID	Q6WBUI	PRELIMINARY;	PRT;	10 AA.

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DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (fragment).
GN Name=COI;
OS Phrynosoma cornutum (Texas horned lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=43610;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297487; AAP84432.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db |::|::|
2 FINRWFFS 9

RESULT 33
Q6WBW8 PRELIMINARY; PRT; 10 AA.
AC Q6WBW8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (fragment).
GN Name=COI;
OS Phrynosoma mcallii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=159094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297486; AAP84429.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db |::|::|
2 FINRWFFS 9

RESULT 34
Q6WBX1 PRELIMINARY; PRT; 10 AA.
AC Q6WBX1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)

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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (fragment).
GN Name=COI;
OS Phrynosoma coronatum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=159093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297485; AAP84426.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db |::|::|
2 FINRWFFS 9

RESULT 35
Q6WBX4 PRELIMINARY; PRT; 10 AA.
AC Q6WBX4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (fragment).
GN Name=COI;
OS Phrynosoma modestum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=43612;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297484; AAP84423.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db |::|::|
2 FINRWFFS 9

RESULT 36
Q6WZN6 PRELIMINARY; PRT; 10 AA.
AC Q6WZN6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 GN Name=COL;
 OS Anolis cybotes (large-headed anole).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=38891;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22990428; PubMed=14628926;
 RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
 RT "Phylogenetic analysis of ecological and morphological diversification
 in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
 RL Evolution 57:2383-2397(2003).
 DR EMBL; AY2631139; AAP94564.1; -.
 DR EMBL; AY2631140; AAP94567.1; -.
 DR EMBL; AY2631144; AAP94579.1; -.
 DR EMBL; AY2631138; AAP94561.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1367 MW; BE3480C9D3640446 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

.QY 1 FXXXWXXX 8
 |:::|:::
 Db 2 FNNRWFFS 9

RESULT 37
 Q6X061
 ID Q6X061 PRELIMINARY; PRT; 10 AA.
 AC Q6X061;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 GN Name=COL;
 GN Anolis haetianus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=237983;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22990428; PubMed=14628926;
 RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
 RT "Phylogenetic analysis of ecological and morphological diversification
 in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
 RL Evolution 57:2383-2397(2003).
 DR EMBL; AY263042; AAP94389.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1288 MW; 0A349CB9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

.QY 1 FXXXWXXX 8
 |:::|:::
 Db 2 FNNRWFFS 9

RESULT 38
 Q6X071
 ID Q6X071 PRELIMINARY; PRT; 10 AA.
 AC Q6X071;

DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment) (Fragment).
 GN Name=COL;
 GN Anolis shrevei.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=237982;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22990428; PubMed=14628926;
 RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
 RT "Phylogenetic analysis of ecological and morphological diversification
 in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
 RL Evolution 57:2383-2397(2003).
 DR EMBL; AY263036; AAP94377.1; -.
 DR EMBL; AY263037; AAP94380.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

.QY 1 FXXXWXXX 8
 |:::|:::
 Db 2 FNNRWFFS 9

RESULT 39
 Q6X0C3
 ID Q6X0C3 PRELIMINARY; PRT; 10 AA.
 AC Q6X0C3;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment) (Fragment).
 GN Name=COL;
 GN Anolis whitemani.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=237981;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22990428; PubMed=14628926;
 RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
 RT "Phylogenetic analysis of ecological and morphological diversification
 in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
 RL Evolution 57:2383-2397(2003).
 DR EMBL; AY263016; AAP94325.1; -.
 DR EMBL; AY263017; AAP94328.1; -.
 DR EMBL; AY263018; AAP94331.1; -.
 DR EMBL; AY263019; AAP94334.1; -.
 DR EMBL; AY263020; AAP94337.1; -.
 DR EMBL; AY263021; AAP94340.1; -.
 DR EMBL; AY263022; AAP94343.1; -.
 DR EMBL; AY263023; AAP94346.1; -.
 DR EMBL; AY263024; AAP94349.1; -.
 DR EMBL; AY263025; AAP94352.1; -.
 DR EMBL; AY263026; AAP94355.1; -.
 DR EMBL; AY263027; AAP94358.1; -.
 DR EMBL; AY263028; AAP94361.1; -.
 DR EMBL; AY263029; AAP94364.1; -.
 DR EMBL; AY263030; AAP94367.1; -.
 DR EMBL; AY263031; AAP94370.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10

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SQ SEQUENCE 10 AA; 1349 MW; 0A3480CD3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db |::|:::
2 FINRWFFS 9

RESULT 40
Q6X0D2
ID Q6X0D2 PRELIMINARY; PRT; 10 AA.
AC Q6X0D2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment) (Fragment).
GN Name=COI;
OS Anolis armouri.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=237980;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990428; PubMed=14628926;
RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
RT "Phylogenetic analysis of ecological and morphological diversification
RT in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
RL Evolution 57:2383-2397(2003).
DR EMBL; AY263011; AAP94316.1; -.
DR EMBL; AY263012; AAP94319.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480CD3640440 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. NO. 5.4e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db |::|:::
2 FINRWFFS 9
```

Search completed: October 19, 2005, 15:45:20
Job time : 105.941 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:26:26 ; Search time 123.353 Seconds
(without alignments)
28.219 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXWXXX 9

Scoring table: BLOSUM62DX!
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	9	2	Aaw37216 Human onc
2	24	100.0	9	2	Aaw37175 Human onc
3	24	100.0	9	2	Aaw37212 Human onc
4	24	100.0	9	2	Aaw37179 Human onc
5	24	100.0	9	2	Aaw37213 Human onc
6	24	100.0	9	2	Aay25555 Human MHC
7	24	100.0	9	2	Aay55520 HLA bindi
8	24	100.0	9	4	Aau24137 Human MHC
9	24	100.0	9	4	Abp15780 HIV A24 s
10	24	100.0	9	4	Abp20958 HIV A03 m
11	24	100.0	9	4	Abp22220 HIV A03 m
12	24	100.0	9	4	Abp23020 HIV A11 m
13	24	100.0	9	4	Abp23978 HIV A11 m
14	24	100.0	9	4	Aam12502 HLA-B8 no
15	24	100.0	9	4	Aam08958 HLA-A *02
16	24	100.0	9	4	Aam08879 HLA-B *07
17	24	100.0	9	4	Aam07847 HLA-A1 no
18	24	100.0	9	4	Aam08894 HLA-B *27
19	24	100.0	9	4	Aam11670 HLA-A26 n
20	24	100.0	9	4	Aam12223 HLA-B *15
21	24	100.0	9	5	Aau80741 Javelin p
22	24	100.0	9	5	Abg35129 Pancreat
23	24	100.0	9	5	Abj04579 Bone marr
24	24	100.0	9	5	Abj06626 Hepatitis
25	24	100.0	9	5	Abj08649 Hepatitis

26	24	100.0	9	5	ABG60517	Abg60517 Selective
27	24	100.0	9	5	AAE31317	Aae31317 Human p53
28	24	100.0	9	5	AAE31347	Aae31347 Human spl
29	24	100.0	9	5	AAE31160	Aae31160 Human spl
30	24	100.0	9	6	ABR56915	Abri56915 Pancreat
31	24	100.0	9	6	ABRI4212	Abri4212 Human can
32	24	100.0	9	6	ABRI3428	Abri3428 Human can
33	24	100.0	9	6	ABRI4464	Abri4464 Human can
34	24	100.0	9	6	ABRI3820	Abri3820 Human can
35	24	100.0	9	6	ABRI4018	Abri4018 Human can
36	24	100.0	9	6	ABRI3445	Abri3445 Human can
37	24	100.0	9	6	ABRI3966	Abri3966 Human can
38	24	100.0	9	6	ABRO4164	Abro4164 Human can
39	24	100.0	9	6	ABRI3839	Abri3839 Human can
40	24	100.0	9	6	ABJ63399	Abj63399 184P1E2-r
41	24	100.0	9	6	ABJ62064	Abj62064 184P1E2-r
42	24	100.0	9	6	ABJ60738	Abj60738 184P1E2-r
43	24	100.0	9	6	ABJ59945	Abj59945 184P1E2-r
44	24	100.0	9	6	ABJ61514	Abj61514 184P1E2-r
45	24	100.0	9	6	ABJ62639	Abj62639 184P1E2-r
46	24	100.0	9	6	ABJ63337	Abj63337 184P1E2-r
47	24	100.0	9	6	ABJ60822	Abj60822 184P1E2-r
48	24	100.0	9	6	ABJ65025	Abj65025 184P1E2-r
49	24	100.0	9	7	ADD26353	Add26353 Staphyloc
50	24	100.0	9	7	ADD56984	Add56984 HLA bindi
51	24	100.0	9	7	ADD57480	Add57480 HLA bindi
52	24	100.0	9	7	ADD57830	Add57830 HLA bindi
53	24	100.0	9	7	ADD56982	Add56982 HLA bindi
54	24	100.0	9	7	ADSE68739	Adse68739 Human 161
55	24	100.0	9	7	ADSE68096	Adse68096 Human 161
56	24	100.0	9	7	ADSE66983	Adse66983 Human 161
57	24	100.0	9	7	ADSE39751	Adse39751 Peptide p
58	24	100.0	9	8	ADI00690	Adi00690 Human rin
59	24	100.0	9	8	ADK39160	Adk39160 Hepatitis
60	24	100.0	9	8	ADK37906	Adk37906 Hepatitis
61	24	100.0	9	8	ADK03265	Adk03265 Hepatitis
62	24	100.0	9	8	ADK09130	Adk09130 Human pap
63	24	100.0	9	8	ADK09595	Adk09595 Human pap
64	24	100.0	9	8	ADN67919	Adn67919 Human 273
65	24	100.0	9	8	ADN65877	Adn65877 HLA bindi
66	24	100.0	9	8	ADQ69664	Adq69664 Cancer re
67	24	100.0	9	8	ADQ72479	Adq72479 Cancer re
68	24	100.0	9	8	ADQ12754	Adq12754 Hepatitis
69	24	100.0	9	8	ADQ12823	Adq12823 Hepatitis
70	24	100.0	9	8	ADQ28798	Adq28798 Human cel
71	24	100.0	9	8	ADP80098	Adp80098 Human HLA
72	24	100.0	10	1	AAP10179	Aap10179 Sequence
73	24	100.0	10	1	AAP10175	Aap10175 Sequence
74	24	100.0	10	1	AAP10175	Aap10175 Sequence
75	24	100.0	10	1	AAP10533	Aap10533 1.6 subet
76	24	100.0	10	1	AAP10532	Aap10532 1.6 subet
77	24	100.0	10	1	AAP10261	Aap10261 Peptide a
78	24	100.0	10	1	AAP10168	Aap10168 Sequence
79	24	100.0	10	1	AAP10166	Aap10166 Sequence
80	24	100.0	10	1	AAP10169	Aap10169 Sequence
81	24	100.0	10	1	AAP30545	Aap30545 Sequence
82	24	100.0	10	1	AAP30525	Aap30525 Sequence
83	24	100.0	10	1	AAP40331	Aap40331 Sequence
84	24	100.0	10	1	AAP40332	Aap40332 Sequence
85	24	100.0	10	1	AAP50790	Aap50790 Sequence
86	24	100.0	10	1	AAP50792	Aap50792 Sequence
87	24	100.0	10	1	AAP50477	Aap50477 Luliberin
88	24	100.0	10	1	AAP70926	Aap70926 Luteinisi
89	24	100.0	10	1	AAP71235	Aap71235 Luteinisi
90	24	100.0	10	1	AAP82754	Aap82754 Example o
91	24	100.0	10	2	AAR14235	Aar14235 Somatosta
92	24	100.0	10	2	AAR77426	Aar77426 Gonadotro
93	24	100.0	10	2	AAR97318	Aar97318 Humanised
94	24	100.0	10	2	AAW03315	Aaw03315 Tyrosinas
95	24	100.0	10	2	AAW25684	Aaw25684 Antinicro
96	24	100.0	10	2	AAW37226	Aaw37226 MDM2 bind
97	24	100.0	10	2	AAW37169	Aaw37169 Human onc
98	24	100.0	10	2		

99	24	100.0	10	2	AAW96797	Aaw96797 Lamprey I	172	24	100.0	10	6	ABR13072	Human can
100	24	100.0	10	2	AAW96796	Aaw96796 Lamprey I	173	24	100.0	10	6	ABR13469	Human can
101	24	100.0	10	2	AAW96798	Aaw96798 Lamprey I	174	24	100.0	10	6	ABR59148	Alzheimer
102	24	100.0	10	2	AAW72987	Aaw72987 Bovine be	175	24	100.0	10	6	ABR47241	Staphyloc
103	24	100.0	10	2	AAW46796	Aay46796 Immunogen	176	24	100.0	10	6	ABJ57466	184PIE2-r
104	24	100.0	10	2	AAV25554	Aay25554 Human MHC	177	24	100.0	10	6	ABJ66221	184PIE2-r
105	24	100.0	10	2	AAV40648	Aay40648 S2 deriva	178	24	100.0	10	6	ABJ69492	184PIE2-r
106	24	100.0	10	3	AAW85376	Aay85376 II-2 deri	179	24	100.0	10	6	ABJ66633	184PIE2-r
107	24	100.0	10	3	AAW93384	Aay93384 Binding m	180	24	100.0	10	6	ABJ68555	184PIE2-r
108	24	100.0	10	3	AAW17086	Aab17086 Mdm/hdm a	181	24	100.0	10	6	ABJ58245	184PIE2-r
109	24	100.0	10	3	AAW02722	Aab02722 Human thr	182	24	100.0	10	6	ABJ68357	184PIE2-r
110	24	100.0	10	3	AAW29987	Aab29987 Scaffold	183	24	100.0	10	6	ABJ58624	184PIE2-r
111	24	100.0	10	4	ABW55959	Abb55959 Vascular	184	24	100.0	10	6	ABJ57961	184PIE2-r
112	24	100.0	10	4	AAW68078	Aag68078 Anticmou	185	24	100.0	10	6	ABJ57757	184PIE2-r
113	24	100.0	10	4	AAW90971	Aag90971 Luteinib1	186	24	100.0	10	6	ABJ67679	184PIE2-r
114	24	100.0	10	4	AAW94594	Aag94594 Human com	187	24	100.0	10	6	ABJ69385	184PIE2-r
115	24	100.0	10	4	AAW94596	Aag94596 Human com	188	24	100.0	10	6	ABJ67907	184PIE2-r
116	24	100.0	10	4	AAW233907	Aau233907 Human MHC	189	24	100.0	10	6	ABJ66586	184PIE2-r
117	24	100.0	10	4	AAW24211	Aau24211 Human MHC	190	24	100.0	10	6	ABJ67609	184PIE2-r
118	24	100.0	10	4	ABP16563	Abp16563 HIV A24 s	191	24	100.0	10	6	ABJ58400	184PIE2-r
119	24	100.0	10	4	ABP23023	Abp23023 HIV A11 m	192	24	100.0	10	6	ABJ68082	184PIE2-r
120	24	100.0	10	4	ABP24000	Abp24000 HIV A11 m	193	24	100.0	10	6	AAO31089	Human D5-
121	24	100.0	10	4	ABP20961	Abp20961 HIV A03 m	194	24	100.0	10	7	ABD79048	Human ant
122	24	100.0	10	4	ABP16564	Abp16564 HIV A24 s	195	24	100.0	10	7	ADD57477	HLA bindi
123	24	100.0	10	4	AAW10630	Aam10630 HLA-A *02	196	24	100.0	10	7	ADD57022	HLA bindi
124	24	100.0	10	4	AAW13130	Aam13130 HLA-A26 d	197	24	100.0	10	7	ADD57478	HLA bindi
125	24	100.0	10	4	AAW12977	Aam12977 HLA-A26 d	198	24	100.0	10	7	ADD57828	HLA bindi
126	24	100.0	10	4	AAW09968	Aam09968 HLA-A1 de	199	24	100.0	10	7	ADD57021	HLA bindi
127	24	100.0	10	4	AAW10289	Aam10289 HLA-A *02	200	24	100.0	10	7	ADD57020	HLA bindi
128	24	100.0	10	4	AAW10317	Aam10317 HLA-A1 de	201	24	100.0	10	7	ADD57827	HLA bindi
129	24	100.0	10	4	AAW10910	Aam10910 HLA-B *07	202	24	100.0	10	7	ADD24677	Lamprey 1
130	24	100.0	10	4	AAW10703	Aam10703 HLA-B *07	203	24	100.0	10	7	ADD24676	Lamprey 1
131	24	100.0	10	4	ABW52377	Abb52377 Human API	204	24	100.0	10	7	ADE10722	Structura
132	24	100.0	10	5	ABW06172	Abb06172 Gonadotro	205	24	100.0	10	7	ADE69879	Human 161
133	24	100.0	10	5	ABW73181	Abb73181 Mdm/hdm a	206	24	100.0	10	7	ADE69670	Human 161
134	24	100.0	10	5	ABJ15205	Abj15205 Immunogen	207	24	100.0	10	7	ADD94632	Human SIM
135	24	100.0	10	5	ABJ13671	Abj13671 Human 125	208	24	100.0	10	7	ADJ73335	Mdm/hdm a
136	24	100.0	10	5	ABJ14074	Abj14074 Human 125	209	24	100.0	10	8	ADJ78885	Human p53
137	24	100.0	10	5	ABJ13684	Abj13684 Human 125	210	24	100.0	10	8	ADH09996	Backbone
138	24	100.0	10	5	ABJ11969	Abj11969 Human 125	211	24	100.0	10	8	ADH09997	Backbone
139	24	100.0	10	5	ABJ13896	Abj13896 Human 125	212	24	100.0	10	8	ADH09999	Backbone
140	24	100.0	10	5	ABJ06759	Abj06759 Hepatitis	213	24	100.0	10	8	ADH09995	Backbone
141	24	100.0	10	5	ABJ06227	Abj06227 Hepatitis	214	24	100.0	10	8	ADG94702	Human JAM
142	24	100.0	10	5	ABJ07697	Abj07697 Hepatitis	215	24	100.0	10	8	ADJ24649	HIV-1 HLA
143	24	100.0	10	5	AAW93233	Aau93233 Granulocy	216	24	100.0	10	8	ADJ52969	CHI delet
144	24	100.0	10	5	AAE15696	Aae15696 Lamprey 1	217	24	100.0	10	8	ADJ51930	CHI delet
145	24	100.0	10	5	AAE15695	Aae15695 Lamprey 1	218	24	100.0	10	8	ADK15741	Fusion pr
146	24	100.0	10	5	ABJ15736	Abj15736 Zinc tran	219	24	100.0	10	8	ADK147088	Perneabil
147	24	100.0	10	5	ABJ17019	Abj17019 Zinc tran	220	24	100.0	10	8	ADK38039	Hepatitis
148	24	100.0	10	5	ABJ15542	Abj15542 Zinc tran	221	24	100.0	10	8	ADK38786	Hepatitis
149	24	100.0	10	6	ABR13871	Abri13871 Human can	222	24	100.0	10	8	ADK37528	Hepatitis
150	24	100.0	10	6	ABR14555	Abri14555 Human can	223	24	100.0	10	8	ADK03263	Hepatitis
151	24	100.0	10	6	ABR25335	Abri25335 Human can	224	24	100.0	10	8	ADK03268	Hepatitis
152	24	100.0	10	6	ABR13738	Abri13738 Human can	225	24	100.0	10	8	ADK09671	Human pap
153	24	100.0	10	6	ABR14071	Abri14071 Human can	226	24	100.0	10	8	ADK09188	Human pap
154	24	100.0	10	6	ABR04038	Abri04038 Human can	227	24	100.0	10	8	ADL21133	125P5C8 p
155	24	100.0	10	6	ABR13704	Abri13704 Human can	228	24	100.0	10	8	ADL20921	125P5C8 p
156	24	100.0	10	6	ABR14279	Abri14279 Human can	229	24	100.0	10	8	ADL19213	125P5C8 p
157	24	100.0	10	6	ABR13318	Abri13318 Human can	230	24	100.0	10	8	ADL21311	125P5C8 p
158	24	100.0	10	6	ABR03638	Abri03638 Human can	231	24	100.0	10	8	ADL20908	125P5C8 p
159	24	100.0	10	6	ABR13308	Abri13308 Human can	232	24	100.0	10	8	ADN32081	Human A1z
160	24	100.0	10	6	ABR13670	Abri13670 Human can	233	24	100.0	10	8	ADN66262	Human 273
161	24	100.0	10	6	ABR04206	Abri04206 Human can	234	24	100.0	10	8	ADN66446	Human 273
162	24	100.0	10	6	ABR13155	Abri13155 Human can	235	24	100.0	10	8	ADN69764	Human 273
163	24	100.0	10	6	ABR13890	Abri13890 Human can	236	24	100.0	10	8	ADN70291	Human 273
164	24	100.0	10	6	ABR14472	Abri14472 Human can	237	24	100.0	10	8	ADN69699	Human 273
165	24	100.0	10	6	ABR03828	Abri03828 Human can	238	24	100.0	10	8	ADN69624	Human 273
166	24	100.0	10	6	ABR14336	Abri14336 Human can	239	24	100.0	10	8	ADN48959	Peptide #
167	24	100.0	10	6	ABR04044	Abri04044 Human can	240	24	100.0	10	8	ADO49156	Human car
168	24	100.0	10	6	ABR13285	Abri13285 Human can	241	24	100.0	10	8	ADN95107	Murine MN
169	24	100.0	10	6	ABR13555	Abri13555 Human can	242	24	100.0	10	8	ADM98316	Humanised
170	24	100.0	10	6	ABR14090	Abri14090 Human can	243	24	100.0	10	8	ADP18399	Neurogene
171	24	100.0	10	6	ABR13505	Abri13505 Human can	244	24	100.0	10	8	ADW77933	Gonadotro

245	24	100.0	10	8	ADQ73638	Adq73638 Cancer re	318	24	100.0	12	2	AAR83344	Aar83344 Kb-bindin
246	24	100.0	10	8	ADQ69764	Adq69764 Cancer re	319	24	100.0	12	2	AAR32655	Aar32655 Human pla
247	24	100.0	10	8	ADQ73285	Adq73285 Cancer re	320	24	100.0	12	2	AAR32654	Aar32654 Human pla
248	24	100.0	10	8	ADQ73425	Adq73425 Cancer re	321	24	100.0	12	2	AAW18715	Aaw18715 C-src exo
249	24	100.0	10	8	ADP87277	Adp87277 Human cla	322	24	100.0	12	2	AAW81309	Aaw81309 Human iNO
250	24	100.0	10	8	ADQ90923	Adq90923 Pancreat	323	24	100.0	12	2	AAW81249	Aaw81249 Human iNO
251	24	100.0	10	8	ADR20482	Adr20482 Aromatic-	324	24	100.0	12	2	AAW71785	Aaw71785 Mimotope
252	24	100.0	10	8	ADR70840	Adr70840 Synthetic	325	24	100.0	12	2	AAW71784	Aaw71784 Mimotope
253	24	100.0	11	1	AAW71510	Aap71510 Growth ho	326	24	100.0	12	2	AAW37190	Aaw37190 Human onc
254	24	100.0	11	1	AAW71234	Aap71234 Luteinisi	327	24	100.0	12	2	AAW37184	Aaw37184 Human onc
255	24	100.0	11	1	AAW82068	Aap82068 Polypepti	328	24	100.0	12	2	AAW37191	Aaw37191 Human onc
256	24	100.0	11	2	AAW41331	Aar41331 HIV gp120	329	24	100.0	12	2	AAW37221	Aaw37221 MD2 bind
257	24	100.0	11	2	AAW74938	Aar74938 H-CDR-3 o	330	24	100.0	12	2	AAW37195	Aaw37195 Human onc
258	24	100.0	11	2	AAW88686	Aar88686 Allergen	331	24	100.0	12	2	AAW37171	Aaw37171 Human onc
259	24	100.0	11	2	AAW24022	Aaw24022 Variable	332	24	100.0	12	2	AAW37182	Aaw37182 Human onc
260	24	100.0	11	2	AAW62112	Aaw62112 Human MDM	333	24	100.0	12	2	AAW37181	Aaw37181 Human p53
261	24	100.0	11	2	AAW62115	Aaw62115 Human MDM	334	24	100.0	12	2	AAW37188	Aaw37188 Human onc
262	24	100.0	11	2	AAW62111	Aaw62111 Human MDM	335	24	100.0	12	2	AAW37196	Aaw37196 Human onc
263	24	100.0	11	2	AAW62113	Aaw62113 Human MDM	336	24	100.0	12	2	AAW37183	Aaw37183 Human onc
264	24	100.0	11	2	AAW62114	Aaw62114 Human MDM	337	24	100.0	12	2	AAW37220	Aaw37220 MD2 bind
265	24	100.0	11	2	AAW25553	Aay25553 Human MHC	338	24	100.0	12	2	AAW37170	Aaw37170 Human onc
266	24	100.0	11	3	AAW85394	Aay85394 IL-2 deri	339	24	100.0	12	2	AAW37189	Aaw37189 Human onc
267	24	100.0	11	3	AAW93383	Aay93383 Binding m	340	24	100.0	12	2	AAW37222	Aaw37222 MD2 bind
268	24	100.0	11	3	AAW93379	Aay93379 Binding m	341	24	100.0	12	2	AAW25552	Aay25552 Human MHC
269	24	100.0	11	3	AAW93377	Aay93377 Binding m	342	24	100.0	12	2	AAW44672	Aay44672 N-termina
270	24	100.0	11	3	AAW93381	Aay93381 Binding m	343	24	100.0	12	2	AAW85378	Aay85378 IL-2 deri
271	24	100.0	11	3	AAW93382	Aay93382 Binding m	344	24	100.0	12	3	AAW85107	Aay85107 HBV surfa
272	24	100.0	11	3	AAW91380	Aay91380 Binding m	345	24	100.0	12	3	AAW85105	Aay85105 HBV surfa
273	24	100.0	11	3	AAW17269	Aab17269 Anti-canc	346	24	100.0	12	3	AAW85104	Aay85104 HBV surfa
274	24	100.0	11	3	AAW86558	Aay86558 Human gen	347	24	100.0	12	3	AAW93376	Aay93376 Binding m
275	24	100.0	11	3	AAW52116	Aab52116 Human sec	348	24	100.0	12	3	AAW93389	Aay93389 Binding m
276	24	100.0	11	4	AAW92383	Aab92383 Miscellan	349	24	100.0	12	3	AAW93387	Aay93387 Binding m
277	24	100.0	11	4	ABP18965	Abp18965 HIV B62 s	350	24	100.0	12	3	AAW93388	Aay93388 Binding m
278	24	100.0	11	5	ABW73347	Abw73347 Exemplary	351	24	100.0	12	3	AAW93386	Aay93386 Binding m
279	24	100.0	11	5	ABP47662	Abp47662 N. mening	352	24	100.0	12	3	AAW17076	Aab17076 Mdm/hdm a
280	24	100.0	11	5	ABG97334	Abg97334 Human leu	353	24	100.0	12	3	AAW17087	Aab17087 Mdm/hdm a
281	24	100.0	11	5	ABJ07782	Abj07782 Hepatitis	354	24	100.0	12	3	AAW17089	Aab17089 Mdm/hdm a
282	24	100.0	11	5	ABJ06960	Abj06960 Hepatitis	355	24	100.0	12	3	AAW17081	Aab17081 Mdm/hdm a
283	24	100.0	11	5	AAW93631	Aau93631 Granulocy	356	24	100.0	12	3	AAW17078	Aab17078 Mdm/hdm a
284	24	100.0	11	5	AAW52269	Aam52269 Miniature	357	24	100.0	12	3	AAW17090	Aab17090 Mdm/hdm a
285	24	100.0	11	5	ABG67493	Abg67493 Human ADP	358	24	100.0	12	3	AAW17079	Aab17079 Mdm/hdm a
286	24	100.0	11	5	AAO18916	Aao18916 Human but	359	24	100.0	12	3	AAW17088	Aab17088 Mdm/hdm a
287	24	100.0	11	6	ADA03306	Ada03306 Angiotens	360	24	100.0	12	3	AAW17075	Aab17075 Mdm/hdm a
288	24	100.0	11	6	ABR56676	AbR56676 Angiotens	361	24	100.0	12	3	AAW17080	Aab17080 Mdm/hdm a
289	24	100.0	11	6	AAE35325	Aae35325 Human CD4	362	24	100.0	12	3	AAW17077	Aab17077 Mdm/hdm a
290	24	100.0	11	6	AAE31825	Aae31825 Androgen	363	24	100.0	12	3	AAW02747	Aab02747 Human thr
291	24	100.0	11	6	AAE31805	Aae31805 Androgen	364	24	100.0	12	3	AAW93867	Aay93867 Reactive
292	24	100.0	11	6	ABR59507	AbR59507 S. aureus	365	24	100.0	12	3	AAW93837	Aay93837 Peptide m
293	24	100.0	11	6	ABO53728	Abo53728 Novel hum	366	24	100.0	12	3	AAW32176	Aab32176 Peptide m
294	24	100.0	11	6	ADA23607	Ada23607 Alzheimer	367	24	100.0	12	3	AAW94486	Aay94486 Human som
295	24	100.0	11	7	ADC07163	Adc07163 Painted l	368	24	100.0	12	3	AAW30372	Aab30372 T. brucei
296	24	100.0	11	7	ADJ73501	Adj73501 Exemplary	369	24	100.0	12	4	AAW07310	Aae07310 Human MMP
297	24	100.0	11	8	ADJ53135	Adj53135 CHI delet	370	24	100.0	12	4	AAW86005	Aab86005 DCM-asso
298	24	100.0	11	8	ADJ52096	Adj52096 CHI delet	371	24	100.0	12	4	ABP24353	Abp24353 HIV A24 m
299	24	100.0	11	8	ADK38758	Adk38758 Hepatitis	372	24	100.0	12	4	ABP24364	Abp24364 HIV A24 m
300	24	100.0	11	8	ADK38240	Adk38240 Hepatitis	373	24	100.0	12	5	ABW06167	Abw06167 Gonadotro
301	24	100.0	11	8	ADL15440	Adl15440 Human cel	374	24	100.0	12	5	ABG78401	Abg78401 Memagin
302	24	100.0	11	8	ADJ25786	Adj25786 MD2 bind	375	24	100.0	12	5	AAW80737	Aau80737 Javelin p
303	24	100.0	11	8	ADJ25784	Adj25784 MD2 bind	376	24	100.0	12	5	AAW80736	Aau80736 Javelin p
304	24	100.0	11	8	ADJ25912	Adj25912 MD2 bind	377	24	100.0	12	5	ABW05292	Abw05292 Collar so
305	24	100.0	11	8	ADJ25913	Adj25913 MD2 bind	378	24	100.0	12	5	ABW05293	Abw05293 Collar so
306	24	100.0	11	8	ADJ25787	Adj25787 MD2 bind	379	24	100.0	12	5	ABW73170	Abw73170 Mdm/hdm a
307	24	100.0	11	8	ADJ25785	Adj25785 MD2 bind	380	24	100.0	12	5	ABW73175	Abw73175 Mdm/hdm a
308	24	100.0	11	8	ADN64806	Adn64806 HLA bindi	381	24	100.0	12	5	ABW73172	Abw73172 Mdm/hdm a
309	24	100.0	11	8	ADO00848	Ado00848 Human CD4	382	24	100.0	12	5	ABW73185	Abw73185 Mdm/hdm a
310	24	100.0	11	8	ADQ11533	Adq11533 Myostatin	383	24	100.0	12	5	ABW73184	Abw73184 Mdm/hdm a
311	24	100.0	11	8	ADR20392	Adr20392 Tryptic d	384	24	100.0	12	5	ABW73174	Abw73174 Mdm/hdm a
312	24	100.0	11	8	ADP80368	Adp80368 Human HLA	385	24	100.0	12	5	ABW73176	Abw73176 Mdm/hdm a
313	24	100.0	12	1	AAW931573	Aap931573 Extracell	386	24	100.0	12	5	ABW73183	Abw73183 Mdm/hdm a
314	24	100.0	12	2	AAW933388	Aar933388 Kml1-bind	387	24	100.0	12	5	ABW73173	Abw73173 Mdm/hdm a
315	24	100.0	12	2	AAW83372	Aar83372 Kml1-bind	388	24	100.0	12	5	ABW73171	Abw73171 Mdm/hdm a
316	24	100.0	12	2	AAW83375	Aar83375 Kml1-bind	389	24	100.0	12	5	ABW73182	Abw73182 Mdm/hdm a
317	24	100.0	12	2	AAW83323	Aar83323 Kb-bindin	390	24	100.0	12	5	AAW29104	Aae29104 Human DBH

391	24	100.0	12	5	AAB29118	Human DBH	Aae29118	464	24	100.0	12	8	ADL23636	ADL23636	RAD51C pr
392	24	100.0	12	5	ABJ05649	Peptide m	Abj05649	465	24	100.0	12	8	ADM96401	ADM96401	Immature
393	24	100.0	12	5	ABG60547	Selective	Abg60547	466	24	100.0	12	8	ADM31958	ADM31958	Eph famil
394	24	100.0	12	5	AAG96272	Class I G	Aau96272	467	24	100.0	12	8	ADN65746	ADN65746	HLA bindi
395	24	100.0	12	5	ABG68991	ABG68991	Abg68991	468	24	100.0	13	2	AAAR49316	AAAR49316	Beta2m po
396	24	100.0	12	5	ABB83231	Hepatitis	Abb83231	469	24	100.0	13	2	AAAR57883	AAAR57883	LCAT mini
397	24	100.0	12	6	AAE30893	MDM2-bind	Aae30893	470	24	100.0	13	2	AAAR70250	AAAR70250	Pan DR-bi
398	24	100.0	12	6	AAE30886	MDM2-bind	Aae30886	471	24	100.0	13	2	AAW25682	AAW25682	Antimicro
399	24	100.0	12	6	AAE30888	MDM2-bind	Aae30888	472	24	100.0	13	2	AAW26066	AAW26066	M30 deriv
400	24	100.0	12	6	AAE30890	MDM2-bind	Aae30890	473	24	100.0	13	2	AAW22121	AAW22121	Padre (pa
401	24	100.0	12	6	AAE30887	MDM2-bind	Aae30887	474	24	100.0	13	2	AAW67036	AAW67036	Pollioviru
402	24	100.0	12	6	AAE30892	MDM2-bind	Aae30892	475	24	100.0	13	2	AAV21821	AAV21821	Mimetic p
403	24	100.0	12	6	AAE34248	Human bra	Aae34248	476	24	100.0	13	2	AAV25551	AAV25551	Human MHC
404	24	100.0	12	6	ABP68069	Bacillus	Abp68069	477	24	100.0	13	3	AAV85093	AAV85093	HBV surfa
405	24	100.0	12	6	ABP83368	G protein	Abp83368	478	24	100.0	13	3	AAV85092	AAV85092	HBV surfa
406	24	100.0	12	6	ABP71371	Anti-OPGL	Abp71371	479	24	100.0	13	3	AAV85095	AAV85095	HBV surfa
407	24	100.0	12	7	ADC28198	Synthetic	Adc28198	480	24	100.0	13	3	AAAB02721	AAAB02721	Human thr
408	24	100.0	12	7	ADD25408	Complemen	Add25408	481	24	100.0	13	3	AAV52558	AAV52558	Universal
409	24	100.0	12	7	ADD25407	Complemen	Add25407	482	24	100.0	13	3	AAV57799	AAV57799	TRAM-inte
410	24	100.0	12	7	ADR39750	Peptide p	Ade39750	483	24	100.0	13	3	AAAB00667	AAAB00667	VRN2 pept
411	24	100.0	12	7	ADJ03010	Human mon	Adi03010	484	24	100.0	13	3	AAAB20975	AAAB20975	Phosphory
412	24	100.0	12	7	ADJ73329	Mdm/hdm a	Adj73329	485	24	100.0	13	3	AAAB36289	AAAB36289	Promiscuo
413	24	100.0	12	7	ADJ73326	Mdm/hdm a	Adj73326	486	24	100.0	13	3	AAAB08611	AAAB08611	Peptide i
414	24	100.0	12	7	ADJ73326	Mdm/hdm a	Adj73326	487	24	100.0	13	4	AAAB20427	AAAB20427	Anti-FIX/
415	24	100.0	12	7	ADJ73330	Interleuk	Adj73330	488	24	100.0	13	4	AAAB20390	AAAB20390	Anti-FIX/
416	24	100.0	12	7	ADJ72619	Interleuk	Adj72619	489	24	100.0	13	4	AAAB99710	AAAB99710	Pan-DR-bi
417	24	100.0	12	7	ADJ73339	Mdm/hdm a	Adj73339	490	24	100.0	13	4	AAE05735	AAE05735	Complemen
418	24	100.0	12	7	ADJ72622	Interleuk	Adj72622	491	24	100.0	13	4	AAE073644	AAE073644	Pan-DR bi
419	24	100.0	12	7	ADJ73324	Mdm/hdm a	Adj73324	492	24	100.0	13	4	AAAB86009	AAAB86009	DCM-asso
420	24	100.0	12	7	ADJ73336	Mdm/hdm a	Adj73336	493	24	100.0	13	4	AAAB86007	AAAB86007	DCM-asso
421	24	100.0	12	7	ADJ73328	Mdm/hdm a	Adj73328	494	24	100.0	13	4	AAAB86006	AAAB86006	DCM-asso
422	24	100.0	12	7	ADJ73327	Mdm/hdm a	Adj73327	495	24	100.0	13	4	AAAB20154	AAAB20154	PADRE pep
423	24	100.0	12	7	ADJ73337	Mdm/hdm a	Adj73337	496	24	100.0	13	4	ABP17586	ABP17586	HIV B27 s
424	24	100.0	12	7	ADJ72608	Interleuk	Adj72608	497	24	100.0	13	4	ABP17587	ABP17587	HIV B27 s
425	24	100.0	12	7	ADJ73338	Interleuk	Adj73338	498	24	100.0	13	5	AAAB48084	AAAB48084	Tie-1 bin
426	24	100.0	12	7	ADJ73338	Mdm/hdm a	Adj73338	499	24	100.0	13	5	AAAB88336	AAAB88336	Marine sn
427	24	100.0	12	7	ADJ73325	Mdm/hdm a	Adj73325	500	24	100.0	13	5	AAU80293	AAU80293	Pan DR ep
428	24	100.0	12	8	ADH50043	Active G	Adh50043	501	24	100.0	13	5	ABG31776	ABG31776	Pan DR ep
429	24	100.0	12	8	ADJ34263	12 mer pe	Adi34263	502	24	100.0	13	5	AAE26369	AAE26369	PADRE pep
430	24	100.0	12	8	ADJ34264	Wild type	Adi34264	503	24	100.0	13	5	ABP52369	ABP52369	Human c-S
431	24	100.0	12	8	ADJ52964	CH1 delet	Adj52964	504	24	100.0	13	5	ABB97697	ABB97697	Human pro
432	24	100.0	12	8	ADJ52564	CH1 delet	Adj52564	505	24	100.0	13	5	ADG67226	ADG67226	Human SGI
433	24	100.0	12	8	ADJ52960	CH1 delet	Adj52960	506	24	100.0	13	5	ADG66202	ADG66202	Human pro
434	24	100.0	12	8	ADJ52959	CH1 delet	Adj52959	507	24	100.0	13	5	ADG67227	ADG67227	Human SGI
435	24	100.0	12	8	ADJ52243	CH1 delet	Adj52243	508	24	100.0	13	5	ADG66203	ADG66203	Human pro
436	24	100.0	12	8	ADJ52556	CH1 delet	Adj52556	509	24	100.0	13	5	ADG67228	ADG67228	Human SGI
437	24	100.0	12	8	ADJ52971	CH1 delet	Adj52971	510	24	100.0	13	5	ADG66201	ADG66201	Human pro
438	24	100.0	12	8	ADJ52962	CH1 delet	Adj52962	511	24	100.0	13	5	ADG67229	ADG67229	Human SGI
439	24	100.0	12	8	ADJ52963	CH1 delet	Adj52963	512	24	100.0	13	6	ABO10766	ABO10766	Murine B9
440	24	100.0	12	8	ADJ52972	CH1 delet	Adj52972	513	24	100.0	13	6	ABG75574	ABG75574	CDR3 pept
441	24	100.0	12	8	ADJ52970	CH1 delet	Adj52970	514	24	100.0	13	6	ADA03307	ADA03307	Angiotens
442	24	100.0	12	8	ADJ52254	CH1 delet	Adj52254	515	24	100.0	13	6	ADA03312	ADA03312	Angiotens
443	24	100.0	12	8	ADJ52258	CH1 delet	Adj52258	516	24	100.0	13	6	ADA03305	ADA03305	Angiotens
444	24	100.0	12	8	ADJ52961	CH1 delet	Adj52961	517	24	100.0	13	6	ADA03310	ADA03310	Angiotens
445	24	100.0	12	8	ADJ52973	CH1 delet	Adj52973	518	24	100.0	13	6	ADA03311	ADA03311	Angiotens
446	24	100.0	12	8	ADJ52257	CH1 delet	Adj52257	519	24	100.0	13	6	ABR56680	ABR56680	Angiotens
447	24	100.0	12	8	ADJ51527	CH1 delet	Adj51527	520	24	100.0	13	6	ABR56677	ABR56677	Angiotens
448	24	100.0	12	8	ADJ51921	CH1 delet	Adj51921	521	24	100.0	13	6	ABR56682	ABR56682	Angiotens
449	24	100.0	12	8	ADJ51922	CH1 delet	Adj51922	522	24	100.0	13	6	ABR56675	ABR56675	Angiotens
450	24	100.0	12	8	ADJ51920	CH1 delet	Adj51920	523	24	100.0	13	6	ABR56681	ABR56681	Angiotens
451	24	100.0	12	8	ADJ51923	CH1 delet	Adj51923	524	24	100.0	13	6	ABP72696	ABP72696	T cell ep
452	24	100.0	12	8	ADJ51932	CH1 delet	Adj51932	525	24	100.0	13	6	ABR44710	ABR44710	Murine B9
453	24	100.0	12	8	ADJ51216	CH1 delet	Adj51216	526	24	100.0	13	6	ABR64118	ABR64118	E. coli 9
454	24	100.0	12	8	ADJ51931	CH1 delet	Adj51931	527	24	100.0	13	6	ABP98589	ABP98589	Beta-barr
455	24	100.0	12	8	ADJ51919	CH1 delet	Adj51919	528	24	100.0	13	6	ABP76124	ABP76124	Human GEN
456	24	100.0	12	8	ADJ51924	CH1 delet	Adj51924	529	24	100.0	13	6	ABP76126	ABP76126	Human GEN
457	24	100.0	12	8	ADJ51934	CH1 delet	Adj51934	530	24	100.0	13	6	ABP76127	ABP76127	Human GEN
458	24	100.0	12	8	ADJ51925	CH1 delet	Adj51925	531	24	100.0	13	6	ABP76125	ABP76125	Human GEN
459	24	100.0	12	8	ADJ51519	CH1 delet	Adj51519	532	24	100.0	13	6	AAO30456	AAO30456	Pan DR ep
460	24	100.0	12	8	ADJ51219	CH1 delet	Adj51219	533	24	100.0	13	6	AAO30463	AAO30463	Pan DR ep
461	24	100.0	12	8	ADJ51205	CH1 delet	Adj51205	534	24	100.0	13	7	ABR82484	ABR82484	Universal
462	24	100.0	12	8	ADJ51933	CH1 delet	Adj51933	535	24	100.0	13	7	ADC36627	ADC36627	Overlappi
463	24	100.0	12	8	ADJ57296	Provasopr	Adj57296	536	24	100.0	13	7	ADC36628	ADC36628	Overlappi

537	24	100.0	13	7	ADC81611	Adc81611	Universal	610	24	100.0	14	4	AAU25847	Aau25847	Human thr
538	24	100.0	13	7	ADE36941	Ade36941	Interfacci	611	24	100.0	14	4	AAB73820	Aab73820	Human LBP
539	24	100.0	13	7	ADE36957	Ade36957	Interfacci	612	24	100.0	14	4	AG98103	Ag98103	Human SNP
540	24	100.0	13	7	ADE36944	Ade36944	Interfacci	613	24	100.0	14	4	AG98104	Ag98104	Human SNP
541	24	100.0	13	7	ADF10455	Adf10455	Serum alb	614	24	100.0	14	4	AAB86012	Aab86012	DCM-aesoc
542	24	100.0	13	7	ADI57984	Adi57984	Anti-TNF-	615	24	100.0	14	4	AAB86020	Aab86020	DCM autoa
543	24	100.0	13	7	ADI57985	Adi57985	Anti-TNF-	616	24	100.0	14	4	ABB05294	Abb05294	Collar so
544	24	100.0	13	7	ADI57986	Adi57986	Anti-TNF-	617	24	100.0	14	5	ABB72898	Abb72898	TPO mimet
545	24	100.0	13	7	ADM75629	Adm75629	Potential	618	24	100.0	14	5	ABR52591	Abr52591	Mouse ARF
546	24	100.0	13	7	ADM74835	Adm74835	Potential	619	24	100.0	14	5	AAU93274	Aau93274	Granulocy
547	24	100.0	13	8	ADH94540	Adh94540	Lecithin	620	24	100.0	14	5	AAU09420	Aau09420	Preferred
548	24	100.0	13	8	ADK39825	Adk39825	PNA molec	621	24	100.0	14	5	ABJ15269	Abj15269	IGF relat
549	24	100.0	13	8	ADK39871	Adk39871	PNA molec	622	24	100.0	14	6	ABJ38281	Abj38281	Preferred
550	24	100.0	13	8	ADJ50658	Adj50658	Human ser	623	24	100.0	14	6	ADA03321	Ada03321	Angiotens
551	24	100.0	13	8	ADJ93375	Adj93375	Human BGS	624	24	100.0	14	6	ADA03317	Ada03317	Angiotens
552	24	100.0	13	8	ADJ73543	Adj73543	Cyclic hu	625	24	100.0	14	6	ADA03318	Ada03318	Angiotens
553	24	100.0	13	8	ADM06893	Adm06893	Pan DR bi	626	24	100.0	14	6	ABR56687	Abr56687	Angiotens
554	24	100.0	13	8	ADO57845	Ado57845	Porcine f	627	24	100.0	14	6	ABR56688	Abr56688	Angiotens
555	24	100.0	13	8	ADO57860	Ado57860	Human for	628	24	100.0	14	6	ABR56691	Abr56691	Angiotens
556	24	100.0	13	8	ADO24819	Ado24819	Polioviru	629	24	100.0	14	6	ABR53524	Abr53524	Human CD4
557	24	100.0	13	8	ADO27050	Ado27050	Human hol	630	24	100.0	14	6	ABP83523	Abp83523	G protein
558	24	100.0	13	8	ADQ27052	Adq27052	Human hol	631	24	100.0	14	6	ABR63806	Abr63806	Sepsis an
559	24	100.0	13	8	ADP73620	Adp73620	PADRE T c	632	24	100.0	14	6	ABO53732	Abo53732	Novel hum
560	24	100.0	13	8	ADP48563	Adp48563	Pan DR ep	633	24	100.0	14	7	ADC14177	Adc14177	Mouse ARF
561	24	100.0	13	8	ADQ90852	Adq90852	Mouse com	634	24	100.0	14	7	ADF28673	Adf28673	Lipocalin
562	24	100.0	13	8	ADR05553	Adr05553	Novel ssd	635	24	100.0	14	7	ADF10458	Adf10458	Serum alb
563	24	100.0	13	8	ADP79777	Adp79777	HLA epit	636	24	100.0	14	7	ADJ73049	Adj73049	TPO mimet
564	24	100.0	14	1	AAp61005	Ap61005	Discoderm	637	24	100.0	14	8	AD141370	Adi41370	Human HGP
565	24	100.0	14	1	AAp61006	Ap61006	Discoderm	638	24	100.0	14	8	ADJ50661	Adj50661	Human ser
566	24	100.0	14	2	AAr62082	Ar62082	Porcine P	639	24	100.0	14	8	ADJ52684	Adj52684	CHI delet
567	24	100.0	14	2	AAr69553	Ar69553	Human CD4	640	24	100.0	14	8	ADJ51645	Adj51645	CHI delet
568	24	100.0	14	2	AAr91596	Ar91596	Synthetic	641	24	100.0	14	8	ADL15439	Adl15439	Human cel
569	24	100.0	14	2	AAW24020	Aaw24020	Variable	642	24	100.0	14	8	ADN48906	Adn48906	Amphipath
570	24	100.0	14	2	AAW25683	Aaw25683	Antimicro	643	24	100.0	14	8	ADN48918	Adn48918	Cellular
571	24	100.0	14	2	AAW09827	Aaw09827	UDP-gluc	644	24	100.0	14	8	ADO00847	Ado00847	Human CD4
572	24	100.0	14	2	AAW24946	Aaw24946	C3/C4/C5-	645	24	100.0	14	8	ADO34382	Ado34382	Synthetic
573	24	100.0	14	2	AAW09477	Aw09477	Thrombopo	646	24	100.0	14	8	ADO34381	Ado34381	Synthetic
574	24	100.0	14	2	AAW16325	Aw16325	Murine AR	647	24	100.0	14	8	ADO34427	Ado34427	Synthetic
575	24	100.0	14	2	AAW01827	Aw01827	CD44 epit	648	24	100.0	14	8	ADO34383	Ado34383	Synthetic
576	24	100.0	14	2	AAW01828	Aw01828	CD44 epit	649	24	100.0	14	8	ADO34419	Ado34419	Synthetic
577	24	100.0	14	2	AAW36764	Aw36764	Thrombopo	650	24	100.0	14	8	ADO34417	Ado34417	Synthetic
578	24	100.0	14	2	AAW36628	Aw36628	Thrombopo	651	24	100.0	14	8	ADO34418	Ado34418	Synthetic
579	24	100.0	14	2	AAW50952	Aw50952	Somatosta	652	24	100.0	14	8	ADQ11555	Adq11555	Myostatin
580	24	100.0	14	2	AAW52538	Aw52538	Cyclic pe	653	24	100.0	14	8	ADQ11527	Adq11527	Myostatin
581	24	100.0	14	2	AAW52539	Aw52539	Cyclic pe	654	24	100.0	14	8	ADQ11526	Adq11526	Myostatin
582	24	100.0	14	2	AAW53471	Aw53471	P2 predom	655	24	100.0	14	8	ADQ11529	Adq11529	Myostatin
583	24	100.0	14	2	AAW37197	Aw37197	Human onc	656	24	100.0	14	8	ADQ11545	Adq11545	Myostatin
584	24	100.0	14	2	AAW25550	Aw25550	Human MHC	657	24	100.0	15	1	AAp20076	Aap20076	Example o
585	24	100.0	14	2	AAW08740	Aw08740	TuMV Nla	658	24	100.0	15	1	AAp82353	Aap82353	Antigenic
586	24	100.0	14	2	AAW08736	Aw08736	TEV Nla p	659	24	100.0	15	2	AAr51379	Aar51379	Immunodm
587	24	100.0	14	2	AAW08735	Aw08735	TEV Nla p	660	24	100.0	15	2	AAr54910	Aar54910	Immunodm
588	24	100.0	14	2	AAW08737	Aw08737	PVY Nla p	661	24	100.0	15	2	AAr63727	Aar63727	BPI deriv
589	24	100.0	14	2	AAW08733	Aw08733	WMV2 Nla	662	24	100.0	15	2	AAr85654	Aar85654	Urinastat
590	24	100.0	14	2	AAW08734	Aw08734	Plum pox	663	24	100.0	15	2	AAr81095	Aar81095	Anti-fung
591	24	100.0	14	2	AAW08738	Aw08738	PRSV Nla	664	24	100.0	15	2	AAr76012	Aar76012	BPI prote
592	24	100.0	14	2	AAW17346	Aw17346	Antimicro	665	24	100.0	15	2	AAr81013	Aar81013	BPI domai
593	24	100.0	14	2	AAW17345	Aw17345	Antimicro	666	24	100.0	15	2	AAr93624	Aar93624	HIV princ
594	24	100.0	14	2	AAW42865	Aw42865	Vpr-bindi	667	24	100.0	15	2	AAr63883	Aar63883	Human tum
595	24	100.0	14	2	AAW42864	Aw42864	Vpr-bindi	668	24	100.0	15	2	AAr62575	Aar62575	Human hep
596	24	100.0	14	2	AAW42867	Aw42867	Vpr-bindi	669	24	100.0	15	2	AAr63882	Aar63882	Human tum
597	24	100.0	14	3	AAW79175	Aw79175	Mouse ARF	670	24	100.0	15	2	AAr63880	Aar63880	Human tum
598	24	100.0	14	3	AAW17012	Aw17012	TPO-mimet	671	24	100.0	15	2	AAr63881	Aar63881	Human tum
599	24	100.0	14	3	AAW13866	Aw13866	L2/HNK1 c	672	24	100.0	15	2	AAr71957	Aar71957	Immunogen
600	24	100.0	14	3	AAW86562	Aw86562	Human gen	673	24	100.0	15	2	AAr80770	Aar80770	Immunogen
601	24	100.0	14	4	AAW97448	Aw97448	Peptide n-	674	24	100.0	15	2	AAr71956	Aar71956	Immunogen
602	24	100.0	14	4	AAW20428	Aw20428	Anti-FIX/	675	24	100.0	15	2	AAr86506	Aar86506	BPI.9 for
603	24	100.0	14	4	AAW98830	Aw98830	Human pep	676	24	100.0	15	2	AAr76293	Aar76293	Bacterial
604	24	100.0	14	4	AAW98837	Aw98837	Human pep	677	24	100.0	15	2	AAW05903	Aaw05903	Recombina
605	24	100.0	14	4	AAW97679	Aw97679	Human pep	678	24	100.0	15	2	AAr94739	Aar94739	SPNE 19b-
606	24	100.0	14	4	AAW98495	Aw98495	Human pep	679	24	100.0	15	2	AAW07992	Aaw07992	gp120 pep
607	24	100.0	14	4	AAW98088	Aw98088	Human pep	680	24	100.0	15	2	AAr97875	Aar97875	Japan ced
608	24	100.0	14	4	AAW98390	Aw98390	Human pep	681	24	100.0	15	2	AAr89914	Aar89914	p53 prote
609	24	100.0	14	4	AAW91005	Aw91005	Somatosta	682	24	100.0	15	2	AAW12885	Aaw12885	Antimicro

683	24	100.0	15	2	AAW43565	Aaw43565 Bacterici	756	24	100.0	15	4	AB886022	AB886022 DCM autoa
684	24	100.0	15	2	AAW75601	Aaw75601 M. tuberc	757	24	100.0	15	4	ABP24922	ABP24922 HIV DR 3a
685	24	100.0	15	2	AAW75656	Aaw75656 M. tuberc	758	24	100.0	15	4	ABP24864	ABP24864 HIV DR su
686	24	100.0	15	2	AAW75602	Aaw75602 M. tuberc	759	24	100.0	15	4	AB52261	AB52261 Peptide B
687	24	100.0	15	2	AAW75657	Aaw75657 M. tuberc	760	24	100.0	15	4	AB67599	AB67599 Peptide f
688	24	100.0	15	2	AAW81244	Aaw81244 Human iNO	761	24	100.0	15	4	AAJ03040	AAJ03040 Hepatitis
689	24	100.0	15	2	AAW81248	Aaw81248 Human iNO	762	24	100.0	15	4	AAJ03346	AAJ03346 Hepatitis
690	24	100.0	15	2	AAW81308	Aaw81308 Human iNO	763	24	100.0	15	4	AAJ03392	AAJ03392 Hepatitis
691	24	100.0	15	2	AAW81324	Aaw81324 Human iNO	764	24	100.0	15	4	AAE03355	AAE03355 Human gen
692	24	100.0	15	2	AAW81243	Aaw81243 Human iNO	765	24	100.0	15	4	AAE98123	AAE98123 Interfero
693	24	100.0	15	2	AAW81304	Aaw81304 Human iNO	766	24	100.0	15	5	AAU76315	AAU76315 Human act
694	24	100.0	15	2	AAW85420	Aaw85420 Helper T-	767	24	100.0	15	5	AAE13702	AAE13702 f88-4 pha
695	24	100.0	15	2	AAW76978	Aaw76978 Fusion im	768	24	100.0	15	5	AAO22325	AAO22325 Anti-CD14
696	24	100.0	15	2	AAW77201	Aaw77201 Pharnaceu	769	24	100.0	15	5	AB873178	AB873178 Mdm/hdm a
697	24	100.0	15	2	AAW63354	Aaw63354 Human BPI	770	24	100.0	15	5	AB873180	AB873180 Mdm/hdm a
698	24	100.0	15	2	AAW37192	Aaw37192 Human onc	771	24	100.0	15	5	AB873177	AB873177 Mdm/hdm a
699	24	100.0	15	2	AAW37193	Aaw37193 Human onc	772	24	100.0	15	5	AB873179	AB873179 Mdm/hdm a
700	24	100.0	15	2	AAW37172	Aaw37172 Human onc	773	24	100.0	15	5	AAE23400	AAE23400 Trichoder
701	24	100.0	15	2	AAW37224	Aaw37224 MDM2 bind	774	24	100.0	15	5	AB897999	AB897999 Pescadill
702	24	100.0	15	2	AAW37223	Aaw37223 MDM2 bind	775	24	100.0	15	5	ABU14522	ABU14522 Human 125
703	24	100.0	15	2	AAW37225	Aaw37225 MDM2 bind	776	24	100.0	15	5	ABU14687	ABU14687 Human 125
704	24	100.0	15	2	AAW37194	Aaw37194 Human onc	777	24	100.0	15	5	ABU14906	ABU14906 Human 125
705	24	100.0	15	2	AAW42068	Aaw42068 Rheumatoi	778	24	100.0	15	5	ABU14401	ABU14401 Human 125
706	24	100.0	15	2	AAW42003	Aaw42003 Rheumatoi	779	24	100.0	15	5	ABU14285	ABU14285 Human 125
707	24	100.0	15	2	AAW25577	Aaw25577 Human MHC	780	24	100.0	15	5	ABU14732	ABU14732 Human 125
708	24	100.0	15	2	AAW25578	Aaw25578 Human MHC	781	24	100.0	15	5	ABU15028	ABU15028 Human 125
709	24	100.0	15	2	AAW25549	Aaw25549 Human MHC	782	24	100.0	15	5	ABU15036	ABU15036 Human 125
710	24	100.0	15	2	AAW06310	Aaw06310 Human p53	783	24	100.0	15	5	ABU14774	ABU14774 Human 125
711	24	100.0	15	2	AAW92534	Aaw92534 Beta-acti	784	24	100.0	15	5	ABU14848	ABU14848 Human 125
712	24	100.0	15	2	AAW92606	Aaw92606 Mouse bet	785	24	100.0	15	5	ABU14860	ABU14860 Human 125
713	24	100.0	15	2	AAW92621	Aaw92621 Rabbit ac	786	24	100.0	15	5	ABU14224	ABU14224 Human 125
714	24	100.0	15	2	AAW33055	Aaw33055 Carbohydr	787	24	100.0	15	5	ABU14408	ABU14408 Human 125
715	24	100.0	15	2	AAW33054	Aaw33054 Carbohydr	788	24	100.0	15	5	ABU14458	ABU14458 Human 125
716	24	100.0	15	2	AAW33058	Aaw33058 Carbohydr	789	24	100.0	15	5	ABU14621	ABU14621 Human 125
717	24	100.0	15	2	AAW33070	Aaw33070 Carbohydr	790	24	100.0	15	5	ABU14861	ABU14861 Human 125
718	24	100.0	15	2	AAW82737	Aaw82737 Hepatitis	791	24	100.0	15	5	ABU14337	ABU14337 Human 125
719	24	100.0	15	3	AAW21652	Aaw21652 HSF regio	792	24	100.0	15	5	ABU14409	ABU14409 Human 125
720	24	100.0	15	3	AAW57059	Aaw57059 Calbindin	793	24	100.0	15	5	ABU14528	ABU14528 Human 125
721	24	100.0	15	3	AAW83120	Aaw83120 Synthetic	794	24	100.0	15	5	ABU14588	ABU14588 Human 125
722	24	100.0	15	3	AAW83119	Aaw83119 Synthetic	795	24	100.0	15	5	ABU14859	ABU14859 Human 125
723	24	100.0	15	3	AAW83121	Aaw83121 Tryptopha	796	24	100.0	15	5	ABU14813	ABU14813 Human 125
724	24	100.0	15	3	AAW65636	Aaw65636 Oestrogen	797	24	100.0	15	5	ABU15027	ABU15027 Human 125
725	24	100.0	15	3	AAW65649	Aaw65649 Oestrogen	798	24	100.0	15	5	ABU08946	ABU08946 Hepatitis
726	24	100.0	15	3	AAW65588	Aaw65588 Oestrogen	799	24	100.0	15	5	ABU09238	ABU09238 Hepatitis
727	24	100.0	15	3	AAW83247	Aaw83247 CYB5RP fa	800	24	100.0	15	5	AAU86386	AAU86386 Oestrogen
728	24	100.0	15	3	AAW17085	Aaw17085 Mdm/hdm a	801	24	100.0	15	5	AAU86325	AAU86325 Oestrogen
729	24	100.0	15	3	AAW17084	Aaw17084 Mdm/hdm a	802	24	100.0	15	5	AAU86373	AAU86373 Oestrogen
730	24	100.0	15	3	AAW17083	Aaw17083 Mdm/hdm a	803	24	100.0	15	5	AAO20307	AAO20307 Human ple
731	24	100.0	15	3	AAW17082	Aaw17082 Mdm/hdm a	804	24	100.0	15	5	AAO20896	AAO20896 N-termina
732	24	100.0	15	3	AAW16091	Aaw16091 Bacterici	805	24	100.0	15	5	AAO20896	AAO20896 N-termina
733	24	100.0	15	3	AAW66444	Aaw66444 HLA-A2-b1	806	24	100.0	15	5	ABO09195	ABO09195 HIV-1 pro
734	24	100.0	15	3	AAW02746	Aaw02746 Human thr	807	24	100.0	15	5	AAU96950	AAU96950 Quadrupl
735	24	100.0	15	3	AAW13869	Aaw13869 L2/HNK1 c	808	24	100.0	15	5	AAW52273	AAW52273 Miniature
736	24	100.0	15	3	AAW13870	Aaw13870 L2/HNK1 c	809	24	100.0	15	5	AAW52275	AAW52275 Miniature
737	24	100.0	15	3	AAW86376	Aaw86376 Human gen	810	24	100.0	15	5	AAW52274	AAW52274 Miniature
738	24	100.0	15	3	AAW85021	Aaw85021 Bovine la	811	24	100.0	15	5	AAW47804	AAW47804 Miniature
739	24	100.0	15	3	AAW85020	Aaw85020 Bovine la	812	24	100.0	15	5	AAW47805	AAW47805 Miniature
740	24	100.0	15	3	AAW85001	Aaw85001 Modified	813	24	100.0	15	5	AAW47809	AAW47809 Miniature
741	24	100.0	15	3	AAW863143	Aaw863143 Human sec	814	24	100.0	15	5	AAW47810	AAW47810 Miniature
742	24	100.0	15	4	AAW63330	Aaw63330 Nucleotid	815	24	100.0	15	5	AAW52271	AAW52271 Miniature
743	24	100.0	15	4	AAW63331	Aaw63331 Nucleotid	816	24	100.0	15	5	AAW52274	AAW52274 Miniature
744	24	100.0	15	4	AAU01041	Aau01041 Human sec	817	24	100.0	15	5	AAW47806	AAW47806 Miniature
745	24	100.0	15	4	AAW45797	Aaw45797 Human aut	818	24	100.0	15	5	AAW47807	AAW47807 Miniature
746	24	100.0	15	4	AAW68137	Aaw68137 Human CD1	819	24	100.0	15	5	AAW52272	AAW52272 Miniature
747	24	100.0	15	4	AAW57714	Aaw57714 D.melanog	820	24	100.0	15	5	AAU99942	AAU99942 Dihydrofo
748	24	100.0	15	4	AAW97733	Aaw97733 gp100 der	821	24	100.0	15	5	AAU47350	AAU47350 Human syn
749	24	100.0	15	4	AAW86028	Aaw86028 DCM autoa	822	24	100.0	15	5	AB899056	AB899056 Human tra
750	24	100.0	15	4	AAW51673	Aaw51673 Human ATP	823	24	100.0	15	5	AAW68350	AAW68350 Mouse mbc
751	24	100.0	15	4	AAW66753	Aaw66753 Human ATP	824	24	100.0	15	5	AAU88033	AAU88033 Mouse mbc
752	24	100.0	15	4	AAW86017	Aaw86017 DCM-assoc	825	24	100.0	15	5	ABG72016	ABG72016 N-termina
753	24	100.0	15	4	AAW86013	Aaw86013 DCM-assoc	826	24	100.0	15	5	ABW76972	ABW76972 4-Hydroxy
754	24	100.0	15	4	AAW86014	Aaw86014 DCM-assoc	827	24	100.0	15	5	ABW77835	ABW77835 Peptide u
755	24	100.0	15	4	AAW86021	Aaw86021 DCM autoa	828	24	100.0	15	5	ABU17702	ABU17702 Zinc tran

829	24	100.0	5	ABJ17745	Abj17745 Zinc tran	902	24	100.0	15	6	ABJ70191	Abj70191 184PIE2-r
830	24	100.0	5	ABJ17466	Abj17466 Zinc tran	903	24	100.0	15	6	ABJ70742	Abj70742 184PIE2-r
831	24	100.0	15	ABJ17905	Abj17905 Zinc tran	904	24	100.0	15	6	ABJ75806	Abj75806 Solid pha
832	24	100.0	15	ABJ17834	Abj17834 Zinc tran	905	24	100.0	15	6	ABU56365	Abu56365 Mycobacte
833	24	100.0	15	ABJ17573	Abj17573 Zinc tran	906	24	100.0	15	6	ABU56366	Abu56366 Mycobacte
834	24	100.0	15	ABJ17656	Abj17656 Zinc tran	907	24	100.0	15	6	ABG73434	Abg73434 Human p53
835	24	100.0	15	ABP55643	Abp55643 Na-K aden	908	24	100.0	15	6	ABU87143	Abu87143 Carbohydr
836	24	100.0	15	ABO19633	Abol19633 F22844 te	909	24	100.0	15	6	ABU87155	Abu87155 Carbohydr
837	24	100.0	15	ABP58627	Abp58627 Human end	910	24	100.0	15	6	ABU87140	Abu87140 Carbohydr
838	24	100.0	15	ABJ38737	Abj38737 Human G-p	911	24	100.0	15	6	ABU87139	Abu87139 Carbohydr
839	24	100.0	15	ABP96426	Abp96426 HIV-1 Vpr	912	24	100.0	15	6	ABO53521	Abos3521 Novel hum
840	24	100.0	15	ABJ37251	Abj37251 Rhodopsin	913	24	100.0	15	6	ADA19573	Ada19573 Human Bet
841	24	100.0	15	ABJ37249	Abj37249 Rhodopsin	914	24	100.0	15	7	ADB67055	Adb67055 Streptavi
842	24	100.0	15	ABJ37271	Abj37271 Rhodopsin	915	24	100.0	15	7	ADC22292	Adc22292 Protein b
843	24	100.0	15	ABJ37259	Abj37259 Rhodopsin	916	24	100.0	15	7	AAE39310	Aae39310 M. tuberc
844	24	100.0	15	ABJ37273	Abj37273 Rhodopsin	917	24	100.0	15	7	AAE39311	Aae39311 M. tuberc
845	24	100.0	15	ABJ37283	Abj37283 Rhodopsin	918	24	100.0	15	7	AAE39375	Aae39375 Peptide #
846	24	100.0	15	ABR35681	AbR35681 Human can	919	24	100.0	15	7	AAE39374	Aae39374 Peptide #
847	24	100.0	15	ABR33516	AbR33516 Human can	920	24	100.0	15	7	ADE70760	AdE70760 Human 161
848	24	100.0	15	ABR33564	AbR33564 Human can	921	24	100.0	15	7	AdE70795	AdE70795 Human 161
849	24	100.0	15	ABR33572	AbR33572 Human can	922	24	100.0	15	7	AdE70392	AdE70392 Human 161
850	24	100.0	15	ABR35444	AbR35444 Human can	923	24	100.0	15	7	AdE70622	AdE70622 Human 161
851	24	100.0	15	ABR36362	AbR36362 Human can	924	24	100.0	15	7	AdE70540	AdE70540 Human 161
852	24	100.0	15	ABR36578	AbR36578 Human can	925	24	100.0	15	7	AdE70838	AdE70838 Human 161
853	24	100.0	15	ABR38002	AbR38002 Human can	926	24	100.0	15	7	AdE70177	AdE70177 Human 161
854	24	100.0	15	ABR33539	AbR33539 Human can	927	24	100.0	15	7	AdE78417	AdE78417 Peptide t
855	24	100.0	15	ABR37718	AbR37718 Human can	928	24	100.0	15	7	ABW02221	ABW02221 HGPBMY14
856	24	100.0	15	ABR37824	AbR37824 Human can	929	24	100.0	15	7	ABW02222	ABW02222 HGPBMY14
857	24	100.0	15	ABR33504	AbR33504 Human can	930	24	100.0	15	7	ADF28666	Adf28666 Lipocalin
858	24	100.0	15	ABR37956	AbR37956 Human can	931	24	100.0	15	7	ADF12276	Adf12276 Drosophill
859	24	100.0	15	ABR33195	AbR33195 Human can	932	24	100.0	15	7	ADF45152	Adf45152 M. tuberc
860	24	100.0	15	ABR33549	AbR33549 Human can	933	24	100.0	15	7	ADf45153	Adf45153 M. tuberc
861	24	100.0	15	ABR35046	AbR35046 Human can	934	24	100.0	15	7	ADf57819	Adf57819 Monoclonal
862	24	100.0	15	ABR35797	AbR35797 Human can	935	24	100.0	15	7	ADf57818	Adf57818 Monoclonal
863	24	100.0	15	ABR35870	AbR35870 Human can	936	24	100.0	15	7	ADf57820	Adf57820 Monoclonal
864	24	100.0	15	ABR30139	AbR30139 Human can	937	24	100.0	15	7	ADf03009	Adf03009 Human mon
865	24	100.0	15	ABR33214	AbR33214 Human can	938	24	100.0	15	7	ADf03005	Adf03005 Human mon
866	24	100.0	15	ABR37285	AbR37285 Human can	939	24	100.0	15	7	ADf03004	Adf03004 Human mon
867	24	100.0	15	ABR36886	AbR36886 Human can	940	24	100.0	15	7	ADf14946	Adf14946 Trypsinog
868	24	100.0	15	ABR33211	AbR33211 Human can	941	24	100.0	15	7	ADf73331	Adf73331 Mdm/hdm a
869	24	100.0	15	ABR33470	AbR33470 Human can	942	24	100.0	15	7	ADf73333	Adf73333 Mdm/hdm a
870	24	100.0	15	ABR33505	AbR33505 Human can	943	24	100.0	15	7	ADf73332	Adf73332 Mdm/hdm a
871	24	100.0	15	ABR37825	AbR37825 Human can	944	24	100.0	15	7	ADf73334	Adf73334 Mdm/hdm a
872	24	100.0	15	ABR37899	AbR37899 Human can	945	24	100.0	15	7	ADk40547	Adk40547 KDR & VEG
873	24	100.0	15	ABR33161	AbR33161 Human can	946	24	100.0	15	8	ADG78883	Adg78883 Human p53
874	24	100.0	15	ABR33193	AbR33193 Human can	947	24	100.0	15	8	ADf24624	Adf24624 HIV-1 HLA
875	24	100.0	15	ABR33263	AbR33263 Human can	948	24	100.0	15	8	ADf66554	Adf66554 Rat bacce
876	24	100.0	15	ABR33457	AbR33457 Human can	949	24	100.0	15	8	ADf41333	Adf41333 Human HGP
877	24	100.0	15	ABR36675	AbR36675 Human can	950	24	100.0	15	8	ADf52965	Adf52965 CH1 delet
878	24	100.0	15	ABR36740	AbR36740 Human can	951	24	100.0	15	8	ADf52967	Adf52967 CH1 delet
879	24	100.0	15	ABR37791	AbR37791 Human can	952	24	100.0	15	8	ADf52968	Adf52968 CH1 delet
880	24	100.0	15	ABR30197	AbR30197 Human can	953	24	100.0	15	8	ADf52966	Adf52966 CH1 delet
881	24	100.0	15	ABR30248	AbR30248 Human can	954	24	100.0	15	8	ADf51926	Adf51926 CH1 delet
882	24	100.0	15	ABR30319	AbR30319 Human can	955	24	100.0	15	8	ADf51929	Adf51929 CH1 delet
883	24	100.0	15	ABR33225	AbR33225 Human can	956	24	100.0	15	8	ADf51928	Adf51928 CH1 delet
884	24	100.0	15	ABR33580	AbR33580 Human can	957	24	100.0	15	8	ADf51927	Adf51927 CH1 delet
885	24	100.0	15	ABR37528	AbR37528 Human can	958	24	100.0	15	8	ADf87982	Adf87982 Bioactive
886	24	100.0	15	ABR37642	AbR37642 Human can	959	24	100.0	15	8	ADf39274	Adf39274 Hepatitis
887	24	100.0	15	ABR37973	AbR37973 Human can	960	24	100.0	15	8	ADf99325	Adf99325 Nanostruc
888	24	100.0	15	ABR30238	AbR30238 Human can	961	24	100.0	15	8	ADf21645	Adf21645 125P5C8 p
889	24	100.0	15	ABR36011	AbR36011 Human can	962	24	100.0	15	8	ADf22143	Adf22143 125P5C8 p
890	24	100.0	15	ABR33215	AbR33215 Human can	963	24	100.0	15	8	ADf21858	Adf21858 125P5C8 p
891	24	100.0	15	ABR37812	AbR37812 Human can	964	24	100.0	15	8	ADf21969	Adf21969 125P5C8 p
892	24	100.0	15	ABP58798	Abp58798 Tumour ce	965	24	100.0	15	8	ADf21461	Adf21461 125P5C8 p
893	24	100.0	15	ABJ71392	Abj71392 184PIE2-r	966	24	100.0	15	8	ADf21759	Adf21759 125P5C8 p
894	24	100.0	15	ABJ71394	Abj71394 184PIE2-r	967	24	100.0	15	8	ADf21695	Adf21695 125P5C8 p
895	24	100.0	15	ABJ71730	Abj71730 184PIE2-r	968	24	100.0	15	8	ADf21825	Adf21825 125P5C8 p
896	24	100.0	15	ABJ71393	Abj71393 184PIE2-r	969	24	100.0	15	8	ADf21924	Adf21924 125P5C8 p
897	24	100.0	15	ABJ72029	Abj72029 184PIE2-r	970	24	100.0	15	8	ADf21522	Adf21522 125P5C8 p
898	24	100.0	15	ABJ70666	Abj70666 184PIE2-r	971	24	100.0	15	8	ADf22098	Adf22098 125P5C8 p
899	24	100.0	15	ABJ69909	Abj69909 184PIE2-r	972	24	100.0	15	8	ADf22264	Adf22264 125P5C8 p
900	24	100.0	15	ABJ70160	Abj70160 184PIE2-r	973	24	100.0	15	8	ADf22011	Adf22011 125P5C8 p
901	24	100.0	15	ABJ70609	Abj70609 184PIE2-r	974	24	100.0	15	8	ADf21574	Adf21574 125P5C8 p

```
975 24 100.0 15 8 ADL22265 Adl22265 125P5C8 p
976 24 100.0 15 8 ADL22273 Adl22273 125P5C8 p
977 24 100.0 15 8 ADL21638 Adl21638 125P5C8 p
978 24 100.0 15 8 ADL22097 Adl22097 125P5C8 p
979 24 100.0 15 8 ADL21765 Adl21765 125P5C8 p
980 24 100.0 15 8 ADL22096 Adl22096 125P5C8 p
981 24 100.0 15 8 ADL21646 Adl21646 125P5C8 p
982 24 100.0 15 8 ADL22050 Adl22050 125P5C8 p
983 24 100.0 15 8 ADL22085 Adl22085 125P5C8 p
984 24 100.0 15 8 ADM79097 Adm79097 Oestrogen
985 24 100.0 15 8 ADM79084 Adm79084 Oestrogen
986 24 100.0 15 8 ADM79036 Adm79036 Oestrogen
987 24 100.0 15 8 ADL26376 Adl26376 Synthetic
988 24 100.0 15 8 ADL17442 Adl17442 Different
989 24 100.0 15 8 ADL17420 Adl17420 Different
990 24 100.0 15 8 ADN71026 Adn71026 Human 273
991 24 100.0 15 8 ADN711360 Adn711360 Human 273
992 24 100.0 15 8 ADN71184 Adn71184 Human 273
993 24 100.0 15 8 ADN70619 Adn70619 Human 273
994 24 100.0 15 8 ADN70752 Adn70752 Human 273
995 24 100.0 15 8 ADN71359 Adn71359 Human 273
996 24 100.0 15 8 ADN70813 Adn70813 Human 273
997 24 100.0 15 8 ADN71858 Adn71858 Human 273
998 24 100.0 15 8 ADN70880 Adn70880 Human 273
999 24 100.0 15 8 ADN71292 Adn71292 Human 273
1000 24 100.0 15 8 ADN71578 Adn71578 Human 273
```

ALIGNMENTS

```
RESULT 1
AAW37216
ID AAW37216 standard; peptide; 9 AA.
```

```
XX AAW37216;
XX
XX 20-JUL-1998 (first entry)
XX
XX Human oncogenic protein MDM2 binding peptide derivative 9.
XX
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection.
XX Synthetic.
XX Homo sapiens.
```

```
XX Key Location/Qualifiers
XX Modified-site 1
XX Modified-site 9 /note= "N-terminal acetyl"
XX Modified-site 9 /note= "C-terminal amide"
```

```
XX WO9801467-A2.
```

```
XX 15-JAN-1998.
```

```
XX 04-JUL-1997; 97WO-EP003549.
```

```
XX 05-JUL-1996; 96GB-00014197.
```

```
XX 07-APR-1997; 97GB-00007041.
```

```
XX (NOVS ) NOVARTIS AG.
```

```
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
```

```
XX Lane D, Boettger V, Boettger A, Pickaley S, Hochkeppel H;
```

```
XX Garcia-Echeverria C, Chene P, Furet P;
```

```
XX WPI; 1998-100996/09.
```

```
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
```

```
XX Example 6; Page 26; 45pp; English.
XX
XX This is a MDM2 binding peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of
XX MDM2/p53 binding. They may also be used to purify binding partners
XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
XX cancer and leukaemia patients and for treatment or prevention of diseases
XX involving p53/MDM2 interactions, especially tumours and viral infections.
XX The peptides can be administered nasally, rectally, orally or by
XX injection. By interfering with MDM2/p53 interaction, the peptides can
XX activate p53 function and accumulation in normal cells. The peptides
XX which mimic the MDM2 binding site in p53, have a significantly greater
XX blocking activity compared with wild-type p53
```

```
XX Sequence 9 AA;
```

```
Query Match 100.0%; Score 24; DB 2; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XPXXXXXXX 9
```

```
Db 1 RFMDYWEGL 9
```

```
RESULT 2
```

```
AAW37175
```

```
ID AAW37175 standard; peptide; 9 AA.
```

```
XX AAW37175;
```

```
XX 20-JUL-1998 (first entry)
```

```
XX Human oncogenic protein MDM2 binding generic peptide sequence 3.
```

```
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection.
```

```
XX Homo sapiens.
```

```
XX Key Location/Qualifiers
```

```
XX Misc-difference 1
```

```
XX /label= Arg, Asp, Ala, Thr or Val
```

```
XX /note= "preferentially Arg"
```

```
XX Misc-difference 3
```

```
XX /label= Met, Ile, Thr, Arg, Ala or Ser
```

```
XX /note= "preferentially Met"
```

```
XX Misc-difference 4
```

```
XX /label= Arg, His, Glu, Cys or Asp
```

```
XX /note= "preferentially Asp"
```

```
XX Misc-difference 5
```

```
XX /label= His, Phe or Tyr
```

```
XX Misc-difference 7
```

```
XX /label= Glu, Thr, Ala, Phe or Ser
```

```
XX /note= "preferentially Glu"
```

```
XX Misc-difference 8
```

```
XX /label= Gly, Thr, Ala or Asp
```

```
XX /note= "preferentially Gly"
```

```
XX Misc-difference 9
```

```
XX /label= Phe, Gln or Leu
```

```
XX WO9801467-A2.
```

```
XX 15-JAN-1998.
```

```
XX 04-JUL-1997; 97WO-EP003549.
```

```
XX
```

PR 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
PA (NOVS) NOVARTIS AG.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX
XX Claim 8; Page 42; 45pp; English.
XX
XX This represents a generic peptide that is capable of binding to an
CC oncogenic protein MDM2 (especially human DM2). The peptide and its
CC derivatives can specifically inhibit or block the binding of MDM2 to the
CC human p53 protein, in vitro or in vivo. Inhibiting the interaction
CC between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
CC cells comprising a wild-type p53 and non-elevated levels of MDM2. The
CC peptide or its derivatives may be used to identify molecules that bind to
CC MDM2 and to identify and design inhibitors of MDM2/p53 binding. They may
CC also be used to purify binding partners especially MDM2, diagnose disease
CC by measuring levels of MDM2 in blood of cancer and leukaemia patients and
CC for treatment or prevention of disease involving p53/MDM2 interactions,
CC especially tumours and viral infections. The peptides can be administered
CC nasally, rectally, orally or by injection. By interfering with MDM2/p53
CC interaction, the peptides can activate p53 function and accumulation in
CC normal cells. The peptides which mimic the MDM2 binding site in p53, have
CC a significantly greater blocking activity compared with wild-type p53
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 24; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXXWXXX 9
Db 1 XFXXXXWXXX 9
RESULT 3
AAW37212
ID AAW37212 standard; peptide; 9 AA.
AC AAW37212;
XX
XX 20-JUL-1998 (first entry)
XX
XX Human oncogenic protein MDM2 binding N-acylated peptide derivative 15.
DE
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 4 /label= Aib
FT /note= "2-Aminoisobutyric acid"
FT Modified-site 7 /label= Aib
FT /note= "2-Aminoisobutyric acid"
FT Modified-site 9 /note= "C-terminal amide"
FT
XX

PN WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
PR 07-APR-1997; 97GB-00007041.
XX
XX (NOVS) NOVARTIS AG.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
PA
XX Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
PI Garcia-Echeverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
PT useful in, e.g. diagnosis and treatment of cancer and viral infections
PT and identifying binding agents.
XX
XX Example 5; Page 25; 45pp; English.
XX
XX This is a MDM2 binding peptide derivative capable of binding to a human
CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
CC molecules that bind to MDM2 and to identify and design inhibitors of
CC MDM2/p53 binding. They may also be used to purify binding partners
CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 24; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.8e+06;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXXWXXX 9
Db 1 RFXXYWXGL 9
RESULT 4
AAW37179
ID AAW37179 standard; peptide; 9 AA.
XX
XX AAW37179;
XX
XX 20-JUL-1998 (first entry)
XX
XX Human oncogenic protein MDM2 binding peptide derivative 7.
DE
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX

PR 05-JUL-1996; 96GB-00014197.
 PR 07-APR-1997; 97GB-00007041.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 XX WPI; 1998-100996/09.
 XX
 XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 XX
 PS Disclosure; Page 8; 45pp; English.
 XX
 CC This peptide is capable of binding to an oncogenic protein MDM2
 CC (especially human DM2). The MDM2 binding peptides can specifically
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC molecules that bind to MDM2 and to identify and design inhibitors of
 CC MDM2/p53 binding. They may also be used to purify binding partners
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC cancer and leukaemia patients and for treatment or prevention of disease
 CC involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 CC injection. By interfering with MDM2/p53 interaction, the peptides can
 CC activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 24; DB 2; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XFXXXWXXX 9
 Db :|:|:|:|:
 1 RFPDIWEGL 9
 RESULT 5
 AAW37213
 ID AAW37213 standard; peptide; 9 AA.
 XX
 AC AAW37213;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Human oncogenic protein MDM2 binding N-acylated peptide derivative 16.
 XX
 KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumour; diagnosis; binding; viral infection.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 4
 FT /label= Aib
 FT /note= "2-Aminoisobutyric acid"
 FT Misc-difference 8
 FT /label= OTHER
 FT /note= "Ac3c (1-amino-cyclopropane-1-carboxylic acid)"
 FT Modified-site 9
 FT /note= "C-terminal amide"
 XX

PN WO9801467-A2.
 XX
 PD 15-JAN-1998.
 XX
 PF 04-JUL-1997; 97WO-EP003549.
 XX
 PR 05-JUL-1996; 96GB-00014197.
 PR 07-APR-1997; 97GB-00007041.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 XX WPI; 1998-100996/09.
 XX
 XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 XX
 PS Example 5; Page 25; 45pp; English.
 XX
 CC This is a MDM2 binding peptide derivative capable of binding to a human
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC molecules that bind to MDM2 and to identify and design inhibitors of
 CC MDM2/p53 binding. They may also be used to purify binding partners
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC cancer and leukaemia patients and for treatment or prevention of disease
 CC involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 CC injection. By interfering with MDM2/p53 interaction, the peptides can
 CC activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 24; DB 2; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.8e+06;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XFXXXWXXX 9
 Db :|:|:|:|:
 1 RFPDIWEGL 9
 RESULT 6
 AAY25555
 ID AAY25555 standard; peptide; 9 AA.
 XX
 AC AAY25555;
 XX
 DT 30-SEP-1999 (first entry)
 XX
 DE Human MHC Class II hypothetical desensitising peptide #13.
 XX
 KW Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
 XX
 OS Synthetic.
 XX
 PN WO9934826-A1.
 XX
 PD 15-JUL-1999.

CC group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0

Qy 1 XFXXXWXXX 9
:|::||:::
Db 1 GFPPDMQNY 9

RESULT 9
ABP15780
ID ABP15780 standard; peptide; 9 AA.
XX
AC ABP15780;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif nef peptide #42.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PS Claim 32; Page 192; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0

Qy 1 XFXXXWXXX 9
:|::||:::
Db 1 GFPPKWSGR 9

RESULT 9
ABP15780
ID ABP15780 standard; peptide; 9 AA.
XX
AC ABP15780;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif nef peptide #42.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PS Claim 32; Page 192; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0

Qy 1 XFXXXWXXX 9
:|::||:::
Db 1 GFPPKWSGR 9

RESULT 9
ABP15780
ID ABP15780 standard; peptide; 9 AA.
XX
AC ABP15780;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif nef peptide #42.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PS Claim 32; Page 192; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0

Qy 1 XFXXXWXXX 9
:|::||:::
Db 1 GFPPKWSGR 9

RESULT 9
ABP15780
ID ABP15780 standard; peptide; 9 AA.
XX
AC ABP15780;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif nef peptide #42.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PS Claim 32; Page 192; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0

Qy 1 XFXXXWXXX 9
:|::||:::
Db 1 GFPPKWSGR 9

RESULT 9
ABP15780
ID ABP15780 standard; peptide; 9 AA.
XX
AC ABP15780;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif nef peptide #42.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.

CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 24; DB 4; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
 Db 1 GFFPDWQNY 9

RESULT 11
 ABP22220
 ID ABP22220 standard; peptide; 9 AA.
 XX
 AC ABP22220;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A03 motif vpr peptide #62.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT
 PS Claim 32; Page 324; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or

CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 24; DB 4; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
 Db 1 HPRPWLII 9

RESULT 12
 ABP23020
 ID ABP23020 standard; peptide; 9 AA.
 XX
 AC ABP23020;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A11 motif nef peptide #67.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT
 PS Claim 32; Page 340; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or

generated APC (III) that presents a peptide of a CYP1B1 in the context of a MHC complex molecule. The method is useful for treating a patient having or is at risk of having a cell that expresses CYP1B1. The method is useful for the prevention, treatment and diagnosis of cancer, e.g. melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can bind to human leukocyte antigens (HLAs), as well as other amino acid sequence used in the exemplification of the present invention

Sequence 9 AA:

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels

Qy	1	X	F	X	X	X	X	9
		:	:	:	:	:	:	
n'b	1	V	F	N	O	S	V	9

RESULT 18
AAM08894
ID AAM08894 standard: peptide: 9 AA.

AA AAM08894:

09-OCT-2001 (first entry)

XX
DE HT.A-B #2705 nonmar #434

XX Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
XX human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; AEC;
XX major histocompatibility complex; antigen presenting cell; melanoma
XX lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

AA
OS
Homo sapiens.

XX
PN
WC200135810-A2XX
DN
25-MAY-2001XX
DE 15 NOV 2000. 2000NOV15031513

XX 2

XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (UTYBO-) UNIV BOSTON.

XX Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
PI PI Von Bergwelt-Baildon M;

DR WPI: 2001-355537/37.

Treating a cancer patient involves administering to patient a cytotoxic T-lymphocyte, an antigen presenting cell that activates T cells, a peptide of cytchrome p450 1B1, or a polynucleotide encoding the peptide.

XX
PS Disclosure: Page 68: 121pp: English:

The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1), which involves administering to the patient a cytotoxic T-lymphocyte (CTL) that kills the cell, an antigen presenting cell (APC) that activates CTL, a peptide of CYP1B1 that binds to major histocompatibility complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or peptide of CYP1B1. Also described are: (1) a method for assessing the level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that binds to MHC complex molecule, involving measuring the level of CTL specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex vivo generated CTL (II) that specifically kills a cell expressing CYP1B1 in a specific of a MHC complex-restricted fashion; and (4) an ex vivo

The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1), which involves administering to the patient a cytotoxic T-lymphocyte (CTL) that kills the cell, an antigen presenting cell (APC) that activates CTL, a peptide of CYP1B1 that binds to major histocompatibility complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or peptide of CYP1B1. Also described are: (1) a method for assessing the level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that binds to MHC complex molecule, involving measuring the level of CTL specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex vivo generated CTL (II) that specifically kills a cell expressing CYP1B1 in a specific of a MHC complex-restricted fashion; and (4) an ex vivo

PF 08-SEP-2000; 2000WO-US024802.
 XX
 PR 08-SEP-2000; 2000WO-US024802.
 XX
 PA (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTE A.
 XX
 XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Cellis E, Kubo RT, Grey HM, Chesnut RW;
 PI WPI; 2002-643192/69.
 DR Vaccine composition for treating or preventing hepatitis B virus (HBV)
 XX infection, and/or for stimulating an immune response to HBV, comprises a
 PT HBV peptide epitope.
 PT
 XX Disclosure; Page 174; 228pp; English.
 XX
 PS The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 24; DB 5; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XFXXXWXXX 9
 DB :|::|::|::
 1 IFCLWVYI 9
 RESULT 26
 ABG60517
 ID ABG60517 standard; peptide; 9 AA.
 XX
 AC ABG60517;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Selective targeting peptide #192.
 XX
 KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
 KW gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO200220769-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US027692.
 XX
 XX 08-SEP-2000; 2000US-0231266P.
 PR 17-JAN-2001; 2001US-00765101.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Arap W, Pasqualini R;
 PI WPI; 2002-415731/44.
 DR
 XX Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease, e.g.
 PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
 PT disease.

XX Claim 22; Page 121; 317pp; English.
 PS
 XX The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting
 CC peptides of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 24; DB 5; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XFXXXWXXX 9
 DB :|::|::|::
 1 CFNRTWIGC 9
 RESULT 27
 AAE31317
 ID AAE31317 standard; peptide; 9 AA.
 XX
 AC AAE31317;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human p53 peptide #2.
 XX
 KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200272627-A2.
 XX
 PD 19-SEP-2002.
 XX
 XX 11-MAR-2002; 2002WO-EP002666.
 PF 09-MAR-2001; 2001US-0274250P.
 PR 14-MAY-2001; 2001US-0290353P.
 PR 18-MAY-2001; 2001US-0291610P.
 XX
 XX (CALL-) CALLISTOGEN AG.
 XX
 XX Wrede P, Walden P, Eichler-Mertens M, Filter M;
 XX WPI; 2002-759836/82.
 DR
 XX Providing, identifying or optimizing peptides for inducing cytotoxic T-
 PT lymphocytes and for treating cancer, comprises selecting conserved
 PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
 PT protein.
 XX
 XX Disclosure; Page 11; 32pp; English.
 PS
 XX The invention relates to a method for providing, identifying or/and
 CC optimising peptides which induce cytotoxic T-lymphocytes and to the uses
 CC of the obtained peptides for vaccination. The method is useful for
 CC providing, identifying and/or optimising peptides that are useful in
 CC manufacturing a pharmaceutical composition for the induction of cytotoxic
 CC T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
 CC or viral infections. The invention is also used in gene therapy. The
 CC present sequence is human p53 peptide used to illustrate the method of

PT cancer patients.
 XX Claim 13; Page 246; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 24; DB 6; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
 DB 1 SPFCVWRL 9

RESULT 33
 ABR14464
 ID ABR14464 standard; peptide; 9 AA.
 XX
 AC ABR14464;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 156P5C12 HLA peptide #1399.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 CC New composition comprising a substance that modulates the structure of
 CC proteins and polynucleotides, useful for therapeutic, prognostic and
 CC diagnostic reagents for eliciting cellular or humoral immune response in
 CC cancer patients.
 XX
 PS Claim 13; Page 256; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein; as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 24; DB 6; Length 9;
 Best Local Similarity 22.2%; Pred. No. 1.8e+06;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
 DB 1 SPFCVWRL 9

RESULT 34
 ABR13820
 ID ABR13820 standard; peptide; 9 AA.
 XX
 AC ABR13820;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 156P5C12 HLA peptide #755.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 CC New composition comprising a substance that modulates the structure of
 CC proteins and polynucleotides, useful for therapeutic, prognostic and
 CC diagnostic reagents for eliciting cellular or humoral immune response in
 CC cancer patients.
 XX
 PS Claim 13; Page 250; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 24; DB 6; Length 9;

```
Best Local Similarity 22.2%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 7;

QY 1 XPXXXWXXX 9
   :|::|::|::
Db 1 LFPALWFLA 9

RESULT 35
ABR14018
ID ABR14018 standard; peptide; 9 AA.
XX AC ABR14018;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 156P5C12 HLA peptide #953.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 252; 1021pp; English.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 252; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC inhibiting the expression of the protein, as tools for modulating or
XX CC directing the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 9 AA;
    Query Match 100.0%; Score 24; DB 6; Length 9;
    Best Local Similarity 22.2%; Pred. No. 1.8e+06;
    Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XPXXXWXXX 9
   :|::|::|::
Db 1 LFPALWFLA 9

RESULT 36
ABR13966
ID ABR13966 standard; peptide; 9 AA.
XX AC ABR13966;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 156P5C12 HLA peptide #901.
XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX PS Claim 13; Page 246; 1021pp; English.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 246; 1021pp; English.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 246; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of the protein, as coding sequences capable of
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 9 AA;
    Query Match 100.0%; Score 24; DB 6; Length 9;
    Best Local Similarity 22.2%; Pred. No. 1.8e+06;
    Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XPXXXWXXX 9
   :|::|::|::
Db 1 LFPALWFLA 9

RESULT 37
ABR13966
ID ABR13966 standard; peptide; 9 AA.
XX AC ABR13966;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 156P5C12 HLA peptide #901.
XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX PS Claim 13; Page 246; 1021pp; English.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 246; 1021pp; English.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 246; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of the protein, as coding sequences capable of
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 9 AA;
    Query Match 100.0%; Score 24; DB 6; Length 9;
    Best Local Similarity 22.2%; Pred. No. 1.8e+06;
    Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XPXXXWXXX 9
   :|::|::|::
Db 1 LFPALWFLA 9
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XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2001; 2001US-0283112P.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX CC Sequence 9 AA;
XX CC
XX CC Query Match 100.0%; Score 24; DB 6; Length 9;
XX CC Best Local Similarity 22.2%; Pred. No. 1.8e+06;
XX CC Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1 XFXXWXXX 9
DB :|::|::|
1 SFFCVWRL 9

RESULT 38
ABR04164
ID ABR04164 standard; peptide; 9 AA.
XX AC ABR04164;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 74P3B3 HLA peptide #2299.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2001; 2001US-0283112P.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0286630P.

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PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response in
XX CC cancer patients.
XX CC Claim 13; Page 153; 1021pp; English.
XX CC
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX CC Sequence 9 AA;
XX CC
XX CC Query Match 100.0%; Score 24; DB 6; Length 9;
XX CC Best Local Similarity 22.2%; Pred. No. 1.8e+06;
XX CC Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1 XFXXWXXX 9
DB :|::|::|
1 QFKTWTDE 9

RESULT 39
ABR13839
ID ABR13839 standard; peptide; 9 AA.
XX AC ABR13839;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 156P5C12 HLA peptide #774.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2001; 2001US-0283112P.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX

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PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX
XX Claim 13; Page 250; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 6; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|::|::|
Db 1 SPFCVWRL 9

RESULT 40
ABJ63999
ID ABJ63999 standard; peptide; 9 AA.
XX
XX AC ABJ63999;
DT 16-OCT-2003 (first entry)
XX
XX DE 184PlE2-related HLA peptide #7046.
XX
XX Gene therapy; vaccine; 184PlE2; cancer; genetic abnormality;
KW cellular immune response; immunisation.
XX Unidentified.
XX
XX PN WO200283919-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011643.
XX
XX PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Chalitta-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
XX DR WPI; 2003-148269/14.
XX
XX PT New 184PlE2 polynucleotide encoding a 184PlE2 protein, useful for
PT diagnosing, prognosing, preventing or treating cancer, in eliciting an
PT immune response, and in chromosome mapping.
XX
XX PS Example 50; Page 218; 394pp; English.
XX
XX The invention comprises the amino acid and coding sequence of a 184PlE2
CC protein. The DNA and protein sequences of the invention are useful for
CC diagnosing, prognosing, preventing and/or treating cancer. The 184PlE2
CC DNA and protein sequences may also be used to elicit a humoral or a
CC cellular immune response in patients and in monitoring genetic

CC abnormalities. Antibodies raised against the 184PlE2 proteins may be used
CC in active or passive immunisation. The present amino acid sequence
CC represents a peptide that is used in the exemplification of the invention
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 24; DB 6; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.8e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXWXXX 9
:|::|::|
Db 1 PPSFKWNN 9

Search completed: October 19, 2005, 15:40:44
Job time : 126.353 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:41:05 ; Search time 31.2353 Seconds
(without alignments)
21.509 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	24	100.0	10	1	US-08-306-546C-24
5	24	100.0	10	1	US-08-242-678D-5
6	24	100.0	10	1	US-08-487-568-88
7	24	100.0	10	2	US-08-530-524A-24
8	24	100.0	10	2	US-08-370-909-17
9	24	100.0	10	2	US-08-318-157B-25
10	24	100.0	10	2	US-08-806-378B-3
11	24	100.0	10	3	US-09-186-958-11
12	24	100.0	10	3	US-09-333-441-3
13	24	100.0	10	3	US-09-669-271A-11
14	24	100.0	10	4	US-09-881-276-11
15	24	100.0	10	4	US-09-428-082B-142
16	24	100.0	10	4	US-09-253-794-25
17	24	100.0	10	4	US-09-239-043D-396
18	24	100.0	10	4	US-09-239-043D-907
19	24	100.0	10	4	US-09-239-043D-1654
20	24	100.0	10	4	US-09-620-091-46
21	24	100.0	11	1	US-08-318-970B-10
22	24	100.0	11	2	US-08-486-839-9
23	24	100.0	11	3	US-08-485-324-14
24	24	100.0	11	3	US-09-151-011-9
25	24	100.0	11	3	US-08-447-506-14
26	24	100.0	11	3	US-08-235-437-14
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29	24	100.0	11	3	US-09-186-958-6	Sequence 6, Appli
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31	24	100.0	11	3	US-09-186-958-8	Sequence 8, Appli
32	24	100.0	11	3	US-09-186-958-9	Sequence 9, Appli
33	24	100.0	11	3	US-09-186-958-10	Sequence 10, Appli
34	24	100.0	11	3	US-09-669-271A-4	Sequence 4, Appli
35	24	100.0	11	3	US-09-669-271A-6	Sequence 6, Appli
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42	24	100.0	11	4	US-09-461-325-504	Sequence 504, App
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84	24	100.0	12	4	US-09-752-165-65	Sequence 65, Appli
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102	24	100.0	13	1	US-08-305-871A-23	Sequence 23, Appl	175	24	100.0	15	1	US-08-424-957-22	Sequence 22, Appl
103	24	100.0	13	1	US-08-487-568-87	Sequence 87, Appl	176	24	100.0	15	1	US-08-487-568-112	Sequence 112, App
104	24	100.0	13	2	US-08-480-190-26	Sequence 26, Appl	177	24	100.0	15	2	US-08-621-803-9	Sequence 9, Appl
105	24	100.0	13	2	US-08-488-379-26	Sequence 26, Appl	178	24	100.0	15	2	US-08-485-445A-51	Sequence 51, Appl
106	24	100.0	13	2	US-08-806-378B-1	Sequence 1, Appl	179	24	100.0	15	2	US-08-553-257A-10	Sequence 10, Appl
107	24	100.0	13	3	US-08-911-79A-3	Sequence 3, Appl	180	24	100.0	15	2	US-08-553-257A-49	Sequence 49, Appl
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109	24	100.0	13	3	US-09-333-441-1	Sequence 11, Appl	182	24	100.0	15	2	US-08-553-257A-51	Sequence 51, Appl
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112	24	100.0	13	3	US-08-788-822A-27	Sequence 27, Appl	185	24	100.0	15	3	US-09-165-042-16	Sequence 16, Appl
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114	24	100.0	13	4	US-09-081-975-9	Sequence 9, Appl	187	24	100.0	15	3	US-08-847-844A-22	Sequence 22, Appl
115	24	100.0	13	4	US-08-475-399A-26	Sequence 26, Appl	188	24	100.0	15	3	US-09-035-686-1	Sequence 1, Appl
116	24	100.0	13	4	US-10-158-847-103	Sequence 103, App	189	24	100.0	15	3	US-09-035-686-21	Sequence 21, Appl
117	24	100.0	13	4	US-10-158-847-105	Sequence 105, App	190	24	100.0	15	3	US-09-035-686-22	Sequence 22, Appl
118	24	100.0	13	4	US-10-158-847-108	Sequence 108, App	191	24	100.0	15	3	US-09-224-480-51	Sequence 51, Appl
119	24	100.0	13	4	US-10-158-847-109	Sequence 109, App	192	24	100.0	15	3	US-08-702-054B-21	Sequence 21, Appl
120	24	100.0	13	4	US-10-158-847-110	Sequence 110, App	193	24	100.0	15	3	US-09-217-352-9	Sequence 9, Appl
121	24	100.0	13	4	US-09-543-608A-27	Sequence 27, App	194	24	100.0	15	3	US-09-063-733A-28	Sequence 28, Appl
122	24	100.0	13	4	US-08-077-255A-26	Sequence 26, App	195	24	100.0	15	4	US-09-009-953-247	Sequence 247, App
123	24	100.0	13	4	US-09-556-818-65	Sequence 65, Appl	196	24	100.0	15	4	US-08-487-795A-2	Sequence 2, Appl
124	24	100.0	13	4	US-09-695-437A-42	Sequence 42, Appl	197	24	100.0	15	4	US-08-487-795A-16	Sequence 16, Appl
125	24	100.0	13	5	PCT-US93-07545-26	Sequence 26, App	198	24	100.0	15	4	US-08-487-795A-17	Sequence 17, Appl
126	24	100.0	13	5	PCT-US94-01234-47	Sequence 47, Appl	199	24	100.0	15	4	US-08-121-105B-2	Sequence 2, Appl
127	24	100.0	13	6	5185431-25	Sequence 47, App	200	24	100.0	15	4	US-08-121-105B-16	Sequence 16, Appl
128	24	100.0	13	6	5185431-25	Patent No. 5185431	201	24	100.0	15	4	US-08-121-105B-17	Sequence 17, Appl
129	24	100.0	14	1	US-08-534-975-10	Sequence 10, Appl	202	24	100.0	15	4	US-09-081-975-24	Sequence 24, Appl
130	24	100.0	14	2	US-08-449-933-11	Sequence 11, Appl	203	24	100.0	15	4	US-09-461-325-295	Sequence 295, App
131	24	100.0	14	2	US-08-392-816-12	Sequence 12, Appl	204	24	100.0	15	4	US-09-914-259-155	Sequence 165, App
132	24	100.0	14	2	US-08-764-640-33	Sequence 33, Appl	205	24	100.0	15	4	US-08-634-332A-64	Sequence 64, Appl
133	24	100.0	14	2	US-08-954-470-10	Sequence 10, Appl	206	24	100.0	15	4	US-08-634-332A-65	Sequence 65, Appl
134	24	100.0	14	2	US-08-750-359-3	Sequence 3, Appl	207	24	100.0	15	4	US-08-634-332A-69	Sequence 69, Appl
135	24	100.0	14	2	US-08-750-359-4	Sequence 4, Appl	208	24	100.0	15	4	US-09-441-992-10	Sequence 10, Appl
136	24	100.0	14	2	US-08-685-589A-132	Sequence 192, App	209	24	100.0	15	4	US-09-441-992-49	Sequence 49, Appl
137	24	100.0	14	2	US-08-685-589A-133	Sequence 193, App	210	24	100.0	15	4	US-09-441-992-50	Sequence 50, Appl
138	24	100.0	14	2	US-08-806-378B-2	Sequence 2, Appl	211	24	100.0	15	4	US-09-441-992-51	Sequence 51, Appl
139	24	100.0	14	3	US-08-564-225-10	Sequence 10, Appl	212	24	100.0	15	4	US-09-441-992-52	Sequence 52, Appl
140	24	100.0	14	3	US-09-129-855A-10	Sequence 10, Appl	213	24	100.0	15	4	US-09-574-749B-54	Sequence 54, Appl
141	24	100.0	14	3	US-08-973-225-33	Sequence 33, Appl	214	24	100.0	15	4	US-09-644-442-7	Sequence 7, Appl
142	24	100.0	14	3	US-08-973-225-213	Sequence 213, App	215	24	100.0	15	4	US-09-157-689-51	Sequence 51, Appl
143	24	100.0	14	3	US-09-244-298A-33	Sequence 33, Appl	216	24	100.0	15	4	US-09-157-689-52	Sequence 52, Appl
144	24	100.0	14	3	US-09-247-154-10	Sequence 10, Appl	217	24	100.0	15	4	US-10-012-542-235	Sequence 235, App
145	24	100.0	14	3	US-07-966-049A-11	Sequence 11, Appl	218	24	100.0	15	4	US-09-428-082B-138	Sequence 138, App
146	24	100.0	14	3	US-09-516-704-33	Sequence 33, Appl	219	24	100.0	15	4	US-09-428-082B-139	Sequence 139, App
147	24	100.0	14	3	US-09-333-441-2	Sequence 2, Appl	220	24	100.0	15	4	US-09-428-082B-140	Sequence 140, App
148	24	100.0	14	4	US-09-480-718-10	Sequence 10, Appl	221	24	100.0	15	4	US-09-428-082B-141	Sequence 141, App
149	24	100.0	14	4	US-09-549-090-33	Sequence 33, Appl	222	24	100.0	15	4	US-09-689-097-53	Sequence 53, Appl
150	24	100.0	14	4	US-09-549-090-213	Sequence 213, App	223	24	100.0	15	4	US-09-239-043D-2142	Sequence 2142, Ap
151	24	100.0	14	4	US-09-461-325-508	Sequence 508, App	224	24	100.0	15	4	US-09-142-524D-88	Sequence 88, Appl
152	24	100.0	14	4	US-10-012-542-508	Sequence 10, Appl	225	24	100.0	15	4	US-10-115-123-295	Sequence 295, App
153	24	100.0	14	4	US-09-832-230A-33	Sequence 33, App	226	24	100.0	15	4	US-09-953-510-51	Sequence 51, Appl
154	24	100.0	14	4	US-09-129-855A-10	Sequence 10, Appl	227	24	100.0	15	4	US-09-953-510-52	Sequence 52, Appl
155	24	100.0	14	4	US-10-158-847-115	Sequence 115, App	228	24	100.0	15	4	US-09-581-472B-4	Sequence 4, Appl
156	24	100.0	14	4	US-10-158-847-116	Sequence 116, App	229	24	100.0	15	4	US-09-732-384-6	Sequence 6, Appl
157	24	100.0	14	4	US-10-158-847-119	Sequence 119, App	230	24	100.0	15	5	PCT-US93-08699-1	Sequence 1, Appl
158	24	100.0	14	4	US-10-012-542-508	Sequence 508, App	231	24	100.0	15	5	PCT-US94-02465-51	Sequence 51, Appl
159	24	100.0	14	4	US-09-428-082B-68	Sequence 68, Appl	232	24	100.0	15	5	PCT-US94-10356-2	Sequence 2, Appl
160	24	100.0	14	4	US-09-620-091-87	Sequence 87, Appl	233	24	100.0	15	5	PCT-US94-10356-6	Sequence 6, Appl
161	24	100.0	14	4	US-10-115-123-508	Sequence 508, App	234	24	100.0	15	5	PCT-US94-10356-20	Sequence 20, Appl
162	24	100.0	15	1	US-08-311-611A-51	Sequence 51, Appl	235	24	100.0	15	5	PCT-US95-00498-51	Sequence 51, Appl
163	24	100.0	15	1	US-08-218-025A-139	Sequence 139, App	236	24	100.0	15	5	PCT-US95-00656-51	Sequence 51, Appl
164	24	100.0	15	1	US-08-372-783-51	Sequence 51, Appl	237	24	100.0	16	1	US-07-959-946-5	Sequence 5, Appl
165	24	100.0	15	1	US-08-372-105-51	Sequence 51, Appl	238	24	100.0	16	1	US-08-079-051-2	Sequence 2, Appl
166	24	100.0	15	1	US-08-148-160-2	Sequence 2, Appl	239	24	100.0	16	1	US-08-077-797A-43	Sequence 43, Appl
167	24	100.0	15	1	US-08-306-473A-51	Sequence 51, Appl	240	24	100.0	16	1	US-08-473-344-51	Sequence 51, Appl
168	24	100.0	15	1	US-08-277-660A-1	Sequence 1, Appl	241	24	100.0	16	1	US-08-333-577-5	Sequence 5, Appl
169	24	100.0	15	1	US-08-277-660A-5	Sequence 5, Appl	242	24	100.0	16	2	US-08-629-291A-19	Sequence 19, Appl
170	24	100.0	15	1	US-08-207-660A-6	Sequence 6, Appl	243	24	100.0	16	2	US-08-658-335B-19	Sequence 19, Appl
171	24	100.0	15	1	US-08-209-762-51	Sequence 51, Appl	244	24	100.0	16	3	US-08-930-776-1	Sequence 1, Appl
172	24	100.0	15	1	US-08-625-691-10	Sequence 10, Appl	245	24	100.0	16	3	US-09-149-303-1	Sequence 1, Appl
173	24	100.0	15	1	US-08-424-957-1	Sequence 1, Appl	246	24	100.0	16	3	US-09-093-539-51	Sequence 51, Appl

247	24	100.0	16	4	US-09-009-953-39	Sequence 39, Appl	320	24	100.0	17	2	US-08-480-150-123	Sequence 123, App
248	24	100.0	16	4	US-09-009-953-230	Sequence 230, Appl	321	24	100.0	17	2	US-08-746-283-7	Sequence 7, Appl
249	24	100.0	16	4	US-09-458-745-1	Sequence 1, Appl	322	24	100.0	17	2	US-08-545-562A-64	Sequence 64, Appl
250	24	100.0	16	4	US-09-330-914A-11	Sequence 11, Appl	323	24	100.0	17	2	US-08-637-759B-238	Sequence 238, App
251	24	100.0	16	4	US-09-406-640-19	Sequence 19, Appl	324	24	100.0	17	2	US-08-746-257A-5	Sequence 5, Appl
252	24	100.0	16	4	US-09-081-975-23	Sequence 23, Appl	325	24	100.0	17	2	US-08-488-379-123	Sequence 123, App
253	24	100.0	16	4	US-09-790-230-51	Sequence 51, Appl	326	24	100.0	17	3	US-08-871-355A-238	Sequence 238, App
254	24	100.0	16	4	US-08-413-233-3	Sequence 3, Appl	327	24	100.0	17	3	US-08-990-823-88	Sequence 88, Appl
255	24	100.0	16	4	US-09-690-454-88	Sequence 88, Appl	328	24	100.0	17	3	US-08-990-823-89	Sequence 89, Appl
256	24	100.0	16	4	US-09-311-784A-308	Sequence 308, App	329	24	100.0	17	3	US-09-082-279B-814	Sequence 814, App
257	24	100.0	16	4	US-09-170-496D-285	Sequence 285, App	330	24	100.0	17	3	US-09-201-945-238	Sequence 238, App
258	24	100.0	16	4	US-09-546-013-72	Sequence 72, Appl	331	24	100.0	17	3	US-09-315-304B-814	Sequence 814, App
259	24	100.0	16	4	US-09-620-091-89	Sequence 89, Appl	332	24	100.0	17	4	US-08-487-795A-15	Sequence 15, Appl
260	24	100.0	16	4	US-09-854-133-587	Sequence 587, App	333	24	100.0	17	4	US-08-121-105B-15	Sequence 15, Appl
261	24	100.0	16	4	US-09-541-345-4	Sequence 4, Appl	334	24	100.0	17	4	US-08-475-399A-123	Sequence 123, App
262	24	100.0	16	4	US-09-541-345-20	Sequence 20, Appl	335	24	100.0	17	4	US-09-170-496D-286	Sequence 286, App
263	24	100.0	16	4	US-09-541-345-35	Sequence 35, Appl	336	24	100.0	17	4	US-09-834-784-814	Sequence 814, App
264	24	100.0	16	4	US-09-541-345-37	Sequence 37, Appl	337	24	100.0	17	4	US-09-477-135A-88	Sequence 88, Appl
265	24	100.0	16	4	US-09-541-345-38	Sequence 38, Appl	338	24	100.0	17	4	US-09-477-135A-89	Sequence 89, Appl
266	24	100.0	16	4	US-09-541-345-39	Sequence 39, Appl	339	24	100.0	17	4	US-09-515-965A-814	Sequence 814, App
267	24	100.0	16	4	US-09-541-345-40	Sequence 40, Appl	340	24	100.0	17	4	US-09-350-641C-814	Sequence 814, App
268	24	100.0	16	4	US-09-541-345-41	Sequence 41, Appl	341	24	100.0	17	4	US-09-428-082B-209	Sequence 209, App
269	24	100.0	16	4	US-09-541-345-42	Sequence 42, Appl	342	24	100.0	17	4	US-08-077-255A-123	Sequence 123, App
270	24	100.0	16	4	US-09-541-345-43	Sequence 43, Appl	343	24	100.0	17	4	US-09-350-841A-814	Sequence 814, App
271	24	100.0	16	4	US-09-541-345-44	Sequence 44, Appl	344	24	100.0	17	4	US-09-695-437A-40	Sequence 40, Appl
272	24	100.0	16	4	US-09-541-345-45	Sequence 45, Appl	345	24	100.0	17	5	PCT-US93-07545-123	Sequence 123, App
273	24	100.0	16	4	US-09-541-345-46	Sequence 46, Appl	346	24	100.0	17	5	PCT-US94-05684-7	Sequence 7, Appl
274	24	100.0	16	4	US-09-541-345-47	Sequence 47, Appl	347	24	100.0	17	5	PCT-US94-10356-19	Sequence 19, Appl
275	24	100.0	16	4	US-09-541-345-48	Sequence 48, Appl	348	24	100.0	18	1	US-08-218-025A-3	Sequence 3, Appl
276	24	100.0	16	4	US-09-541-345-50	Sequence 50, Appl	349	24	100.0	18	1	US-08-375-100-3	Sequence 3, Appl
277	24	100.0	16	4	US-09-541-345-51	Sequence 51, Appl	350	24	100.0	18	2	US-08-248-839C-166	Sequence 166, App
278	24	100.0	16	4	US-09-541-345-52	Sequence 52, Appl	351	24	100.0	18	2	US-08-934-915-125	Sequence 125, App
279	24	100.0	16	4	US-09-541-345-53	Sequence 53, Appl	352	24	100.0	18	3	US-08-940-095-199	Sequence 199, App
280	24	100.0	16	4	US-09-541-345-55	Sequence 55, Appl	353	24	100.0	18	3	US-08-940-095-224	Sequence 224, App
281	24	100.0	16	4	US-09-541-345-56	Sequence 56, Appl	354	24	100.0	18	3	US-08-940-093-199	Sequence 199, App
282	24	100.0	16	4	US-09-541-345-57	Sequence 57, Appl	355	24	100.0	18	3	US-08-940-093-224	Sequence 224, App
283	24	100.0	16	4	US-09-541-345-58	Sequence 58, Appl	356	24	100.0	18	3	US-08-940-096-199	Sequence 199, App
284	24	100.0	16	4	US-09-541-345-59	Sequence 59, Appl	357	24	100.0	18	3	US-08-940-096-224	Sequence 224, App
285	24	100.0	16	4	US-09-541-345-61	Sequence 61, Appl	358	24	100.0	18	3	US-08-513-968-40	Sequence 40, Appl
286	24	100.0	16	4	US-09-541-345-62	Sequence 62, Appl	359	24	100.0	18	3	US-09-082-279B-1147	Sequence 1147, App
287	24	100.0	16	4	US-09-541-345-63	Sequence 63, Appl	360	24	100.0	18	3	US-09-465-719-199	Sequence 199, App
288	24	100.0	16	4	US-09-541-345-64	Sequence 64, Appl	361	24	100.0	18	3	US-09-465-719-224	Sequence 224, App
289	24	100.0	16	4	US-09-541-345-66	Sequence 66, Appl	362	24	100.0	18	3	US-09-025-769B-249	Sequence 249, App
290	24	100.0	16	4	US-09-541-345-68	Sequence 68, Appl	363	24	100.0	18	3	US-09-453-605-199	Sequence 199, App
291	24	100.0	16	4	US-09-541-345-69	Sequence 69, Appl	364	24	100.0	18	3	US-09-453-605-224	Sequence 224, App
292	24	100.0	16	4	US-09-541-345-71	Sequence 71, Appl	365	24	100.0	18	3	US-09-315-304B-1147	Sequence 1147, App
293	24	100.0	16	4	US-09-541-345-73	Sequence 73, Appl	366	24	100.0	18	3	US-09-453-838-199	Sequence 199, App
294	24	100.0	16	4	US-09-541-345-74	Sequence 74, Appl	367	24	100.0	18	3	US-09-453-838-224	Sequence 224, App
295	24	100.0	16	4	US-09-541-345-75	Sequence 75, Appl	368	24	100.0	18	4	US-09-081-975-22	Sequence 22, Appl
296	24	100.0	16	4	US-09-541-345-76	Sequence 76, Appl	369	24	100.0	18	4	US-08-940-136-199	Sequence 199, App
297	24	100.0	16	4	US-09-541-345-77	Sequence 77, Appl	370	24	100.0	18	4	US-08-940-136-224	Sequence 224, App
298	24	100.0	16	4	US-09-541-345-79	Sequence 79, Appl	371	24	100.0	18	4	US-08-634-332A-8	Sequence 8, Appl
299	24	100.0	16	4	US-09-541-345-81	Sequence 81, Appl	372	24	100.0	18	4	US-08-634-332A-9	Sequence 9, Appl
300	24	100.0	16	4	US-09-541-345-83	Sequence 83, Appl	373	24	100.0	18	4	US-08-634-332A-10	Sequence 10, Appl
301	24	100.0	16	4	US-09-541-345-84	Sequence 84, Appl	374	24	100.0	18	4	US-08-634-332A-11	Sequence 11, Appl
302	24	100.0	16	4	US-09-541-345-85	Sequence 85, Appl	375	24	100.0	18	4	US-08-634-332A-12	Sequence 12, Appl
303	24	100.0	16	4	US-09-541-345-86	Sequence 86, Appl	376	24	100.0	18	4	US-08-634-332A-13	Sequence 13, Appl
304	24	100.0	16	4	US-09-541-345-89	Sequence 89, Appl	377	24	100.0	18	4	US-08-634-332A-24	Sequence 24, Appl
305	24	100.0	16	4	US-09-541-345-91	Sequence 91, Appl	378	24	100.0	18	4	US-08-634-332A-25	Sequence 25, Appl
306	24	100.0	16	4	US-09-541-345-92	Sequence 92, Appl	379	24	100.0	18	4	US-08-634-332A-62	Sequence 62, Appl
307	24	100.0	16	4	US-09-541-345-96	Sequence 96, Appl	380	24	100.0	18	4	US-08-634-332A-63	Sequence 63, Appl
308	24	100.0	16	4	US-09-541-345-98	Sequence 98, Appl	381	24	100.0	18	4	US-09-834-784-1147	Sequence 1147, App
309	24	100.0	16	4	US-09-541-345-99	Sequence 99, Appl	382	24	100.0	18	4	US-09-453-841-199	Sequence 199, App
310	24	100.0	16	4	US-09-541-345-100	Sequence 100, App	383	24	100.0	18	4	US-09-453-841-224	Sequence 224, App
311	24	100.0	16	4	US-09-541-345-104	Sequence 104, App	384	24	100.0	18	4	US-10-158-847-78	Sequence 78, Appl
312	24	100.0	16	4	US-09-541-345-105	Sequence 105, App	385	24	100.0	18	4	US-10-158-847-88	Sequence 88, Appl
313	24	100.0	16	4	US-09-541-345-106	Sequence 106, App	386	24	100.0	18	4	US-10-158-847-120	Sequence 120, App
314	24	100.0	16	4	US-09-269-703A-1	Sequence 1, Appl	387	24	100.0	18	4	US-09-453-833-199	Sequence 199, App
315	24	100.0	16	5	PCT-US92-08634-5	Sequence 5, Appl	388	24	100.0	18	4	US-09-453-833-224	Sequence 224, App
316	24	100.0	16	5	PCT-US94-01238-43	Sequence 43, Appl	389	24	100.0	18	4	US-09-515-965A-1147	Sequence 1147, App
317	24	100.0	16	5	PCT-US94-06994-2	Sequence 2, Appl	390	24	100.0	18	4	US-09-453-826-199	Sequence 199, App
318	24	100.0	17	1	US-08-370-567-7	Sequence 7, Appl	391	24	100.0	18	4	US-09-453-826-224	Sequence 224, App
319	24	100.0	17	1	US-08-438-759-7	Sequence 7, Appl	392	24	100.0	18	4	US-09-350-641C-1147	Sequence 1147, App

393	24	100.0	18	4	US-09-490-070A-249	Sequence 249, App	466	24	100.0	20	1	US-08-306-473A-151	Sequence 151, App
394	24	100.0	18	4	US-09-490-153-249	Sequence 249, App	467	24	100.0	20	1	US-08-306-473A-152	Sequence 152, App
395	24	100.0	18	4	US-09-620-091-195	Sequence 195, App	468	24	100.0	20	1	US-08-306-473A-159	Sequence 159, App
396	24	100.0	18	4	US-09-453-840-199	Sequence 199, App	469	24	100.0	20	1	US-08-306-473A-160	Sequence 160, App
397	24	100.0	18	4	US-09-453-840-224	Sequence 224, App	470	24	100.0	20	1	US-08-209-762-54	Sequence 54, Appl
398	24	100.0	18	4	US-09-865-989-199	Sequence 199, App	471	24	100.0	20	1	US-08-209-762-57	Sequence 57, Appl
399	24	100.0	18	4	US-09-865-989-224	Sequence 224, App	472	24	100.0	20	1	US-08-209-762-58	Sequence 58, Appl
400	24	100.0	18	4	US-09-350-841A-1147	Sequence 1147, App	473	24	100.0	20	1	US-08-209-762-59	Sequence 59, Appl
401	24	100.0	18	4	US-09-453-834-199	Sequence 199, App	474	24	100.0	20	1	US-08-473-344-54	Sequence 54, Appl
402	24	100.0	18	4	US-09-453-834-224	Sequence 224, App	475	24	100.0	20	2	US-08-493-235-31	Sequence 31, Appl
403	24	100.0	18	4	US-09-695-437A-63	Sequence 63, Appl	476	24	100.0	20	2	US-08-621-803-7	Sequence 7, Appl
404	24	100.0	18	4	US-09-695-437A-64	Sequence 64, Appl	477	24	100.0	20	2	US-08-621-803-47	Sequence 47, Appl
405	24	100.0	18	4	US-09-774-639-236	Sequence 236, App	478	24	100.0	20	2	US-08-621-803-48	Sequence 48, Appl
406	24	100.0	18	4	US-09-490-324-249	Sequence 249, App	479	24	100.0	20	2	US-08-621-803-49	Sequence 49, Appl
407	24	100.0	19	2	US-08-537-400-35	Sequence 35, Appl	480	24	100.0	20	2	US-08-621-803-120	Sequence 120, App
408	24	100.0	19	3	US-08-574-549A-118	Sequence 118, App	481	24	100.0	20	2	US-08-621-803-148	Sequence 148, App
409	24	100.0	19	3	US-09-252-149B-8	Sequence 8, Appl	482	24	100.0	20	2	US-08-485-445A-54	Sequence 54, Appl
410	24	100.0	19	4	US-09-081-975-13	Sequence 13, Appl	483	24	100.0	20	2	US-08-485-445A-57	Sequence 57, Appl
411	24	100.0	19	4	US-09-461-325-291	Sequence 291, App	484	24	100.0	20	2	US-08-485-445A-58	Sequence 58, Appl
412	24	100.0	19	4	US-09-489-847-359	Sequence 359, App	485	24	100.0	20	2	US-08-485-445A-59	Sequence 59, Appl
413	24	100.0	19	4	US-09-489-847-360	Sequence 360, App	486	24	100.0	20	2	US-08-485-445A-101	Sequence 101, App
414	24	100.0	19	4	US-09-402-181B-118	Sequence 118, App	487	24	100.0	20	2	US-08-485-445A-150	Sequence 150, App
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416	24	100.0	19	4	US-10-012-542-291	Sequence 291, App	489	24	100.0	20	2	US-08-485-445A-152	Sequence 152, App
417	24	100.0	19	4	US-09-794-529B-9	Sequence 9, Appl	490	24	100.0	20	2	US-08-485-445A-159	Sequence 159, App
418	24	100.0	19	4	US-09-794-517A-9	Sequence 9, Appl	491	24	100.0	20	2	US-08-485-445A-160	Sequence 160, App
419	24	100.0	19	4	US-09-011-645B-9	Sequence 9, Appl	492	24	100.0	20	2	US-08-253-751-1	Sequence 1, Appl
420	24	100.0	19	4	US-09-794-834-9	Sequence 9, Appl	493	24	100.0	20	2	US-08-253-751-2	Sequence 2, Appl
421	24	100.0	19	4	US-09-732-357B-9	Sequence 9, Appl	494	24	100.0	20	2	US-08-714-677-17	Sequence 17, Appl
422	24	100.0	19	4	US-09-680-806A-9	Sequence 9, Appl	495	24	100.0	20	2	US-08-393-540-17	Sequence 17, Appl
423	24	100.0	19	4	US-09-552-868-9	Sequence 9, Appl	496	24	100.0	20	2	US-08-714-537-17	Sequence 17, Appl
424	24	100.0	19	4	US-09-636-295-9	Sequence 9, Appl	497	24	100.0	20	2	US-08-637-759B-294	Sequence 294, App
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435	24	100.0	20	1	US-08-311-611A-152	Sequence 152, App	508	24	100.0	20	3	US-09-119-263-57	Sequence 57, Appl
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437	24	100.0	20	1	US-08-311-611A-160	Sequence 160, App	510	24	100.0	20	3	US-09-119-263-59	Sequence 59, App
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454	24	100.0	20	1	US-08-372-105-150	Sequence 150, App	527	24	100.0	20	3	US-08-612-973-83	Sequence 83, Appl
455	24	100.0	20	1	US-08-372-105-151	Sequence 151, App	528	24	100.0	20	3	US-09-224-480-54	Sequence 54, Appl
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689	23	95.8	8	4	US-09-552-866-4	Sequence 4, Appli	762	23	95.8	10	2	US-08-922-048-135	Sequence 134, App
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693	23	95.8	8	6	5514646-28	Patent No. 5514646	766	23	95.8	10	2	US-08-922-048-138	Sequence 138, App
694	23	95.8	8	6	5514646-28	Patent No. 5514646	767	23	95.8	10	2	US-08-922-048-139	Sequence 139, App
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698	23	95.8	9	1	US-08-350-884-14	Sequence 14, Appl	771	23	95.8	10	2	US-08-922-048-143	Sequence 143, App
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701	23	95.8	9	1	US-08-709-173-11	Sequence 11, Appl	774	23	95.8	10	2	US-08-922-048-146	Sequence 146, App
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707	23	95.8	9	1	US-08-638-911A-21	Sequence 21, Appl	780	23	95.8	10	3	US-08-974-899-10	Sequence 10, Appl
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ALIGNMENTS

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; APPLICANT: Kubo, Ralph T.
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; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 985:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-985

Query Match 100.0%; Score 24; DB 3; Length 9;
Best Local Similarity 22.2%; Pred. No. 4.1e+05;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|:::|:::
Db 1 KFWLWVKAK 9

RESULT 2
US-09-239-043D-774
; Sequence 774, Application US/09239043D
; Patent No. 6689383
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-774

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred. No. 4.1e+05;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|:::|:::
Db 1 IPFCLWVVI 9


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RESULT 3
US-09-239-043D-2028
; Sequence 2028, Application US/092339043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Eteban
; APPLICANT: Kubo, Howard M.
; APPLICANT: Grey, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2028
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2028

Query Match 100.0%; Score 24; DB 4; Length 9;
Best Local Similarity 22.2%; Pred. No. 4.1e+05;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 IPFCLWVI 9

RESULT 4
US-08-306-546C-24
; Sequence 24, Application US/08306546C
; Patent No. 5605797
; GENERAL INFORMATION:
; APPLICANT: Friderici, Karen
; APPLICANT: Jones, Margaret
; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,546C
; FILING DATE: September 15, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-306-546C-24

Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 VFFYPWKM 10

RESULT 5
US-08-242-678D-5
; Sequence 5, Application US/08242678D
; Patent No. 5760000
; GENERAL INFORMATION:
; APPLICANT: HABIBI, Hamid R.
; TITLE OF INVENTION: INHIBITION OF LIVER CANCER BY THE USE OF
; TITLE OF INVENTION: GNRH AND GNRH ANALOGS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,678D
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 028722-103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= AA1
OTHER INFORMATION: /note= "AA1 is D-AA, and is PYROGLUTAMIC ACID"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= AA2
OTHER INFORMATION: /note= "AA2 is D-AA"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /label= AA3
OTHER INFORMATION: /note= "AA3 is D-AA"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= AA6
OTHER INFORMATION: /note= "AA6 is D-Trp"
US-08-242-678D-5

Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 2.1e+03;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
DB 1 XFWYWLRP 9

RESULT 6
US-08-487-568-88
Sequence 88, Application US/08487568
Patent No. 5770563
GENERAL INFORMATION:
APPLICANT: Roberts, David D.
APPLICANT: Browning, Philip J.
APPLICANT: Bryant, Joseph L.
APPLICANT: Inman, John K.
APPLICANT: Kruttsch, Henry C.
APPLICANT: Guo, Nenghua
TITLE OF INVENTION: Heparin and Sulfatide Binding Peptides
TITLE OF INVENTION: from the Type-I Repeats of Human Trombospondin and
TITLE OF INVENTION: Conjugates Thereof
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,568
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,085
FILING DATE: 21-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,812
FILING DATE: 06-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 015280-023310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Xaa = Lys or
OTHER INFORMATION: alpha-N-acetyl-lysine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /note= "Xaa = Gln or Ala"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Xaa = Asp or Ala"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Xaa = His or Pro"
US-08-487-568-88
Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.1e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXWXXX 9
DB 2 KFXXXWSXW 10
RESULT 7
US-08-530-524A-24
Sequence 24, Application US/08530524A
Patent No. 5837836
GENERAL INFORMATION:
APPLICANT: Friderici, Karen
APPLICANT: Jones, Margaret
APPLICANT: Chen, Hong
APPLICANT: Cavanagh, Kevin
TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,524A
FILING DATE: September 19, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36,683

REFERENCE/DOCKET NUMBER: 6550-00003DVA
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-530-524A-24

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 2 VFYPWKPM 10

RESULT 8
US-08-370-909-17
Sequence 17, Application US/08370909
Patent No. 5843648
GENERAL INFORMATION:
APPLICANT: ROBBINS, PAUL F.; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: p15 AND TYROSINASE
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC
TITLE OF INVENTION: AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,909
FILING DATE: 10-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4155
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-370-909-17

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 1 LFLLRWEQ 9

RESULT 9
US-08-318-157B-25
Sequence 25, Application US/08318157B
Patent No. 5874540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-157B-25

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 2 YGFFWFAY 10

RESULT 10
US-08-806-378B-3
Sequence 3, Application US/08806378B
Patent No. 5994308
GENERAL INFORMATION:
APPLICANT: Lawyer M.D., Carl H
APPLICANT: Watabe, Kounosuke
TITLE OF INVENTION: BROAD SPECTRUM ANTIMICROBIAL
TITLE OF INVENTION: PEPTIDES CONTAINING A TRYPTOPHAN TRIPLET AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Senniger, Powers, Leavitt & Roedel
STREET: One Metropolitan Square, 16th floor
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

; GENERAL INFORMATION:
; APPLICANT: LAWYER, CARL H.
; APPLICANT: WATABE, KOUNOSUKE
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTIMICROBIAL PEPTIDES
; FILE REFERENCES: SIU7391

```

```

; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayette
; TITLE OF INVENTION: Binding Moisties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881.276

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; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ IDNOS: 27

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; SOFTWARE: Microsoft Word 97
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polype
US-09-881-276-11

Query Match 100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
Db 1 FFCQYWNC 9

RESULT 15
US-09-428-082B-142
; Sequence 142, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 142
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDV/HDM ANTAGONIST PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (2, 4, 8)..(9)
; OTHER INFORMATION: Xaa = any amino acid
US-09-428-082B-142

Query Match 100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
Db 2 XFXYWXXL 10

RESULT 16
US-09-253-794-25
; Sequence 25, Application US/09253794
; Patent No. 6676524
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-253-794-25

Query Match 100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
Db 2 YFGPWFAY 10

RESULT 17
US-09-239-043D-396
; Sequence 396, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060, 0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
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/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/197,484
/ PRIOR FILING DATE: 1994-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 396
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-396

Query Match      100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 IFPCLWVYI 10

RESULT 18
US-09-239-043D-907
/ Sequence 907, Application US/092339043D
/ Patent No. 6689363
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Vitiello, Maria A.
/ APPLICANT: Livingston, Brian D.
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
/ FILE REFERENCE: 2060.0060007
/ CURRENT APPLICATION NUMBER: US/09/239,043D
/ CURRENT FILING DATE: 1999-01-27
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/978,291
/ PRIOR FILING DATE: 1997-11-25
/ PRIOR APPLICATION NUMBER: US 08/820,360
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: US 60/013,363
/ PRIOR FILING DATE: 1996-03-13
/ PRIOR APPLICATION NUMBER: US 08/461,603
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ PRIOR APPLICATION NUMBER: US 08/344,824
/ PRIOR FILING DATE: 1994-11-23
/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/197,484
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 907
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-907

Query Match      100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 IFPCLWVYI 10

RESULT 19
US-09-239-043D-1654
/ Sequence 1654, Application US/09239043D
/ Patent No. 6689363
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Vitiello, Maria A.
/ APPLICANT: Livingston, Brian D.
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
/ FILE REFERENCE: 2060.0060007
/ CURRENT APPLICATION NUMBER: US/09/239,043D
/ CURRENT FILING DATE: 1999-01-27
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/978,291
/ PRIOR FILING DATE: 1997-11-25
/ PRIOR APPLICATION NUMBER: US 08/820,360
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: US 60/013,363
/ PRIOR FILING DATE: 1996-03-13
/ PRIOR APPLICATION NUMBER: US 08/461,603
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ PRIOR APPLICATION NUMBER: US 08/344,824
/ PRIOR FILING DATE: 1994-11-23
/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/197,484
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1654
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1654

Query Match      100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 IFPCLWVYI 10

RESULT 20
US-09-620-091-46
/ Sequence 46, Application US/09620091
/ Patent No. 6716811
/ GENERAL INFORMATION:
/ APPLICANT: CWIRLA, STEVEN E.
```

APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: PIPLANI, SUNILA
APPLICANT: MERRILL, BARBARA MCEOWEN
APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
FILE REFERENCE: 0300-0014
CURRENT APPLICATION NUMBER: US/09/620,091
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-620-091-46

Query Match 100.0%; Score 24; DB 4; Length 10;
Best Local Similarity 22.2%; Pred. No. 2.1e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|::|::|::
Db 1 CFWSDWGQT 9

RESULT 21
US-08-318-970B-10
Sequence 10, Application US/08318970B
Patent No. 5589573
GENERAL INFORMATION:
APPLICANT: HIGEAKI HAGIWARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: S-2371
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: H-CDR3-3
OTHER INFORMATION: hypervariable region

US-08-318-970B-10

Query Match 100.0%; Score 24; DB 1; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|::|::|::
Db 2 GFLRDWYFD 10

RESULT 22
US-08-486-839-9
Sequence 9, Application US/08486839
Patent No. 5928928
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
TITLE OF INVENTION: production, its use for decomposing chitin, its use
TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07 - June - 1995
ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-486-839-9

Query Match 100.0%; Score 24; DB 2; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|::|::|::
Db 3 GFLDWEYP 11

RESULT 23
US-08-485-324-14
Sequence 14, Application US/08485324
Patent No. 6043093
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford

ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-324-14

Query Match 100.0%; Score 24; DB 3; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
Db 1 QFINMWQEV 9

RESULT 24
US-09-151-011-9
Sequence 9, Application US/09151011
Patent No. 6057142
GENERAL INFORMATION:
APPLICANT: A Human Chitinase, Its Recombinant
TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use in
TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 6900 Jericho Turnpike
CITY: Syosset
STATE: New York
COUNTRY: United States of America
ZIP: 11791
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
NAME: Morris, Robert C.
REGISTRATION NUMBER: 42,910

REFERENCE/DOCKET NUMBER: 294-32 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-151-011-9

Query Match 100.0%; Score 24; DB 3; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
Db 3 GFDDWDEYP 11

RESULT 25
US-08-447-506-14
Sequence 14, Application US/08447506
Patent No. 6066499
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-506-14

Query Match 100.0%; Score 24; DB 3; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9

	Db	: :: :::	1 QFINMWQEV 9	
		RESULT 26		
		US-08-235-437-14		
		; Sequence 14, Application US/08235437		
		; Patent No. 6087177		
		; GENERAL INFORMATION:		
		; APPLICANT: Wohlstadter, Jacob		
		; TITLE OF INVENTION: SELECTION METHODS		
		; NUMBER OF SEQUENCES: 31		
		; CORRESPONDENCE ADDRESS:		
		; ADDRESSEE: Curtis, Morris, & Safford		
		; ADDRESSEE: c/o Barry Evans		
		; STREET: 530 Fifth Avenue		
		; CITY: New York		
		; STATE: New York		
		; COUNTRY: USA		
		; ZIP: 10036		
		; COMPUTER READABLE FORM:		
		; MEDIUM TYPE: Floppy disk		
		; OPERATING SYSTEM: PC-DOS/MS-DOS		
		; SOFTWARE: PatentIn Release #1.0, Version #1.25		
		; CURRENT APPLICATION DATA:		
		; APPLICATION NUMBER: US/08/235,437		
		; FILING DATE: 29-APR-1994		
		; CLASSIFICATION: 435		
		; PRIOR APPLICATION NUMBER: US 07/852,412		
		; FILING DATE: 16-MAR-1992		
		; NAME: Evans, Barry		
		; ATTORNEY/AGENT INFORMATION:		
		; REGISTRATION NUMBER: 22,802		
		; REFERENCE/DOCKET NUMBER: 370132-2000		
		; TELECOMMUNICATION INFORMATION:		
		; TELEPHONE: (212) 840-3333		
		; TELEFAX: (212) 840-0712		
		; INFORMATION FOR SEQ ID NO: 14:		
		; SEQUENCE CHARACTERISTICS:		
		; LENGTH: 11 amino acids		
		; TYPE: amino acid		
		; STRANDEDNESS: single		
		; TOPOLOGY: linear		
		US-08-235-437-14		
		Query Match 100.0%; Score 24; DB 3; Length 11;		
		Best Local Similarity 22.2%; Pred.No. 2.3e+03;		
		Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;		
		QY 1 XFXXXWXXX 9		
		: :: :::		
		Db 1 QFINMWQEV 9		
		RESULT 27		
		US-08-447-515-14		
		; Sequence 14, Application US/08447515		
		; Patent No. 6162640		
		; GENERAL INFORMATION:		
		; APPLICANT: Wohlstadter, Jacob		
		; TITLE OF INVENTION: SELECTION METHODS		
		; NUMBER OF SEQUENCES: 31		
		; CORRESPONDENCE ADDRESS:		
		; ADDRESSEE: Curtis, Morris, & Safford		
		; ADDRESSEE: c/o Barry Evans		
		; STREET: 530 Fifth Avenue		
		; CITY: New York		
		; STATE: New York		
		; COUNTRY: USA		
		; ZIP: 10036		
		; COMPUTER READABLE FORM:		
		; MEDIUM TYPE: Floppy disk		
		; OPERATING SYSTEM: PC-DOS/MS-DOS		
		; SOFTWARE: PatentIn Release #1.0, Version #1.25		
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		; FILING DATE: 29-APR-1994		
		; CLASSIFICATION: 435		
		; PRIOR APPLICATION NUMBER: US 07/852,412		
		; FILING DATE: 16-MAR-1992		
		; NAME: Evans, Barry		
		; ATTORNEY/AGENT INFORMATION:		
		; REGISTRATION NUMBER: 22,802		
		; REFERENCE/DOCKET NUMBER: 370132-2000		
		; TELECOMMUNICATION INFORMATION:		
		; TELEPHONE: (212) 840-3333		
		; TELEFAX: (212) 840-0712		
		; INFORMATION FOR SEQ ID NO: 14:		
		; SEQUENCE CHARACTERISTICS:		
		; LENGTH: 11 amino acids		
		; TYPE: amino acid		
		; STRANDEDNESS: single		
		; TOPOLOGY: linear		
		US-08-235-437-14		
		Query Match 100.0%; Score 24; DB 3; Length 11;		
		Best Local Similarity 22.2%; Pred.No. 2.3e+03;		
		Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;		
		QY 1 XFXXXWXXX 9		
		: :: :::		
		Db 1 QFINMWQEV 9		
		RESULT 28		
		US-09-186-958-4		
		; Sequence 4, Application US/09186958B		
		; Patent No. 6238860		
		; GENERAL INFORMATION:		
		; APPLICANT: Whelihan, E. Payelle		
		; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19		
		; FILE REFERENCE: Dyax-009.0 US sequence listing		
		; CURRENT APPLICATION NUMBER: US/09/186,958B		
		; CURRENT FILING DATE: 1998-11-05		
		; NUMBER OF SEQ ID NOS: 27		
		; SOFTWARE: Patentin Ver. 2.1		
		; SEQ ID NO 4		
		; LENGTH: 11		
		; TYPE: PRT		
		; ORGANISM: Artificial Sequence		
		; FEATURE:		
		; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide		
		US-09-186-958-4		
		Query Match 100.0%; Score 24; DB 3; Length 11;		


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? CURRENT APPLICATION NUMBER: US/09/869,127/1A
?
? CURRENT FILING DATE: 2000-09-26
? PRIOR APPLICATION NUMBER: 09/186,958
? PRIOR FILING DATE: 1998-11-05
?
? NUMBER OF SEQ ID NOS: 27
? SOFTWARE: PatentIn ver. 2.1
? SEQ ID NO 9
? LENGTH: 11
? TYPE: PRT
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19

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; OTHER INFORMATION: binding polypeptide
US-09-669-271A-9

Query Match 100.0%; Score 24; DB 3; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
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Db 1 LFCSPWYNC 9

RESULT 39

US-09-669-271A-10
; Sequence 10, Application US/09669271A
; Patent No. 6291197
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyex-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/669,271A
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; OTHER INFORMATION: binding polypeptide
US-09-669-271A-10

Query Match 100.0%; Score 24; DB 3; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|::|::|::
Db 1 LFCRFWYNC 9

RESULT 40

US-09-343-623-9
; Sequence 9, Application US/09343623
; Patent No. 6303118
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for decomposing chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/343,623
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,839
; FILING DATE: 07-June-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-343-623-9

Query Match 100.0%; Score 24; DB 3; Length 11;
Best Local Similarity 22.2%; Pred. No. 2.3e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
:|::|::|::
Db 3 GFDDLWYYP 11

Search completed: October 19, 2005, 15:52:05
Job time : 32.2353 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:37:00 ; Search time 114.882 Seconds
(without alignments)
32.655 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFXXWXXX 9

Scoring table: BLOSUM62DX
Gapop 10.0 ; Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 377382

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	24	100.0	9	9 US-09-214-371-55	Sequence 55, Appl
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5	24	100.0	9	9 US-09-214-371-59	Sequence 59, Appl
6	24	100.0	9	10 US-09-793-451-336	Sequence 336, Appl
7	24	100.0	9	14 US-10-062-109A-372	Sequence 372, Appl
8	24	100.0	9	14 US-10-005-480A-372	Sequence 372, Appl
9	24	100.0	9	14 US-10-283-722-336	Sequence 336, Appl
10	24	100.0	9	15 US-10-334-726-212	Sequence 212, Appl
11	24	100.0	9	15 US-10-283-903-336	Sequence 336, Appl

12	24	100.0	9	15 US-10-363-208-237	Sequence 237, Appl
13	24	100.0	9	15 US-10-258-146A-177	Sequence 177, Appl
14	24	100.0	9	16 US-10-340-179-1	Sequence 1, Appl
15	24	100.0	9	16 US-10-363-204-198	Sequence 198, Appl
16	24	100.0	9	16 US-10-685-838-12	Sequence 12, Appl
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254	24	100.0	12	17	US-10-873-848B-1	Sequence 1, App	327	24	100.0	13	16	US-10-158-825-108	Sequence 108, App
255	24	100.0	12	17	US-10-873-848B-2	Sequence 2, App	328	24	100.0	13	16	US-10-158-825-109	Sequence 109, App
256	24	100.0	12	17	US-10-968-732-27	Sequence 27, App	329	24	100.0	13	16	US-10-158-825-110	Sequence 110, App
257	24	100.0	12	17	US-10-968-732-78	Sequence 78, App	330	24	100.0	13	16	US-10-688-015-101	Sequence 101, App
258	24	100.0	12	18	US-10-645-784-131	Sequence 131, App	331	24	100.0	13	16	US-10-441-779C-33	Sequence 33, Appl
259	24	100.0	12	18	US-10-645-784-132	Sequence 132, App	332	24	100.0	13	16	US-10-470-957-7	Sequence 7, Appl
260	24	100.0	12	18	US-10-645-784-133	Sequence 133, App	333	24	100.0	13	16	US-10-363-954A-18	Sequence 18, Appl
261	24	100.0	12	18	US-10-645-784-134	Sequence 134, App	334	24	100.0	13	16	US-10-838-226-275	Sequence 275, App
262	24	100.0	12	18	US-10-645-784-135	Sequence 135, App	335	24	100.0	13	16	US-10-468-496-693	Sequence 693, App
263	24	100.0	12	18	US-10-645-784-136	Sequence 136, App	336	24	100.0	13	16	US-10-468-496-694	Sequence 694, App
264	24	100.0	12	18	US-10-645-784-137	Sequence 137, App	337	24	100.0	13	16	US-10-468-496-695	Sequence 695, App
265	24	100.0	12	18	US-10-645-784-143	Sequence 143, App	338	24	100.0	13	16	US-10-468-496-1718	Sequence 1718, Ap
266	24	100.0	12	18	US-10-645-784-144	Sequence 144, App	339	24	100.0	13	16	US-10-468-496-1719	Sequence 1719, Ap
267	24	100.0	12	18	US-10-645-784-145	Sequence 145, App	340	24	100.0	13	16	US-10-468-496-1720	Sequence 1720, Ap
268	24	100.0	12	18	US-10-645-784-146	Sequence 146, App	341	24	100.0	13	16	US-10-468-496-1721	Sequence 1721, Ap
269	24	100.0	12	18	US-10-927-262A-6	Sequence 6, Appl	342	24	100.0	13	16	US-10-643-103-3	Sequence 3, Appl
270	24	100.0	12	18	US-10-927-262A-7	Sequence 7, Appl	343	24	100.0	13	16	US-10-160-505-101	Sequence 101, App
271	24	100.0	12	18	US-10-927-262A-17	Sequence 17, Appl	344	24	100.0	13	16	US-10-474-960A-69	Sequence 69, Appl
272	24	100.0	12	18	US-10-927-262A-18	Sequence 18, Appl	345	24	100.0	13	16	US-10-846-911-7	Sequence 7, Appl
273	24	100.0	12	18	US-10-927-262A-19	Sequence 19, Appl	346	24	100.0	13	16	US-10-846-911-20	Sequence 20, Appl
274	24	100.0	12	18	US-10-927-262A-20	Sequence 20, Appl	347	24	100.0	13	16	US-10-495-146-186	Sequence 186, App
275	24	100.0	12	18	US-10-927-262A-24	Sequence 24, Appl	348	24	100.0	13	16	US-10-495-146-187	Sequence 187, App
276	24	100.0	12	18	US-10-927-262A-25	Sequence 25, Appl	349	24	100.0	13	16	US-10-495-146-188	Sequence 188, App
277	24	100.0	12	18	US-10-927-262A-26	Sequence 26, Appl	350	24	100.0	13	17	US-10-884-355A-50	Sequence 50, Appl
278	24	100.0	12	18	US-10-927-262A-27	Sequence 27, Appl	351	24	100.0	13	17	US-10-893-018-15	Sequence 15, Appl
279	24	100.0	12	18	US-10-927-262A-31	Sequence 31, Appl	352	24	100.0	13	18	US-10-942-711-40	Sequence 40, Appl
280	24	100.0	12	18	US-10-927-262A-32	Sequence 32, Appl	353	24	100.0	13	18	US-10-732-862A-233	Sequence 233, App
281	24	100.0	12	18	US-10-927-262A-63	Sequence 63, Appl	354	24	100.0	13	18	US-10-783-177A-17	Sequence 17, Appl
282	24	100.0	12	18	US-10-927-262A-64	Sequence 64, Appl	355	24	100.0	13	18	US-10-939-107-7	Sequence 7, Appl
283	24	100.0	12	18	US-10-312-637-1	Sequence 1, Appl	356	24	100.0	13	18	US-10-939-107-20	Sequence 20, Appl
284	24	100.0	12	18	US-10-993-906-12	Sequence 12, Appl	357	24	100.0	13	20	US-11-093-103-7	Sequence 7, Appl
285	24	100.0	12	20	US-11-003-951-32	Sequence 32, Appl	358	24	100.0	14	9	US-09-214-371-33	Sequence 33, Appl
286	24	100.0	12	20	US-11-003-951-33	Sequence 33, Appl	359	24	100.0	14	9	US-09-214-371-34	Sequence 34, Appl
287	24	100.0	13	9	US-09-935-682-61	Sequence 61, Appl	360	24	100.0	14	9	US-09-214-371-65	Sequence 65, Appl
288	24	100.0	13	9	US-09-894-018-69	Sequence 69, Appl	361	24	100.0	14	9	US-09-832-723-28	Sequence 28, Appl
289	24	100.0	13	9	US-09-949-375A-18	Sequence 18, Appl	362	24	100.0	14	13	US-10-003-858-20	Sequence 20, Appl
290	24	100.0	13	9	US-09-785-215-19	Sequence 19, Appl	363	24	100.0	14	14	US-10-012-542-508	Sequence 508, App
291	24	100.0	13	9	US-09-852-455-68	Sequence 68, Appl	364	24	100.0	14	14	US-10-115-123-508	Sequence 508, App
292	24	100.0	13	13	US-10-155-059-9	Sequence 9, Appl	365	24	100.0	14	14	US-10-094-401-230	Sequence 230, App
293	24	100.0	13	14	US-10-094-401-227	Sequence 227, App	366	24	100.0	14	14	US-10-158-847-115	Sequence 115, App
294	24	100.0	13	14	US-10-170-645-2	Sequence 2, App	367	24	100.0	14	14	US-10-158-847-116	Sequence 116, App
295	24	100.0	13	14	US-10-158-847-103	Sequence 103, App	368	24	100.0	14	14	US-10-158-847-119	Sequence 119, App
296	24	100.0	13	14	US-10-158-847-105	Sequence 105, App	369	24	100.0	14	14	US-10-098-093-45	Sequence 45, Appl
297	24	100.0	13	14	US-10-158-847-108	Sequence 108, App	370	24	100.0	14	14	US-10-186-867-7	Sequence 7, Appl
298	24	100.0	13	14	US-10-158-847-109	Sequence 109, App	371	24	100.0	14	14	US-10-150-475A-2	Sequence 2, Appl
299	24	100.0	13	14	US-10-158-847-110	Sequence 110, App	372	24	100.0	14	14	US-10-225-567A-2196	Sequence 2196, Ap
300	24	100.0	13	14	US-10-253-532-28	Sequence 28, App	373	24	100.0	14	14	US-10-158-825-115	Sequence 115, App
301	24	100.0	13	14	US-10-253-532-29	Sequence 29, App	374	24	100.0	14	14	US-10-158-825-116	Sequence 116, App
302	24	100.0	13	14	US-10-158-825-103	Sequence 103, App	375	24	100.0	14	14	US-10-158-825-119	Sequence 119, App
303	24	100.0	13	14	US-10-158-825-105	Sequence 105, App	376	24	100.0	14	14	US-10-303-331-28	Sequence 28, Appl

377	14	14	14	US-10-083-768-33	Sequence 33, Appl	450	24	100.0	15	10	US-09-840-085-34	Sequence 34, Appl
378	24	100.0	24	US-10-083-768-213	Sequence 213, App	451	24	100.0	15	10	US-09-840-085-35	Sequence 35, Appl
379	24	100.0	14	US-10-083-259-14	Sequence 14, Appl	452	24	100.0	15	10	US-09-840-085-36	Sequence 36, Appl
380	24	100.0	14	US-10-145-206-29	Sequence 29, Appl	453	24	100.0	15	10	US-09-840-085-37	Sequence 37, Appl
381	24	100.0	14	US-10-109-274A-14	Sequence 14, Appl	454	24	100.0	15	11	US-09-953-413-51	Sequence 51, Appl
382	24	100.0	14	US-10-308-905A-23	Sequence 23, Appl	455	24	100.0	15	11	US-09-953-413-52	Sequence 52, Appl
383	24	100.0	14	US-10-462-262-198	Sequence 198, App	456	24	100.0	15	13	US-10-155-059-24	Sequence 24, Appl
384	24	100.0	14	US-10-436-715-430	Sequence 430, App	457	24	100.0	15	13	US-10-103-395-247	Sequence 247, App
385	24	100.0	14	US-10-224-595-16	Sequence 16, Appl	458	24	100.0	15	14	US-10-005-530-28	Sequence 28, Appl
386	24	100.0	14	US-10-609-217-68	Sequence 68, Appl	459	24	100.0	15	14	US-10-012-542-295	Sequence 295, App
387	24	100.0	14	US-10-632-388-68	Sequence 68, Appl	460	24	100.0	15	14	US-10-115-123-295	Sequence 295, App
388	24	100.0	14	US-10-651-723-68	Sequence 68, Appl	461	24	100.0	15	14	US-10-120-604-219	Sequence 219, App
389	24	100.0	14	US-10-328-953-320	Sequence 320, App	462	24	100.0	15	14	US-10-161-097-54	Sequence 54, Appl
390	24	100.0	14	US-10-328-953-321	Sequence 321, App	463	24	100.0	15	14	US-10-067-649-89	Sequence 89, Appl
391	24	100.0	14	US-10-328-953-332	Sequence 322, App	464	24	100.0	15	14	US-10-067-649-90	Sequence 90, Appl
392	24	100.0	14	US-10-645-761-68	Sequence 68, Appl	465	24	100.0	15	14	US-10-186-867-28	Sequence 28, Appl
393	24	100.0	14	US-10-240-641-22	Sequence 22, Appl	466	24	100.0	15	14	US-10-186-867-29	Sequence 29, Appl
394	24	100.0	14	US-10-666-696-68	Sequence 68, Appl	467	24	100.0	15	14	US-10-133-210-251	Sequence 251, App
395	24	100.0	14	US-10-653-048-68	Sequence 68, Appl	468	24	100.0	15	14	US-10-1211-088-141	Sequence 141, App
396	24	100.0	14	US-10-704-532-2	Sequence 2, Appli	469	24	100.0	15	14	US-10-091-724-48	Sequence 48, Appl
397	24	100.0	14	US-10-158-825-115	Sequence 115, App	470	24	100.0	15	14	US-10-216-122-22	Sequence 22, Appl
398	24	100.0	14	US-10-158-825-116	Sequence 116, App	471	24	100.0	15	14	US-10-147-255-51	Sequence 51, Appl
399	24	100.0	14	US-10-158-825-119	Sequence 119, App	472	24	100.0	15	14	US-10-147-255-52	Sequence 52, Appl
400	24	100.0	14	US-10-645-215-2	Sequence 2, Appli	473	24	100.0	15	14	US-10-354-240-58	Sequence 88, Appl
401	24	100.0	14	US-10-661-471-23	Sequence 23, Appl	474	24	100.0	15	14	US-10-080-608A-165	Sequence 165, App
402	24	100.0	14	US-10-742-379-7	Sequence 7, Appli	475	24	100.0	15	14	US-10-295-693-89	Sequence 89, Appl
403	24	100.0	14	US-10-742-379-8	Sequence 8, Appli	476	24	100.0	15	14	US-10-295-693-90	Sequence 90, Appl
404	24	100.0	14	US-10-742-379-10	Sequence 10, Appl	477	24	100.0	15	15	US-10-370-685-74	Sequence 74, Appl
405	24	100.0	14	US-10-742-379-26	Sequence 26, Appl	478	24	100.0	15	15	US-10-222-463-25	Sequence 25, Appl
406	24	100.0	14	US-10-742-379-36	Sequence 36, Appl	479	24	100.0	15	15	US-10-024-652-2104	Sequence 2104, Ap
407	24	100.0	14	US-10-712-447-158	Sequence 158, App	480	24	100.0	15	15	US-10-024-652-2211	Sequence 2211, Ap
408	24	100.0	14	US-10-712-447-159	Sequence 159, App	481	24	100.0	15	15	US-10-024-652-2294	Sequence 2294, Ap
409	24	100.0	14	US-10-712-447-160	Sequence 160, App	482	24	100.0	15	15	US-10-024-652-2340	Sequence 2340, Ap
410	24	100.0	14	US-10-712-447-194	Sequence 194, App	483	24	100.0	15	15	US-10-024-652-2383	Sequence 2383, Ap
411	24	100.0	14	US-10-712-447-195	Sequence 195, App	484	24	100.0	15	15	US-10-024-652-2472	Sequence 2472, Ap
412	24	100.0	14	US-10-712-447-196	Sequence 196, App	485	24	100.0	15	15	US-10-024-652-2543	Sequence 2543, Ap
413	24	100.0	14	US-10-712-447-204	Sequence 204, App	486	24	100.0	15	15	US-10-346-162-158	Sequence 158, App
414	24	100.0	14	US-10-865-478-745	Sequence 745, App	487	24	100.0	15	15	US-10-346-162-206	Sequence 206, App
415	24	100.0	14	US-10-868-478-746	Sequence 746, App	488	24	100.0	15	15	US-10-346-162-219	Sequence 219, App
416	24	100.0	14	US-10-808-187-1052	Sequence 1052, Ap	489	24	100.0	15	15	US-10-442-909-41	Sequence 41, Appl
417	24	100.0	14	US-10-659-207-87	Sequence 87, Appl	490	24	100.0	15	15	US-10-431-048-48	Sequence 48, Appl
418	24	100.0	14	US-10-930-313-16	Sequence 16, Appl	491	24	100.0	15	15	US-10-436-715-393	Sequence 393, App
419	24	100.0	14	US-10-968-732-28	Sequence 28, Appl	492	24	100.0	15	15	US-10-403-104-21	Sequence 21, Appl
420	24	100.0	14	US-10-645-784-68	Sequence 68, Appl	493	24	100.0	15	15	US-10-446-628-51	Sequence 51, Appl
421	24	100.0	14	US-10-927-262A-33	Sequence 33, Appl	494	24	100.0	15	15	US-10-609-217-138	Sequence 138, App
422	24	100.0	14	US-10-927-262A-34	Sequence 34, Appl	495	24	100.0	15	15	US-10-609-217-139	Sequence 139, App
423	24	100.0	14	US-10-800-834-508	Sequence 508, App	496	24	100.0	15	15	US-10-609-217-140	Sequence 140, App
424	24	100.0	14	US-10-807-807-1052	Sequence 1052, Ap	497	24	100.0	15	15	US-10-609-217-141	Sequence 141, App
425	24	100.0	14	US-10-946-647-1237	Sequence 1237, Ap	498	24	100.0	15	15	US-10-651-723-139	Sequence 139, App
426	24	100.0	14	US-10-496-905-583	Sequence 583, App	499	24	100.0	15	15	US-10-651-723-140	Sequence 140, App
427	24	100.0	14	US-11-066-697-179	Sequence 179, App	500	24	100.0	15	15	US-10-632-388-138	Sequence 138, App
428	24	100.0	14	US-11-093-103-45	Sequence 45, Appl	501	24	100.0	15	15	US-10-632-388-139	Sequence 139, App
429	24	100.0	15	US-09-214-371-8	Sequence 8, Appli	502	24	100.0	15	15	US-10-632-388-140	Sequence 140, App
430	24	100.0	15	US-09-214-371-28	Sequence 28, Appl	503	24	100.0	15	15	US-10-632-388-141	Sequence 141, App
431	24	100.0	15	US-09-214-371-29	Sequence 29, Appl	504	24	100.0	15	15	US-10-632-388-142	Sequence 142, App
432	24	100.0	15	US-09-214-371-30	Sequence 30, Appl	505	24	100.0	15	15	US-10-651-723-138	Sequence 138, App
433	24	100.0	15	US-09-214-371-66	Sequence 66, Appl	506	24	100.0	15	15	US-10-651-723-139	Sequence 139, App
434	24	100.0	15	US-09-765-527-9	Sequence 9, Appli	507	24	100.0	15	15	US-10-651-723-141	Sequence 141, App
435	24	100.0	15	US-09-829-549A-23	Sequence 23, Appl	508	24	100.0	15	15	US-10-645-761-138	Sequence 138, App
436	24	100.0	15	US-09-953-510-51	Sequence 51, Appl	509	24	100.0	15	15	US-10-645-761-139	Sequence 139, App
437	24	100.0	15	US-09-953-510-52	Sequence 52, Appl	510	24	100.0	15	15	US-10-645-761-140	Sequence 140, App
438	24	100.0	15	US-09-732-384-6	Sequence 6, Appli	511	24	100.0	15	15	US-10-645-761-141	Sequence 141, App
439	24	100.0	15	US-09-894-594-27	Sequence 27, Appl	512	24	100.0	15	15	US-10-666-696-138	Sequence 138, App
440	24	100.0	15	US-09-894-594-28	Sequence 28, Appl	513	24	100.0	15	15	US-10-666-696-139	Sequence 139, App
441	24	100.0	15	US-09-894-594-31	Sequence 31, Appl	514	24	100.0	15	15	US-10-666-696-140	Sequence 140, App
442	24	100.0	15	US-09-894-594-43	Sequence 43, Appl	515	24	100.0	15	15	US-10-666-696-141	Sequence 141, App
443	24	100.0	15	US-09-798-869-6	Sequence 6, Appli	516	24	100.0	15	15	US-10-653-048-138	Sequence 138, App
444	24	100.0	15	US-09-798-869-29	Sequence 29, Appl	517	24	100.0	15	15	US-10-653-048-139	Sequence 139, App
445	24	100.0	15	US-09-798-869-30	Sequence 30, Appl	518	24	100.0	15	15	US-10-653-048-140	Sequence 140, App
446	24	100.0	15	US-09-798-026B-6	Sequence 6, Appli	519	24	100.0	15	15	US-10-432-236-16	Sequence 16, Appl
447	24	100.0	15	US-09-798-026B-30	Sequence 30, Appl	520	24	100.0	15	15	US-10-240-403-15	Sequence 15, Appl
448	24	100.0	15	US-09-798-026B-31	Sequence 31, Appl	521	24	100.0	15	15	US-10-695-155-51	Sequence 51, Appl
449	24	100.0	15	US-09-840-085-33	Sequence 33, Appl	522	24	100.0	15	16		

523	24	100.0	15	16	US-10-695-155-52	Sequence 52, Appl	596	24	100.0	16	10	US-09-825-517A-77	Sequence 77, Appl
524	24	100.0	15	16	US-10-695-155-110	Sequence 110, Appl	597	24	100.0	16	10	US-09-825-517A-79	Sequence 79, Appl
525	24	100.0	15	16	US-10-695-155-111	Sequence 111, Appl	598	24	100.0	16	10	US-09-825-517A-81	Sequence 81, Appl
526	24	100.0	15	16	US-10-495-146-24	Sequence 24, Appl	599	24	100.0	16	10	US-09-825-517A-83	Sequence 83, Appl
527	24	100.0	15	16	US-10-495-146-24	Sequence 24, Appl	600	24	100.0	16	10	US-09-825-517A-84	Sequence 84, Appl
528	24	100.0	15	16	US-10-495-146-25	Sequence 25, Appl	601	24	100.0	16	10	US-09-825-517A-85	Sequence 85, Appl
529	24	100.0	15	16	US-10-495-146-26	Sequence 26, Appl	602	24	100.0	16	10	US-09-825-517A-86	Sequence 86, Appl
530	24	100.0	15	17	US-10-654-601-2142	Sequence 2142, Ap	603	24	100.0	16	10	US-09-825-517A-89	Sequence 89, Appl
531	24	100.0	15	17	US-10-661-156-198	Sequence 158, Ap	604	24	100.0	16	10	US-09-825-517A-91	Sequence 91, Appl
532	24	100.0	15	17	US-10-182-613A-7	Sequence 7, Appl	605	24	100.0	16	10	US-09-825-517A-92	Sequence 92, Appl
533	24	100.0	15	18	US-10-645-784-138	Sequence 138, Appl	606	24	100.0	16	10	US-09-825-517A-96	Sequence 96, Appl
534	24	100.0	15	18	US-10-645-784-139	Sequence 139, Appl	607	24	100.0	16	10	US-09-825-517A-98	Sequence 98, Appl
535	24	100.0	15	18	US-10-645-784-140	Sequence 140, Appl	608	24	100.0	16	10	US-09-825-517A-99	Sequence 99, Appl
536	24	100.0	15	18	US-10-645-784-141	Sequence 141, Appl	609	24	100.0	16	10	US-09-825-517A-100	Sequence 100, Appl
537	24	100.0	15	18	US-10-645-784-141	Sequence 8, Appl	610	24	100.0	16	10	US-09-825-517A-104	Sequence 104, Appl
538	24	100.0	15	18	US-10-927-262A-8	Sequence 28, Appl	611	24	100.0	16	10	US-09-825-517A-105	Sequence 105, Appl
539	24	100.0	15	18	US-10-927-262A-28	Sequence 29, Appl	612	24	100.0	16	10	US-09-825-517A-106	Sequence 106, Appl
540	24	100.0	15	18	US-10-927-262A-29	Sequence 30, Appl	613	24	100.0	16	10	US-09-825-517A-108	Sequence 108, Appl
541	24	100.0	15	18	US-10-927-262A-30	Sequence 30, Appl	614	24	100.0	16	10	US-09-825-517A-109	Sequence 109, Appl
542	24	100.0	15	18	US-10-927-262A-65	Sequence 65, Appl	615	24	100.0	16	10	US-09-825-517A-115	Sequence 115, Appl
543	24	100.0	15	18	US-10-800-834-295	Sequence 295, Appl	616	24	100.0	16	10	US-09-825-517A-119	Sequence 119, Appl
544	24	100.0	15	18	US-10-800-834-295	Sequence 295, Appl	617	24	100.0	16	10	US-09-825-517A-120	Sequence 120, Appl
545	24	100.0	15	18	US-10-946-647-790	Sequence 790, Appl	618	24	100.0	16	10	US-09-825-517A-121	Sequence 121, Appl
546	24	100.0	15	18	US-10-946-647-957	Sequence 957, Appl	619	24	100.0	16	10	US-09-825-517A-124	Sequence 124, Appl
547	24	100.0	15	18	US-10-496-905-576	Sequence 576, Appl	620	24	100.0	16	10	US-09-825-517A-128	Sequence 128, Appl
548	24	100.0	15	18	US-10-920-244A-286	Sequence 286, Appl	621	24	100.0	16	10	US-09-825-517A-129	Sequence 129, Appl
549	24	100.0	15	18	US-10-705-165-9	Sequence 9, Appl	622	24	100.0	16	10	US-09-825-517A-130	Sequence 130, Appl
550	24	100.0	15	20	US-10-754-473-30	Sequence 30, Appl	623	24	100.0	16	10	US-09-825-517A-131	Sequence 131, Appl
551	24	100.0	15	20	US-11-070-456-219	Sequence 219, Appl	624	24	100.0	16	10	US-09-825-517A-132	Sequence 132, Appl
552	24	100.0	16	9	US-11-011-422-76	Sequence 76, Appl	625	24	100.0	16	10	US-09-825-517A-134	Sequence 134, Appl
553	24	100.0	16	9	US-09-214-371-39	Sequence 39, Appl	626	24	100.0	16	10	US-09-825-517A-136	Sequence 136, Appl
554	24	100.0	16	9	US-09-214-371-40	Sequence 40, Appl	627	24	100.0	16	10	US-09-825-517A-137	Sequence 137, Appl
555	24	100.0	16	9	US-09-214-371-41	Sequence 41, Appl	628	24	100.0	16	10	US-09-825-517A-139	Sequence 139, Appl
556	24	100.0	16	9	US-09-962-805-13	Sequence 13, Appl	629	24	100.0	16	10	US-09-825-517A-145	Sequence 145, Appl
557	24	100.0	16	9	US-09-920-552-109	Sequence 109, Appl	630	24	100.0	16	10	US-09-825-517A-150	Sequence 150, Appl
558	24	100.0	16	9	US-09-738-373-587	Sequence 587, Appl	631	24	100.0	16	13	US-10-155-059-23	Sequence 23, Appl
559	24	100.0	16	9	US-09-894-018-199	Sequence 199, Appl	632	24	100.0	16	13	US-10-103-395-39	Sequence 39, Appl
560	24	100.0	16	10	US-09-854-133-587	Sequence 587, Appl	633	24	100.0	16	13	US-10-103-395-230	Sequence 230, Appl
561	24	100.0	16	10	US-09-825-517A-4	Sequence 4, Appl	634	24	100.0	16	14	US-10-223-047-19	Sequence 19, Appl
562	24	100.0	16	10	US-09-825-517A-20	Sequence 20, Appl	635	24	100.0	16	14	US-10-094-401-218	Sequence 218, Appl
563	24	100.0	16	10	US-09-825-517A-35	Sequence 35, Appl	636	24	100.0	16	14	US-10-094-401-220	Sequence 220, Appl
564	24	100.0	16	10	US-09-825-517A-37	Sequence 37, Appl	637	24	100.0	16	14	US-10-193-795-11	Sequence 11, Appl
565	24	100.0	16	10	US-09-825-517A-38	Sequence 38, Appl	638	24	100.0	16	14	US-10-219-834-102	Sequence 102, Appl
566	24	100.0	16	10	US-09-825-517A-39	Sequence 39, Appl	639	24	100.0	16	14	US-10-251-385-285	Sequence 285, Appl
567	24	100.0	16	10	US-09-825-517A-40	Sequence 40, Appl	640	24	100.0	16	14	US-10-062-831-88	Sequence 88, Appl
568	24	100.0	16	10	US-09-825-517A-41	Sequence 41, Appl	641	24	100.0	16	14	US-10-225-567A-942	Sequence 942, Appl
569	24	100.0	16	10	US-09-825-517A-42	Sequence 42, Appl	642	24	100.0	16	14	US-10-144-649A-587	Sequence 587, Appl
570	24	100.0	16	10	US-09-825-517A-43	Sequence 43, Appl	643	24	100.0	16	14	US-10-267-251-4	Sequence 4, Appl
571	24	100.0	16	10	US-09-825-517A-44	Sequence 44, Appl	644	24	100.0	16	14	US-10-224-156-36	Sequence 36, Appl
572	24	100.0	16	10	US-09-825-517A-45	Sequence 45, Appl	645	24	100.0	16	14	US-10-058-053A-309	Sequence 309, Appl
573	24	100.0	16	10	US-09-825-517A-46	Sequence 46, Appl	646	24	100.0	16	14	US-10-047-264A-16	Sequence 16, Appl
574	24	100.0	16	10	US-09-825-517A-47	Sequence 47, Appl	647	24	100.0	16	14	US-10-062-599-88	Sequence 88, Appl
575	24	100.0	16	10	US-09-825-517A-48	Sequence 48, Appl	648	24	100.0	16	15	US-10-371-525-308	Sequence 308, Appl
576	24	100.0	16	10	US-09-825-517A-50	Sequence 50, Appl	649	24	100.0	16	15	US-10-371-069-308	Sequence 308, Appl
577	24	100.0	16	10	US-09-825-517A-51	Sequence 51, Appl	650	24	100.0	16	15	US-10-371-645-308	Sequence 308, Appl
578	24	100.0	16	10	US-09-825-517A-52	Sequence 52, Appl	651	24	100.0	16	15	US-10-371-645-308	Sequence 308, Appl
579	24	100.0	16	10	US-09-825-517A-53	Sequence 53, Appl	652	24	100.0	16	15	US-10-371-260-308	Sequence 308, Appl
580	24	100.0	16	10	US-09-825-517A-55	Sequence 55, Appl	653	24	100.0	16	15	US-10-369-214-6	Sequence 6, Appl
581	24	100.0	16	10	US-09-825-517A-56	Sequence 56, Appl	654	24	100.0	16	15	US-10-462-262-186	Sequence 186, Appl
582	24	100.0	16	10	US-09-825-517A-57	Sequence 57, Appl	655	24	100.0	16	15	US-10-462-262-188	Sequence 188, Appl
583	24	100.0	16	10	US-09-825-517A-58	Sequence 58, Appl	656	24	100.0	16	15	US-10-436-715-288	Sequence 288, Appl
584	24	100.0	16	10	US-09-825-517A-59	Sequence 59, Appl	657	24	100.0	16	15	US-10-436-715-288	Sequence 288, Appl
585	24	100.0	16	10	US-09-825-517A-61	Sequence 61, Appl	658	24	100.0	16	15	US-10-373-238-68	Sequence 68, Appl
586	24	100.0	16	10	US-09-825-517A-62	Sequence 62, Appl	659	24	100.0	16	15	US-10-436-715-288	Sequence 288, Appl
587	24	100.0	16	10	US-09-825-517A-63	Sequence 63, Appl	660	24	100.0	16	15	US-10-436-715-313	Sequence 313, Appl
588	24	100.0	16	10	US-09-825-517A-64	Sequence 64, Appl	661	24	100.0	16	15	US-10-319-786-51	Sequence 51, Appl
589	24	100.0	16	10	US-09-825-517A-66	Sequence 66, Appl	662	24	100.0	16	16	US-10-258-144-277	Sequence 277, Appl
590	24	100.0	16	10	US-09-825-517A-68	Sequence 68, Appl	663	24	100.0	16	16	US-10-467-758-14	Sequence 14, Appl
591	24	100.0	16	10	US-09-825-517A-69	Sequence 69, Appl	664	24	100.0	16	16	US-10-096-525-1	Sequence 1, Appl
592	24	100.0	16	10	US-09-825-517A-71	Sequence 71, Appl	665	24	100.0	16	16	US-10-838-226-309	Sequence 309, Appl
593	24	100.0	16	10	US-09-825-517A-73	Sequence 73, Appl	666	24	100.0	16	16	US-10-474-960A-199	Sequence 199, Appl
594	24	100.0	16	10	US-09-825-517A-74	Sequence 74, Appl	667	24	100.0	16	17	US-10-659-207-89	Sequence 89, Appl
595	24	100.0	16	10	US-09-825-517A-75	Sequence 75, Appl	668	24	100.0	16	18	US-10-927-262A-39	Sequence 39, Appl
596	24	100.0	16	10	US-09-825-517A-76	Sequence 76, Appl	669	24	100.0	16	18	US-10-927-262A-40	Sequence 40, Appl

669	24	100.0	16	18	US-10-927-262A-41	Sequence 41, Appl	742	24	100.0	16	20	US-11-045-477-134	Sequence 134, App
670	24	100.0	16	18	US-10-962-760-11	Sequence 11, Appl	743	24	100.0	16	20	US-11-045-477-136	Sequence 136, App
671	24	100.0	16	18	US-10-470-045-47	Sequence 47, Appl	744	24	100.0	16	20	US-11-045-477-137	Sequence 137, App
672	24	100.0	16	18	US-10-946-647-65	Sequence 65, Appl	745	24	100.0	16	20	US-11-045-477-139	Sequence 139, App
673	24	100.0	16	18	US-10-946-647-368	Sequence 368, App	746	24	100.0	16	20	US-11-045-477-140	Sequence 140, App
674	24	100.0	16	18	US-10-946-647-517	Sequence 517, App	747	24	100.0	16	20	US-11-045-477-145	Sequence 145, App
675	24	100.0	16	18	US-10-946-647-635	Sequence 635, App	748	24	100.0	16	20	US-11-045-477-150	Sequence 150, App
676	24	100.0	16	18	US-10-792-582-7	Sequence 7, Appl	749	24	100.0	17	9	US-09-205-658-198	Sequence 198, App
677	24	100.0	16	20	US-11-045-477-4	Sequence 4, Appl	750	24	100.0	17	9	US-09-775-805-74	Sequence 74, Appl
678	24	100.0	16	20	US-11-045-477-20	Sequence 20, Appl	751	24	100.0	17	9	US-09-996-634-88	Sequence 88, Appl
679	24	100.0	16	20	US-11-045-477-35	Sequence 35, Appl	752	24	100.0	17	10	US-09-997-182-88	Sequence 88, Appl
680	24	100.0	16	20	US-11-045-477-37	Sequence 37, Appl	753	24	100.0	17	10	US-09-997-182-89	Sequence 89, Appl
681	24	100.0	16	20	US-11-045-477-38	Sequence 38, Appl	754	24	100.0	17	10	US-09-997-181-88	Sequence 88, Appl
682	24	100.0	16	20	US-11-045-477-39	Sequence 39, Appl	755	24	100.0	17	10	US-09-997-181-89	Sequence 89, Appl
683	24	100.0	16	20	US-11-045-477-40	Sequence 40, Appl	756	24	100.0	17	10	US-09-963-693-198	Sequence 198, App
684	24	100.0	16	20	US-11-045-477-41	Sequence 41, Appl	757	24	100.0	17	10	US-09-962-756-712	Sequence 712, App
685	24	100.0	16	20	US-11-045-477-42	Sequence 42, Appl	758	24	100.0	17	10	US-09-962-756-1205	Sequence 1205, App
686	24	100.0	16	20	US-11-045-477-43	Sequence 43, Appl	759	24	100.0	17	10	US-09-962-756-1757	Sequence 1757, App
687	24	100.0	16	20	US-11-045-477-44	Sequence 44, Appl	760	24	100.0	17	10	US-09-962-756-1911	Sequence 1911, App
688	24	100.0	16	20	US-11-045-477-45	Sequence 45, Appl	761	24	100.0	17	14	US-10-094-401-195	Sequence 195, App
689	24	100.0	16	20	US-11-045-477-46	Sequence 46, Appl	762	24	100.0	17	14	US-10-251-385-286	Sequence 286, App
690	24	100.0	16	20	US-11-045-477-47	Sequence 47, Appl	763	24	100.0	17	14	US-10-106-698-8186	Sequence 8186, App
691	24	100.0	16	20	US-11-045-477-48	Sequence 48, Appl	764	24	100.0	17	14	US-10-280-066-83	Sequence 83, Appl
692	24	100.0	16	20	US-11-045-477-50	Sequence 50, Appl	765	24	100.0	17	14	US-10-351-641-814	Sequence 814, App
693	24	100.0	16	20	US-11-045-477-51	Sequence 51, Appl	766	24	100.0	17	14	US-10-031-874A-59	Sequence 59, Appl
694	24	100.0	16	20	US-11-045-477-52	Sequence 52, Appl	767	24	100.0	17	14	US-10-029-386-27504	Sequence 27504, A
695	24	100.0	16	20	US-11-045-477-53	Sequence 53, Appl	768	24	100.0	17	14	US-10-029-386-29993	Sequence 29993, A
696	24	100.0	16	20	US-11-045-477-55	Sequence 55, Appl	769	24	100.0	17	14	US-10-029-386-31536	Sequence 31536, A
697	24	100.0	16	20	US-11-045-477-56	Sequence 56, Appl	770	24	100.0	17	14	US-10-029-386-31903	Sequence 31903, A
698	24	100.0	16	20	US-11-045-477-57	Sequence 57, Appl	771	24	100.0	17	14	US-10-125-869A-134	Sequence 134, App
699	24	100.0	16	20	US-11-045-477-58	Sequence 58, Appl	772	24	100.0	17	15	US-10-120-885A-44	Sequence 44, Appl
700	24	100.0	16	20	US-11-045-477-59	Sequence 59, Appl	773	24	100.0	17	15	US-10-409-643-53	Sequence 53, Appl
701	24	100.0	16	20	US-11-045-477-61	Sequence 61, Appl	774	24	100.0	17	15	US-10-253-471-712	Sequence 712, App
702	24	100.0	16	20	US-11-045-477-62	Sequence 62, Appl	775	24	100.0	17	15	US-10-253-471-1205	Sequence 1205, App
703	24	100.0	16	20	US-11-045-477-63	Sequence 63, Appl	776	24	100.0	17	15	US-10-253-471-1757	Sequence 1757, App
704	24	100.0	16	20	US-11-045-477-64	Sequence 64, Appl	777	24	100.0	17	15	US-10-253-471-1911	Sequence 1911, App
705	24	100.0	16	20	US-11-045-477-66	Sequence 66, Appl	778	24	100.0	17	15	US-10-462-262-163	Sequence 163, App
706	24	100.0	16	20	US-11-045-477-68	Sequence 68, Appl	779	24	100.0	17	15	US-10-462-262-358	Sequence 358, App
707	24	100.0	16	20	US-11-045-477-69	Sequence 69, Appl	780	24	100.0	17	15	US-10-253-493-712	Sequence 712, App
708	24	100.0	16	20	US-11-045-477-71	Sequence 71, Appl	781	24	100.0	17	15	US-10-253-493-1205	Sequence 1205, App
709	24	100.0	16	20	US-11-045-477-73	Sequence 73, Appl	782	24	100.0	17	15	US-10-253-493-1757	Sequence 1757, App
710	24	100.0	16	20	US-11-045-477-74	Sequence 74, Appl	783	24	100.0	17	15	US-10-253-493-1911	Sequence 1911, App
711	24	100.0	16	20	US-11-045-477-75	Sequence 75, Appl	784	24	100.0	17	15	US-10-609-217-209	Sequence 209, App
712	24	100.0	16	20	US-11-045-477-76	Sequence 76, Appl	785	24	100.0	17	15	US-10-632-388-209	Sequence 209, App
713	24	100.0	16	20	US-11-045-477-77	Sequence 77, Appl	786	24	100.0	17	15	US-10-651-723-209	Sequence 209, App
714	24	100.0	16	20	US-11-045-477-79	Sequence 79, Appl	787	24	100.0	17	15	US-10-645-761-209	Sequence 209, App
715	24	100.0	16	20	US-11-045-477-81	Sequence 81, Appl	788	24	100.0	17	15	US-10-666-696-209	Sequence 209, App
716	24	100.0	16	20	US-11-045-477-83	Sequence 83, Appl	789	24	100.0	17	15	US-10-653-048-209	Sequence 209, App
717	24	100.0	16	20	US-11-045-477-84	Sequence 84, Appl	790	24	100.0	17	15	US-10-432-465-103	Sequence 103, App
718	24	100.0	16	20	US-11-045-477-85	Sequence 85, Appl	791	24	100.0	17	16	US-10-258-144-208	Sequence 208, App
719	24	100.0	16	20	US-11-045-477-86	Sequence 86, Appl	792	24	100.0	17	16	US-10-258-144-217	Sequence 217, App
720	24	100.0	16	20	US-11-045-477-89	Sequence 89, Appl	793	24	100.0	17	16	US-10-258-144-227	Sequence 227, App
721	24	100.0	16	20	US-11-045-477-91	Sequence 91, Appl	794	24	100.0	17	16	US-10-258-144-237	Sequence 237, App
722	24	100.0	16	20	US-11-045-477-92	Sequence 92, Appl	795	24	100.0	17	16	US-10-258-144-247	Sequence 247, App
723	24	100.0	16	20	US-11-045-477-96	Sequence 96, Appl	796	24	100.0	17	16	US-10-258-144-248	Sequence 248, App
724	24	100.0	16	20	US-11-045-477-98	Sequence 98, Appl	797	24	100.0	17	16	US-10-258-144-257	Sequence 257, App
725	24	100.0	16	20	US-11-045-477-99	Sequence 99, Appl	798	24	100.0	17	16	US-10-258-144-258	Sequence 258, App
726	24	100.0	16	20	US-11-045-477-100	Sequence 100, Appl	799	24	100.0	17	16	US-10-258-144-287	Sequence 287, App
727	24	100.0	16	20	US-11-045-477-104	Sequence 104, App	800	24	100.0	17	16	US-10-258-144-297	Sequence 297, App
728	24	100.0	16	20	US-11-045-477-105	Sequence 105, App	801	24	100.0	17	16	US-10-258-144-317	Sequence 317, App
729	24	100.0	16	20	US-11-045-477-106	Sequence 106, App	802	24	100.0	17	16	US-10-258-144-327	Sequence 327, App
730	24	100.0	16	20	US-11-045-477-108	Sequence 108, App	803	24	100.0	17	16	US-10-258-144-387	Sequence 387, App
731	24	100.0	16	20	US-11-045-477-109	Sequence 109, App	804	24	100.0	17	16	US-10-258-144-417	Sequence 417, App
732	24	100.0	16	20	US-11-045-477-115	Sequence 115, App	805	24	100.0	17	16	US-10-258-144-427	Sequence 427, App
733	24	100.0	16	20	US-11-045-477-119	Sequence 119, App	806	24	100.0	17	16	US-10-258-144-437	Sequence 437, App
734	24	100.0	16	20	US-11-045-477-120	Sequence 120, App	807	24	100.0	17	16	US-10-258-144-442	Sequence 442, App
735	24	100.0	16	20	US-11-045-477-121	Sequence 121, App	808	24	100.0	17	16	US-10-258-144-467	Sequence 467, App
736	24	100.0	16	20	US-11-045-477-124	Sequence 124, App	809	24	100.0	17	16	US-10-258-144-497	Sequence 497, App
737	24	100.0	16	20	US-11-045-477-128	Sequence 128, App	810	24	100.0	17	16	US-10-433-091-72	Sequence 72, Appl
738	24	100.0	16	20	US-11-045-477-129	Sequence 129, App	811	24	100.0	17	16	US-10-450-036A-59	Sequence 59, Appl
739	24	100.0	16	20	US-11-045-477-130	Sequence 130, App	812	24	100.0	17	16	US-10-472-860-2	Sequence 2, Appl
740	24	100.0	16	20	US-11-045-477-131	Sequence 131, App	813	24	100.0	17	16	US-10-753-339-74	Sequence 74, Appl
741	24	100.0	16	20	US-11-045-477-132	Sequence 132, App	814	24	100.0	17	16	US-10-695-155-155	Sequence 155, App

815	24	100.0	17	17	US-10-661-156-93	Sequence 93, Appl	888	24	100.0	18	16	US-10-158-625-120	Sequence 120, App
816	24	100.0	17	18	US-10-645-784-209	Sequence 209, App	889	24	100.0	18	16	US-10-742-379-88	Sequence 88, Appl
817	24	100.0	17	18	US-10-946-647-1240	Sequence 1240, Ap	890	24	100.0	18	16	US-10-802-080-139	Sequence 199, App
818	24	100.0	17	20	US-11-066-697-1593	Sequence 1593, Ap	891	24	100.0	18	16	US-10-802-080-224	Sequence 224, App
819	24	100.0	18	9	US-09-214-371-74	Sequence 74, Appl	892	24	100.0	18	16	US-10-801-897-129	Sequence 199, App
820	24	100.0	18	9	US-09-774-639-236	Sequence 236, App	893	24	100.0	18	16	US-10-801-897-224	Sequence 224, App
821	24	100.0	18	10	US-09-865-989-199	Sequence 199, App	894	24	100.0	18	16	US-10-649-378A-51	Sequence 51, Appl
822	24	100.0	18	10	US-09-865-989-224	Sequence 224, App	895	24	100.0	18	16	US-10-649-378A-52	Sequence 52, Appl
823	24	100.0	18	10	US-09-865-989-224	Sequence 224, App	896	24	100.0	18	16	US-10-649-378A-53	Sequence 53, Appl
824	24	100.0	18	10	US-09-865-989-224	Sequence 224, App	897	24	100.0	18	16	US-10-649-378A-54	Sequence 54, Appl
825	24	100.0	18	10	US-09-865-989-224	Sequence 224, App	898	24	100.0	18	16	US-10-423-830-48	Sequence 48, Appl
826	24	100.0	18	10	US-09-865-989-224	Sequence 224, App	899	24	100.0	18	16	US-10-423-830-49	Sequence 49, Appl
827	24	100.0	18	10	US-09-865-989-224	Sequence 224, App	900	24	100.0	18	16	US-10-423-830-50	Sequence 50, Appl
828	24	100.0	18	11	US-09-833-245-1958	Sequence 1958, Ap	901	24	100.0	18	16	US-10-423-830-51	Sequence 51, Appl
829	24	100.0	18	11	US-09-833-245-1959	Sequence 1959, Ap	902	24	100.0	18	17	US-10-659-207-195	Sequence 195, App
830	24	100.0	18	11	US-09-865-989-199	Sequence 199, App	903	24	100.0	18	17	US-10-937-767-139	Sequence 199, App
831	24	100.0	18	11	US-09-865-989-224	Sequence 224, App	904	24	100.0	18	17	US-10-937-767-224	Sequence 224, App
832	24	100.0	18	13	US-10-155-059-22	Sequence 22, Appl	905	24	100.0	18	17	US-10-927-262A-74	Sequence 74, Appl
833	24	100.0	18	14	US-10-099-574A-199	Sequence 199, App	906	24	100.0	18	18	US-10-991-217-199	Sequence 199, App
834	24	100.0	18	14	US-10-099-574A-224	Sequence 224, App	907	24	100.0	18	18	US-10-991-217-224	Sequence 224, App
835	24	100.0	18	14	US-10-084-813-176	Sequence 176, App	908	24	100.0	18	18	US-10-099-574A-199	Sequence 199, App
836	24	100.0	18	14	US-10-084-813-177	Sequence 177, App	909	24	100.0	18	18	US-10-099-574A-224	Sequence 224, App
837	24	100.0	18	14	US-10-094-401-190	Sequence 190, App	910	24	100.0	18	18	US-10-715-895-139	Sequence 199, App
838	24	100.0	18	14	US-10-094-401-197	Sequence 197, App	911	24	100.0	18	18	US-10-715-895-224	Sequence 224, App
839	24	100.0	18	14	US-10-158-847-78	Sequence 78, Appl	912	24	100.0	18	18	US-10-792-582-12	Sequence 12, App
840	24	100.0	18	14	US-10-158-847-88	Sequence 88, Appl	913	24	100.0	18	18	US-10-792-582-33	Sequence 33, Appl
841	24	100.0	18	14	US-10-158-847-120	Sequence 120, App	914	24	100.0	18	18	US-10-792-582-47	Sequence 47, Appl
842	24	100.0	18	14	US-10-225-567A-1512	Sequence 1512, Ap	915	24	100.0	18	20	US-11-093-103-47	Sequence 47, Appl
843	24	100.0	18	14	US-10-225-567A-2147	Sequence 2147, Ap	916	24	100.0	18	20	US-11-093-103-48	Sequence 48, Appl
844	24	100.0	18	14	US-10-158-825-78	Sequence 78, Appl	917	24	100.0	19	9	US-09-214-371-1	Sequence 1, Appl
845	24	100.0	18	14	US-10-158-825-88	Sequence 88, Appl	918	24	100.0	19	9	US-09-732-357A-9	Sequence 9, Appl
846	24	100.0	18	14	US-10-158-825-120	Sequence 120, App	919	24	100.0	19	9	US-09-864-761-39185	Sequence 39185, A
847	24	100.0	18	14	US-10-224-356-17	Sequence 17, Appl	920	24	100.0	19	9	US-09-732-384-7	Sequence 7, Appl
848	24	100.0	18	14	US-10-105-545-15	Sequence 15, Appl	921	24	100.0	19	10	US-09-774-639-342	Sequence 342, App
849	24	100.0	18	14	US-10-187-215-48	Sequence 48, Appl	922	24	100.0	19	10	US-09-794-517-9	Sequence 9, Appl
850	24	100.0	18	14	US-10-187-215-49	Sequence 49, Appl	923	24	100.0	19	10	US-09-229-173-45	Sequence 45, Appl
851	24	100.0	18	14	US-10-187-215-50	Sequence 50, Appl	924	24	100.0	19	10	US-09-977-797A-116	Sequence 116, App
852	24	100.0	18	14	US-10-187-215-51	Sequence 51, Appl	925	24	100.0	19	10	US-09-963-339-9	Sequence 9, Appl
853	24	100.0	18	14	US-10-351-641-1147	Sequence 1147, Ap	926	24	100.0	19	10	US-09-963-339-10	Sequence 10, Appl
854	24	100.0	18	14	US-10-239-423-37	Sequence 37, Appl	927	24	100.0	19	10	US-09-963-339-289	Sequence 289, App
855	24	100.0	18	14	US-10-125-869A-135	Sequence 135, App	928	24	100.0	19	10	US-09-794-529-9	Sequence 9, Appl
856	24	100.0	18	15	US-10-099-836B-199	Sequence 199, App	929	24	100.0	19	10	US-09-794-832-9	Sequence 9, Appl
857	24	100.0	18	15	US-10-099-836B-224	Sequence 224, App	930	24	100.0	19	10	US-09-915-914B-4	Sequence 4, Appl
858	24	100.0	18	15	US-10-283-599-199	Sequence 199, App	931	24	100.0	19	10	US-09-915-914B-5	Sequence 5, Appl
859	24	100.0	18	15	US-10-283-599-224	Sequence 224, App	932	24	100.0	19	10	US-09-915-914B-41	Sequence 41, Appl
860	24	100.0	18	15	US-10-273-386-48	Sequence 48, Appl	933	24	100.0	19	13	US-10-155-059-13	Sequence 13, Appl
861	24	100.0	18	15	US-10-273-386-49	Sequence 49, Appl	934	24	100.0	19	14	US-10-012-542-291	Sequence 291, App
862	24	100.0	18	15	US-10-273-386-50	Sequence 50, Appl	935	24	100.0	19	14	US-10-074-152-8	Sequence 8, Appl
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864	24	100.0	18	15	US-10-462-262-158	Sequence 158, App	937	24	100.0	19	14	US-10-225-567A-1318	Sequence 1318, Ap
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868	24	100.0	18	15	US-10-381-112-3	Sequence 3, Appl	941	24	100.0	19	14	US-10-170-713A-9	Sequence 9, Appl
869	24	100.0	18	16	US-10-258-144-267	Sequence 267, App	942	24	100.0	19	14	US-10-171-734-9	Sequence 9, Appl
870	24	100.0	18	16	US-10-258-144-268	Sequence 268, App	943	24	100.0	19	14	US-10-300-694A-39	Sequence 39, Appl
871	24	100.0	18	16	US-10-258-144-307	Sequence 307, App	944	24	100.0	19	14	US-10-300-694A-42	Sequence 42, Appl
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876	24	100.0	18	16	US-10-258-144-367	Sequence 367, App	949	24	100.0	19	15	US-10-346-162-208	Sequence 208, App
877	24	100.0	18	16	US-10-258-144-372	Sequence 372, App	950	24	100.0	19	15	US-10-120-885A-45	Sequence 45, Appl
878	24	100.0	18	16	US-10-258-144-377	Sequence 377, App	951	24	100.0	19	15	US-10-186-229-41	Sequence 41, Appl
879	24	100.0	18	16	US-10-258-144-397	Sequence 397, App	952	24	100.0	19	15	US-10-621-363-289	Sequence 289, App
880	24	100.0	18	16	US-10-258-144-407	Sequence 407, App	953	24	100.0	19	15	US-10-616-279-9	Sequence 9, Appl
881	24	100.0	18	16	US-10-258-144-447	Sequence 447, App	954	24	100.0	19	15	US-10-424-599-145516	Sequence 145516
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885	24	100.0	18	16	US-10-600-816-50	Sequence 50, Appl	958	24	100.0	19	15	US-10-258-147-22	Sequence 22, Appl
886	24	100.0	18	16	US-10-158-825-78	Sequence 78, Appl	959	24	100.0	19	15	US-10-257-864A-100	Sequence 100, App
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961 24 100.0 19 15 US-10-328-953-14
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965 24 100.0 19 15 US-10-367-654-9
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ALIGNMENTS

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RESULT 1
US-09-214-371-11
; Sequence 11, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT

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; LOCATION: (1)
; OTHER INFORMATION: X = arginine, asparagine, alanine, threonine or
; NAME/KEY: VARIANT
; LOCATION: (3)
; OTHER INFORMATION: X = methionine, isoleucine, threonine, arginine,
; OTHER INFORMATION: alanine or serine, preferably methionine
; NAME/KEY: VARIANT
; LOCATION: (4)
; OTHER INFORMATION: X = arginine, histidine, glutamic acid, cysteine,
; OTHER INFORMATION: serine or preferably aspartic acid.
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa = histidine, phenylalanine or preferably
; NAME/KEY: VARIANT
; LOCATION: (7)
; OTHER INFORMATION: X = glutamic acid, threonine, alanine,
; OTHER INFORMATION: phenylalanine or serine, preferably glutamic acid.
; NAME/KEY: VARIANT
; LOCATION: (8)
; OTHER INFORMATION: X = glycine, glutamine, threonine, alanine or
; OTHER INFORMATION: aspartic acid preferably glycine.
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: X = phenylalanine, glutamine or preferably
; OTHER INFORMATION: leucine.
US-09-214-371-11

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Query Match 100.0%; Score 24; DB 9; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 XFXXXWXXX 9
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Db 1 XFXXXWXXX 9

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RESULT 2
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; Sequence 15, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-15

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Query Match 100.0%; Score 24; DB 9; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXWXXX 9
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Db      1 RFMDYWEGL 9

RESULT 3
US-09-214-371-55
; Sequence 55, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:peptide
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; LOCATION: (1)
; OTHER INFORMATION: Product = Aib
; NAME/KEY: VARIANT
; LOCATION: (4)
; OTHER INFORMATION: Product = Aib
; NAME/KEY: VARIANT
; LOCATION: (7)
; OTHER INFORMATION: Product = Aib
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: X = Leu-NH2
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; Query Match          100.0%; Score 24; DB 9; Length 9;
; Best Local Similarity 66.7%; Pred. No. 1.7e+06;
; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
        ||:||:|
Db      1 XFMDYWEXX 9

RESULT 5
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; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: x = Ac-Arg
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: x = Leu-NH2
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; Query Match          100.0%; Score 24; DB 9; Length 9;
; Best Local Similarity 44.4%; Pred. No. 1.7e+06;
; Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
        ||:||:|
Db      1 XFMDYWEXX 9

RESULT 4
US-09-214-371-56
; Sequence 56, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
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RESULT 6
US-09-793-451-336
; Sequence 336, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Hubert, Rene S.
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-336

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Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 GFFPKWSGR 9

RESULT 7
US-10-062-109A-372
; Sequence 372, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-372

Query Match 100.0%; Score 24; DB 14; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 GFFPKWSGR 9

RESULT 8
US-10-005-480A-372
; Sequence 372, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-372

Query Match 100.0%; Score 24; DB 14; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 BFRKWDYF 9

RESULT 9
US-10-283-722-336
; Sequence 336, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR FILING DATE: US/09/793,451
; PRIOR APPLICATION NUMBER: 2001-02-26
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-336

Query Match 100.0%; Score 24; DB 14; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 BFRKWDYF 9
```

Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXXWXXX 9
:|::|:::
Db 1 GFPKWSGR 9

RESULT 10

```

US-10-334-726-212
; Sequence 212, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
; TITLE OF INVENTION: BREAST CANCER ANTIGEN
; FILE REFERENCE: 1090-36
; CURRENT APPLICATION NUMBER: US/10/334,726
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/645,446
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00866
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: GB 9805877.9
; PRIOR FILING DATE: 1998-09-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artifi
; OTHER INFORMATION: peptide
US-10-334-726-212

```

Query Match 100.0%; Score 24; DB 15; Length 9;
Best Local Similarity 22.2%; Pred.No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels

Qy	1 XFXXWXXX 9 : :: :::
Dd	1 VFEPSEEEF 9

RESULT 11

```

RESUL 11
US-10-283-903-336
; Sequence 336, Application US/10283903
; Publication No. US20030219766A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,903
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens

```

US-10-283-903-336

Query Match 100.0%; Score 24; DB 15; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels

Qy 1 XFXXXWXXX 9
:|::|:::
Db 1 GFPpKWSGR 9

RESULT 12

```

US-10-363-208-237
; Sequence 237, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-237

```

Query Match 100.0%; Score 24; DB 15; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy	1	X	F	X	X	X	X	9
		:	:	:	:	:	:	
Db	1	C	F	N	R	T	W	9

RESULT 13

```

US-10-258-146A-177
; Sequence 177, Application US/10258146A
; Publication No. US20040052812A1
; GENERAL INFORMATION:
; APPLICANT: Mee Hoe
; APPLICANT: Frank Landberger
; TITLE OF INVENTION: HEAT SHOCK PROTEIN-BASED ANTIVIRAL
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: 11390/46301
; CURRENT APPLICATION NUMBER: US/10/258,146A
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/US01/125568
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/197,462
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 177
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: obtained from a phage synthetic peptide
US-10-258-146A-177

```

```
Query Match      100.0%; Score 24; DB 15; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2: Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

Ov 1 XFXXXXXXX 9

```
Db          1 CFWGLWPWE 9
|||||:|:|:
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-685-838-12

Query Match          100.0%; Score 24; DB 16; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XPXXXWXXX 9
|||||:|:|:
Db 1 TFSDLWKL 9

RESULT 15
US-10-363-204-198
; Sequence 198, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 198
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)-(9)
; OTHER INFORMATION: synthetic construct
; US-10-363-204-198

Query Match          100.0%; Score 24; DB 16; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XPXXXWXXX 9
|||||:|:|:
Db 1 CFNRTWIGC 9

RESULT 16
US-10-685-838-12
; Sequence 12, Application US/10685838
; Publication No. US20040197893A1
; GENERAL INFORMATION:
; APPLICANT: SHUBERT, CARSTEN
```

```
; APPLICANT: GRASBERGER, BRUCE
; APPLICANT: MAGUIRE, DIANE
; APPLICANT: DECKMAN, INGRID
; APPLICANT: SPURLINO, JOHN
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF
; FILE REFERENCE: PRD-2137-USANP
; CURRENT APPLICATION NUMBER: US/10/685,838
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,350
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-685-838-12

Query Match          100.0%; Score 24; DB 16; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XPXXXWXXX 9
|||||:|:|:
Db 1 RPDYWEGL 9

RESULT 17
US-10-654-601-774
; Sequence 774, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
```



```
; SEQ ID NO 774
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-774

Query Match      100.0%; Score 24; DB 17; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
Db      1 IFFCLWVYI 9

RESULT 18
US-10-654-601-2028
; Sequence 2028, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2028
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-2028

Query Match      100.0%; Score 24; DB 17; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
Db      1 IFFCLWVYI 9
```

```
RESULT 19
US-10-916-064-91
; Sequence 91, Application US/10916064
; Publication No. US20050069930A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Tahara, Hideaki
; APPLICANT: Tsunoda, Takuya
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: Japan as represented by
; APPLICANT: The President of The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Human Colon Cancers
; FILE REFERENCE: 082379-000300US
; CURRENT APPLICATION NUMBER: US/10/916,064
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/415,209
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/451,013
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: WO PCT/JP03/07006
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized peptide sequence
US-10-916-064-91

Query Match      100.0%; Score 24; DB 17; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
Db      1 NFQPVWLCL 9

RESULT 20
US-10-363-205-230
; Sequence 230, Application US/10363205
; Publication No. US20050074747A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: US/10/363,205
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-205-230

Query Match      100.0%; Score 24; DB 17; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
Db      1 CFFRVWSRC 9
```

RESULT 21
US-10-927-262A-11
; Sequence 11, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTGER, VOLKER
; APPLICANT: BOTTGER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Arg, Asn, Ala, Thr, or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Met, Ile, Thr, Arg, Ala, or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: Arg, His, Glu, Cys, Ser, or Asp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Glu, Thr, Ala, Phe, or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: Glu, Thr, Ala, Phe, or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Gly, Gln, Thr, Ala, or Asp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Phe, Gln, or Leu
US-10-927-262A-11

Query Match 100.0%; Score 24; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXWXXX 9
DB 1 XFXXXWXXX 9

RESULT 22
US-10-927-262A-15
; Sequence 15, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTGER, VOLKER
; APPLICANT: BOTTGER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-927-262A-15

Query Match 100.0%; Score 24; DB 18; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XFXXXWXXX 9
DB 1 RFMDYWEGL 9

RESULT 23
US-10-927-262A-55
; Sequence 55, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTGER, VOLKER
; APPLICANT: BOTTGER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 55
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: Peptide

NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: Aib
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: Aib
US-10-927-262A-55

Query Match 100.0%; Score 24; DB 18; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:
Db 1 RFXYWXL 9

RESULT 24
US-10-927-262A-56
; Sequence 56, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTGER, VOLKER
; APPLICANT: BOTTGER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PASCAL
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-927-262A-56

Query Match 100.0%; Score 24; DB 18; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:
Db 1 RFXYWXL 9

QY 1 XFXXWXXX 9
:|:|:|:
Db 1 RFXYWXL 9

RESULT 25
US-10-927-262A-59
; Sequence 59, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTGER, VOLKER
; APPLICANT: BOTTGER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PASCAL
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749.0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-927-262A-59

Query Match 100.0%; Score 24; DB 18; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:
Db 1 RFXYWXL 9

RESULT 26
US-10-924-377-25
; Sequence 25, Application US/10924377
; Publication No. US20050181458A1
; GENERAL INFORMATION:
; APPLICANT: Harding, Fiona
; APPLICANT: Mucha, Jeanette Marie
; TITLE OF INVENTION: HPV CD8+ T-Cell Epitopes
; FILE REFERENCE: GC811-2US
; CURRENT APPLICATION NUMBER: US/10/924,377
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/500,452
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-924-377-25

Query Match 100.0%; Score 24; DB 18; Length 9;

Best Local Similarity 22.2%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 7;

QY 1 XFXXXWXXX 9
Db 1 SFVCPWCAS 9

RESULT 27

US-11-051-411-346
; Sequence 346, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: p53 Using Peptide And Nucleic Acid Compositions
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 346
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-346

Query Match 100.0%; Score 24; DB 20; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 TFSDLWKLL 9

RESULT 28

US-11-051-411-1053
; Sequence 1053, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: p53 Using Peptide And Nucleic Acid Compositions
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03

; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1053
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-1053

Query Match 100.0%; Score 24; DB 20; Length 9;
Best Local Similarity 22.2%; Pred. No. 1.7e+06;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 TFSDLWKLL 9

RESULT 29

US-09-214-371-3
; Sequence 3, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickesley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-209377/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Xaa represents any amino acid and proline,
; OTHER INFORMATION: phenylalanine, aspartic acid, tyrosine,
; OTHER INFORMATION: tryptophan and leucine are L-amino acids
US-09-214-371-3

Query Match 100.0%; Score 24; DB 9; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 XFEXDYWXXL 10

RESULT 30

US-09-214-371-4
; Sequence 4, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickesley, Stephen

```
/ APPLICANT: Chene, Patrick
/ APPLICANT: Hochkeppel, Heinz-Kurt
/ APPLICANT: Garcia-Echeverria, Carlos
/ APPLICANT: Furet, Pascal
/ TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
/ FILE REFERENCE: 4-20937/A/PCT
/ CURRENT APPLICATION NUMBER: US/09/214,371B
/ CURRENT FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: PCT/EP97/03549
/ PRIOR FILING DATE: 1997-07-04
/ NUMBER OF SEQ ID NOS: 83
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:peptide
/ NAME/KEY: VARIANT
/ LOCATION: (1)
/ OTHER INFORMATION: x=proline, leucine, glutamic acid, cysteine or
/ OTHER INFORMATION: glutamine
/ NAME/KEY: VARIANT
/ LOCATION: (5)
/ OTHER INFORMATION: x = histidine, phenylalanine, or preferably
/ OTHER INFORMATION: tyrosine
/ NAME/KEY: VARIANT
/ LOCATION: (6)
/ OTHER INFORMATION: x = arginine, histidine, glutamic acid, cysteine,
/ OTHER INFORMATION: serine or preferably aspartic acid.
/ NAME/KEY: VARIANT
/ LOCATION: (10)
/ OTHER INFORMATION: x=phenylalanine, glutamine or preferably leucine
/ OTHER INFORMATION: Xaa at position 2, 4, 8 and 9 is any amino acid
US-09-214-371-4

Query Match 100.0%; Score 24; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 XFXXXWXXX 10

RESULT 31
US-09-214-371-5
; Sequence 5, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickelley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
```

```
/ LOCATION: (1)
/ OTHER INFORMATION: x = proline, leucine, glutamic acid, cysteine or
/ OTHER INFORMATION: glutamine
/ NAME/KEY: VARIANT
/ LOCATION: (2)
/ OTHER INFORMATION: x = arginine, asparagine, alanine, threonine or
/ OTHER INFORMATION: valine
/ NAME/KEY: VARIANT
/ LOCATION: (4)
/ OTHER INFORMATION: X = methionine, isoleucine, threonine, arginine,
/ OTHER INFORMATION: alanine or serine
/ NAME/KEY: VARIANT
/ LOCATION: (5)
/ OTHER INFORMATION: X= arginine, histidine, glutamic acid, cysteine,
/ OTHER INFORMATION: serine or preferably aspartic acid.
/ NAME/KEY: VARIANT
/ LOCATION: (6)
/ OTHER INFORMATION: X = histidine, phenylalanine or preferably
/ OTHER INFORMATION: tyrosine
/ NAME/KEY: VARIANT
/ LOCATION: (8)
/ OTHER INFORMATION: X = glutamic acid, threonine, alanine,
/ OTHER INFORMATION: phenylalanine or serine
/ NAME/KEY: VARIANT
/ LOCATION: (9)
/ OTHER INFORMATION: X= glycine, glutamine, threonine, alanine or
/ OTHER INFORMATION: aspartic acid
/ NAME/KEY: VARIANT
/ LOCATION: (10)
/ OTHER INFORMATION: Xaa = phenylalanine, glutamine or preferably
/ OTHER INFORMATION: leucine
US-09-214-371-5

Query Match 100.0%; Score 24; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 2 XFXXXWXXX 10

RESULT 32
US-09-253-794-25
; Sequence 25, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
```

```
;
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-253-794-25
```

```
Query Match 100.0%; Score 24; DB 9; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XFXXWXXX 9
:|:|:|:|:
Db 2 YFGFPWFAY 10
```

RESULT 33

```
US-09-881-276-11
; Sequence 11, Application US/09881276
; Patent No. US20020031761A1
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DIX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polype
US-09-881-276-11
```

```
Query Match 100.0%; Score 24; DB 9; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XFXXWXXX 9
:|:|:|:|:
Db 1 PFCQYWNC 9
```

RESULT 34

```
US-09-826-290-390
; Sequence 390, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhkhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
```

```
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-390
```

```
Query Match 100.0%; Score 24; DB 9; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XFXXWXXX 9
:|:|:|:|:
Db 1 VFSLQWGEV 9
```

RESULT 35

```
US-09-809-638-483
; Sequence 483, Application US/09809638
; Publication No. US20030059895A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Arthur B. Raitano
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.35US01
; CURRENT APPLICATION NUMBER: US/09/809,638
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 483
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-638-483
```

```
Query Match 100.0%; Score 24; DB 10; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XFXXWXXX 9
:|:|:|:|:
Db 1 IFFCAWCTA 9
```

RESULT 36

```
US-09-572-404B-788
; Sequence 788, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
```

; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 788
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PAI1 OR PLANH1 at 193-202 and may interact with
; US-09-572-404B-788
; SEQUENCE 787 in this patent.

Query Match 100.0%; Score 24; DB 10; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 1 YFNGQWKTP 9

RESULT 37
US-09-572-404B-790
; Sequence 790, Application US/09572404B
; Publication No. US2003007837A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 790
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PAI1 OR PLANH1 at 192-201 and may interact with
; US-09-572-404B-790
; SEQUENCE 789 in this patent.

Query Match 100.0%; Score 24; DB 10; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 2 YFNGQWKTP 10

RESULT 38
US-09-793-451-106
; Sequence 106, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2US02
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-793-451-106

Query Match 100.0%; Score 24; DB 10; Length 10;
Best Local Similarity 22.3%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 2 GPPPKWSGR 10

RESULT 39
US-09-793-451-410
; Sequence 410, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2US02
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-793-451-410

Query Match 100.0%; Score 24; DB 10; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
Db 2 GPPPKWSGR 10

RESULT 40
US-10-005-646-13
; Sequence 13, Application US/10005646
; Publication No. US20020151496A1
; GENERAL INFORMATION:
; APPLICANT: BRINGMANN, PETER W.
; APPLICANT: FAULDS, DARYL
; APPLICANT: MITROVIC, BRANISLAVA
; APPLICANT: SRINIVASAN, SUBHA
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS
; FILE REFERENCE: BERLX 87
; CURRENT APPLICATION NUMBER: US/10/005,646
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/251,837
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-10-005-646-13

Query Match      100.0%; Score 24, DB 13; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.1e+04;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
Db 1 QFENWINT 9
```

Search completed: October 19, 2005, 15:51:00
Job time : 115.882 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:31:09 ; Search time 118.059 Seconds
(without alignments)
39.037 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	10	2	Q70F01 sus scrofa
2	24	100.0	10	2	Q79885 anolis pate
3	24	100.0	10	2	Q79897 hoplocercus
4	24	100.0	10	2	Q79903 oplurus cuv
5	24	100.0	10	2	Q79906 phrynosoma
6	24	100.0	10	2	P92707 platysaurus
7	24	100.0	10	2	Q8W7U4 anolis nite
8	24	100.0	10	2	Q8W8Q2 anolis punc
9	24	100.0	10	2	Q8W8Q3 anolis nite
10	24	100.0	10	2	Q8W8Q4 anolis punc
11	24	100.0	10	2	Q8W969 anolis orto
12	24	100.0	10	2	Q8W970 anolis nite
13	24	100.0	10	2	Q8W971 anolis fusc
14	24	100.0	10	2	Q8WDG6 anolis trac
15	24	100.0	10	2	Q8WDH0 anolis limi
16	24	100.0	10	2	Q8WDH2 anolis lemu
17	24	100.0	10	2	Q8WDH4 anolis carp
18	24	100.0	10	2	Q8WDH6 anolis wood
19	24	100.0	10	2	Q8WDH8 anolis mest
20	24	100.0	10	2	Q8WDI8 anolis tran
21	24	100.0	10	2	Q6UJL5 strophurus
22	24	100.0	10	2	Q6WBN7 sceloporur
23	24	100.0	10	2	Q6WBR1 sceloporur
24	24	100.0	10	2	Q6WBR4 sceloporur
25	24	100.0	10	2	Q6WBS3 sceloporur
26	24	100.0	10	2	Q6WBT8 sceloporur
27	24	100.0	10	2	Q6WBU1 sceloporur
28	24	100.0	10	2	Q6WBU4 sceloporur
29	24	100.0	10	2	Q6WBW2 phrynosoma
30	24	100.0	10	2	Q6WBW5 phrynosoma
31	24	100.0	10	2	Q6WBW8 phrynosoma

32	24	100.0	10	2	Q6WBX1
33	24	100.0	10	2	Q6WBX4
34	24	100.0	10	2	Q6WZN6
35	24	100.0	10	2	Q6X061
36	24	100.0	10	2	Q6X071
37	24	100.0	10	2	Q6X0C3
38	24	100.0	10	2	Q6X0D2
39	24	100.0	10	2	Q6X0D8
40	24	100.0	10	2	Q6X0E7
41	24	100.0	10	2	Q71DR5
42	24	100.0	10	2	Q71DR8
43	24	100.0	10	2	Q71DS4
44	24	100.0	10	2	Q71DS7
45	24	100.0	10	2	Q71DT0
46	24	100.0	10	2	Q71DT3
47	24	100.0	10	2	Q71DT6
48	24	100.0	10	2	Q71DT9
49	24	100.0	10	2	Q71DU2
50	24	100.0	10	2	Q71DU5
51	24	100.0	10	2	Q71DU8
52	24	100.0	10	2	Q71DW0
53	24	100.0	10	2	Q71DW3
54	24	100.0	10	2	Q71DW6
55	24	100.0	10	2	Q71DW9
56	24	100.0	10	2	Q71DX5
57	24	100.0	10	2	Q71DX8
58	24	100.0	10	2	Q71DY1
59	24	100.0	10	2	Q71DY4
60	24	100.0	10	2	Q71DY7
61	24	100.0	10	2	Q71DZ0
62	24	100.0	10	2	Q71DZ3
63	24	100.0	10	2	Q71E08
64	24	100.0	10	2	Q71E11
65	24	100.0	10	2	Q71E17
66	24	100.0	10	2	Q71E20
67	24	100.0	10	2	Q71E23
68	24	100.0	10	2	Q71E35
69	24	100.0	10	2	Q71SD0
70	24	100.0	10	2	Q9T8U8
71	24	100.0	10	2	Q9T8X1
72	24	100.0	10	2	Q9ZYS6
73	24	100.0	10	2	Q9ZYT2
74	24	100.0	11	2	Q8WES0
75	24	100.0	11	2	Q6E5N4
76	24	100.0	11	2	Q9G365
77	24	100.0	11	2	Q9G368
78	24	100.0	11	2	Q9G3Y9
79	24	100.0	11	2	Q9G5Z2
80	24	100.0	11	2	Q9G601
81	24	100.0	11	2	Q9G625
82	24	100.0	11	2	Q9G628
83	24	100.0	11	2	Q9G631
84	24	100.0	11	2	Q9G634
85	24	100.0	11	2	Q9G640
86	24	100.0	11	2	Q9G643
87	24	100.0	11	2	Q9G646
88	24	100.0	11	2	Q9G649
89	24	100.0	12	2	Q6WR31
90	24	100.0	12	2	Q6WR34
91	24	100.0	12	2	Q6WR37
92	24	100.0	12	2	Q6WR43
93	24	100.0	12	2	Q6WR52
94	24	100.0	12	2	Q6WR55
95	24	100.0	12	2	Q6WR58
96	24	100.0	12	2	Q6WR67
97	24	100.0	12	2	Q6WR73
98	24	100.0	12	2	Q6WR79
99	24	100.0	12	2	Q6WR82
100	24	100.0	12	2	Q6WR88
101	24	100.0	12	2	Q6WR91
102	24	100.0	12	2	Q6WR94
103	24	100.0	12	2	Q6WR97
104	24	100.0	12	2	Q6WRA0

Q6wbx1	phrynosoma
Q6wbx4	phrynosoma
Q6wzn6	anolis cybo
Q6x061	anolis haet
Q6x071	anolis shre
Q6x0c3	anolis whit
Q6x0d2	anolis armo
Q6x0d8	anolis long
Q6x0e7	anolis marc
Q71dr5	leiocephalu
Q71dr8	leiocephalu
Q71ds4	tropidurus
Q71ds7	tropidurus
Q71dt0	uranoscodon
Q71dt3	tropidurus
Q71dt6	uracentron
Q71dt9	stenocercus
Q71du2	stenocercus
Q71du5	stenocercus
Q71du8	sceloporus
Q71dw0	phrynosoma
Q71dw3	polychrus m
Q71dw6	polychrus a
Q71dw9	anisocephalus
Q71dx5	urostrophus
Q71dx8	enyalis le
Q71dy1	priestidacty
Q71dy4	leiosaurus
Q71dy7	leiosaurus
Q71dz0	diplolaemus
Q71dz3	diplolaemus
Q71e08	anolis cybo
Q71e11	chalarodon
Q71e17	morunasauru
Q71e20	enyaloides
Q71e23	corytophane
Q71e35	basiliscus
Q71sd0	liolaemus w
Q9t8u8	liolaemus p
Q9t8x1	liolaemus a
Q9zy86	stenocercus
Q9zyt2	leiocephalu
Q8wes0	ceratophora
Q6esn4	mantheyus p
Q9g365	calotes emm
Q9g368	draco blanf
Q9g3y9	pseudocalot
Q9g5z2	pseudocalot
Q9g601	bronchocela
Q9g625	calotes ver
Q9g628	calotes mys
Q9g631	calotes nig
Q9g634	calotes lio
Q9g640	calotes cey
Q9g643	calotes cal
Q9g646	sitana pont
Q9g649	otocryptis
Q6wr31	mycetera am
Q6wr34	phoenicopte
Q6wr37	buteo jamai
Q6wr43	scolopax mi
Q6wr52	asio otus
Q6wr55	crinifer pi
Q6wr58	musophaga v
Q6wr67	neomorphus
Q6wr73	coccyzus er
Q6wr79	cuculus can
Q6wr82	urocolius m
Q6wr88	coracias ep
Q6wr91	trogon curu
Q6wr94	tockus eryt
Q6wr97	anseranas s
Q6wra0	chauna torq

105	24	100.0	12	2	Q6WRA3	G6wra3 megapodius	178	23	95.8	19	2	Q9TU41	Q9tu41 loxodonta a
106	24	100.0	12	2	Q6WRA6	G6wra6 alectura la	179	23	95.8	19	2	Q9TU42	Q9tu42 mammothus p
107	24	100.0	12	2	Q6WRA9	G6wra9 cray rubra	180	23	95.8	19	2	Q99722	Q99722 lamprotorn
108	24	100.0	12	2	Q8HN63	Q8hn63 sayornis ph	181	23	95.8	20	2	Q673D5	Q673d5 dehalococco
109	24	100.0	12	2	Q8HN66	Q8hn66 acryllium v	182	22	91.7	9	1	AKH_HELZE	P67787 heliothis z
110	24	100.0	12	2	Q53579	Q53579 rhodobacter	183	22	91.7	15	2	Q9UC22	Q9uc22 homo sapien
111	24	100.0	13	1	BML2_BOMVA	P84211 bombina var	184	22	91.7	20	1	GBB4_RAT	Q35353 rattus norv
112	24	100.0	13	1	YPNE_PHOLU	P41122 photorhabdu	185	21	87.5	6	1	E101_LITRU	P82096 litorea rub
113	24	100.0	13	2	Q9XLI2	Q9xli2 bemisia tab	186	21	87.5	8	1	AKHG_GRYBI	P67785 gryllus bim
114	24	100.0	13	2	Q7MLIF5	Q7mlif5 freeisia ref	187	21	87.5	8	1	AKH_LIBAU	P25418 libellula a
115	24	100.0	13	2	Q6GNE7	Q6gne7 borrelia bu	188	21	87.5	8	1	AKH_PROTE	P61856 protophormi
116	24	100.0	15	2	Q53580	Q53580 rhodobacter	189	21	87.5	8	1	AKH_ROMMI	P67786 romalea mic
117	24	100.0	15	2	Q9R5D6	Q9r5d6 chromatium	190	21	87.5	8	1	AKH_TABAT	P14595 tabanus atr
118	24	100.0	16	2	Q760I9	Q760i9 aspergillus	191	21	87.5	8	1	HTFI_FERAM	P04548 periplaneta
119	24	100.0	16	2	Q79B06	Q79b06 helicobacte	192	21	87.5	8	1	HTF2_PERAM	P04549 periplaneta
120	24	100.0	16	2	Q8QGA1	Q8qga1 brachydanio	193	21	87.5	8	1	HTF_TENMO	P67789 tenebrio mo
121	24	100.0	17	2	Q8MIG9	Q8mig9 cynopterus	194	21	87.5	8	1	HTF_ZOPRU	P67790 zophobas ru
122	24	100.0	17	2	Q9QUJ4	Q9quj4 mus sp. mep	195	21	87.5	8	1	RPCH_PANBO	P08939 pandalus bo
123	24	100.0	17	2	Q6QLL7	Q6qli7 influenza a	196	21	87.5	8	2	Q7M4H6	Q7m4h6 ischnura se
124	24	100.0	17	2	Q6QLL9	Q6qli9 influenza a	197	21	87.5	8	2	Q7M4H7	Q7m4h7 pseudagrion
125	24	100.0	17	2	Q6QLM0	Q6qlm0 influenza a	198	21	87.5	9	2	Q7M3N6	Q7m3n6 gryllus bim
126	24	100.0	17	2	Q6QLM1	Q6qlm1 influenza a	199	21	87.5	10	1	GON1_PETWA	P04378 petromyzon
127	24	100.0	18	2	Q92YW4	Q92yw4 habrobracon	200	21	87.5	10	2	Q6UJL2	Q6ujl2 strophurus
128	24	100.0	18	2	Q92YX7	Q92yx7 perga conde	201	21	87.5	10	2	Q6X0B4	Q6x0e4 anolis stra
129	24	100.0	19	2	Q7S645	Q7s645 neurospora	202	21	87.5	10	2	Q9ZYU4	Q9zyu4 sceloporos
130	24	100.0	19	2	P83003	P83003 entamosba h	203	21	87.5	11	1	CA31_LITCI	P82089 litorea cit
131	24	100.0	19	2	Q9NLW2	Q9nlw2 equus cabal	204	21	87.5	11	1	CA32_LITCI	P82090 litorea cit
132	24	100.0	19	2	Q9RTV5	Q9rtv5 crithidia f	205	21	87.5	11	2	Q6E5M8	Q6e5m8 pyctolaemu
133	24	100.0	19	2	Q9ZYW7	Q9zyw7 ichneutes ro	206	21	87.5	11	2	Q9G359	Q9g359 japalura fl
134	24	100.0	19	2	Q9ZYW8	Q9zyw8 ichneutes b	207	21	87.5	11	2	Q9G607	Q9g607 aphanotis
135	24	100.0	19	2	Q44506	Q44506 anabaena va	208	21	87.5	12	2	P92680	P92680 trimeresuru
136	24	100.0	19	2	Q6QLM2	Q6qlm2 influenza a	209	21	87.5	13	2	Q9MQK0	Q9mqk0 cervus elap
137	24	100.0	19	2	Q9I329	Q9i329 human immun	210	21	87.5	13	2	Q9MQK6	Q9mqk6 rupicapra r
138	24	100.0	19	2	Q9WJBI	Q9wjbi human immun	211	21	87.5	14	2	Q9TQZ1	Q9tqz1 bos taurus
139	24	100.0	20	1	COXA_THUOB	P80972 thunus obe	212	21	87.5	15	2	Q6LCZ7	Q6lc27 homo sapien
140	24	100.0	20	1	CRTC_SPIOL	P30806 spinacia ol	213	21	87.5	15	2	Q99386	Q99386 sus scrofa
141	24	100.0	20	2	Q95M77	Q95mj7 tarsius syr	214	21	87.5	16	2	Q9N237	Q9n237 pan troglod
142	24	100.0	20	2	Q95MJ8	Q95mj8 galago moho	215	21	87.5	16	2	Q9T2Q8	Q9t2q8 solanum tub
143	24	100.0	20	2	Q95MJ9	Q95mj9 pan troglod	216	21	87.5	16	2	Q9R4F2	Q9r4f2 streptomyce
144	24	100.0	20	2	Q95MK0	Q95mk0 porgo pygma	217	21	87.5	16	2	Q9QW76	Q9qw76 mus sp. hom
145	24	100.0	20	2	Q95MK1	Q95mk1 colobus ang	218	21	87.5	17	2	Q7RM54	Q7rm54 plasmodium
146	24	100.0	20	2	Q95MK2	Q95mk2 papio cynoc	219	21	87.5	17	2	Q8MJ33	Q8mj33 sus scrofa
147	24	100.0	20	2	Q95MK3	Q95mk3 ateles belz	220	21	87.5	17	2	Q72017	Q72017 human immun
148	24	100.0	20	2	Q95MK4	Q95mk4 cheirogaleu	221	21	87.5	18	2	Q8N0X8	Q8n0x8 homo sapien
149	24	100.0	20	2	Q95MK5	Q95mk5 varecia var	222	21	87.5	18	2	Q9ZYW6	Q9zyw6 aleiodes sp
150	24	100.0	20	2	Q95MK6	Q95mk6 eulemur cor	223	21	87.5	18	2	Q8RU82	Q8ru82 zea mays fm
151	24	100.0	20	2	Q9TRAA	Q9traa sus scrofa	224	21	87.5	18	2	Q8NVH2	Q8nvh2 staphylococ
152	24	100.0	20	2	Q9R5E8	Q9r5e8 bacillus sp	225	21	87.5	18	2	Q9QW51	Q9qw51 mus sp. . a
153	24	100.0	20	2	Q6LD18	Q6ld18 mus musculu	226	21	87.5	19	2	Q7REE1	Q7ree1 plasmodium
154	24	100.0	20	2	Q6G548	Q6g548 human herpe	227	21	87.5	20	2	Q8WYR5	Q8wyr5 homo sapien
155	24	100.0	20	2	Q90X92	Q90x92 gallus gall	228	21	83.3	8	2	Q7GEM6	Q7gem6 branchiosto
156	23	95.8	9	2	Q28121	Q28121 bos taurus	229	20	83.3	9	2	Q71EB9	Q71eb9 homo sapien
157	23	95.8	9	2	Q8WGE6	Q8wge6 procambarus	230	20	83.3	9	2	Q9UCQ9	Q9ucq9 homo sapien
158	23	95.8	10	1	AKHX_LOCMI	P81626 locusta mig	231	20	83.3	10	2	Q7J5U5	Q7j5u5 ovias aries
159	23	95.8	10	1	HTFI_ROMMI	P18110 romalea mic	232	20	83.3	11	1	CORZ_PERAM	P11496 periplaneta
160	23	95.8	10	1	HTF2_CARMO	P62542 carausius m	233	20	83.3	11	2	Q6T302	Q6t302 chlamydomon
161	23	95.8	10	1	HTF2_EXITI	P62543 extatosoma	234	20	83.3	15	2	Q6LBS9	Q6lbs9 raja erinac
162	23	95.8	10	1	HTF2_BLAGO	P84220 blattella g	235	20	83.3	18	2	Q47246	Q47246 escherichia
163	23	95.8	10	1	HTF GROPO	P84221 gromphadori	236	20	83.3	20	2	Q9R4Y6	Q9r4y6 porphyromon
164	23	95.8	10	1	HTF_HELZE	P16353 heliothis z	237	19	79.2	10	1	GON2_ALLMI	P68073 alligator m
165	23	95.8	10	1	HTF_LEUMA	P84219 leucophaea	238	19	79.2	10	1	GON2_CHICK	P68072 gallus gall
166	23	95.8	10	1	HTF_NAUCI	P84218 nauphoeta c	239	19	79.2	10	1	GON2_CUOPA	P68075 clupea pall
167	23	95.8	10	1	HTF_TABAT	P14596 tabanus atr	240	19	79.2	10	1	GON2_HYDCC	P68076 hydroclagus
168	23	95.8	10	2	Q7M465	Q7m465 platyleura	241	19	79.2	10	1	GON2_SQUAC	P68074 squalus aca
169	23	95.8	14	2	Q71H30	Q71h30 andrena bra	242	19	79.2	10	1	GON3_ONCKE	P20367 oncorhynch
170	23	95.8	15	2	Q6JCQ4	Q6jcq4 tetraleurod	243	19	79.2	10	1	GON3_PETWA	P20348 petromyzon
171	23	95.8	15	2	Q6JCS2	Q6jcs2 aleuroplatu	244	19	79.2	10	1	GONL_SQUAC	P27429 squalus aca
172	23	95.8	16	2	Q697F2	Q697f2 bemisia sp.	245	19	79.2	10	2	Q79912	Q79912 chamaeleo f
173	23	95.8	16	2	Q9XNP6	Q9xnp6 boophilus m	246	19	79.2	10	2	Q8SH83	Q8sh83 brookeesia t
174	23	95.8	17	2	O15276	O15276 homo sapien	247	19	79.2	10	2	Q8SH85	Q8sh85 brookeesia t
175	23	95.8	17	2	Q7YIX8	Q7yix8 lilium long	248	19	79.2	10	2	Q8SH88	Q8sh88 brookeesia t
176	23	95.8	18	2	Q7S173	Q7s173 neurospora	249	19	79.2	10	2	Q8SH90	Q8sh90 brookeesia s
177	23	95.8	18	2	Q71U72	Q71u72 homo sapien	250	19	79.2	10	2	Q8SH96	Q8sh96 brookeesia p

251	19	79.2	10	2	Q8SH99	Q8sh99 brookesia n	324	18	75.0	10	2	Q958J8	Q958j8 rana muscos
252	19	79.2	10	2	Q8SHA2	Q8sha2 brookesia b	325	18	75.0	10	2	Q958K0	Q958k0 rana caecad
253	19	79.2	10	2	Q8SHA5	Q8sha5 brookesia a	326	18	75.0	10	2	Q958K3	Q958k3 rana aurora
254	19	79.2	10	2	Q8SHB1	Q8shb1 rhampoleon	327	18	75.0	10	2	Q958K6	Q958k6 rana pretio
255	19	79.2	10	2	Q8SHB4	Q8shb4 furcifer ve	328	18	75.0	10	2	Q958K9	Q958k9 rana boylii
256	19	79.2	10	2	Q8SHB7	Q8shb7 furcifer ou	329	18	75.0	10	2	Q958L2	Q958l2 rana tempor
257	19	79.2	10	2	Q8SHC0	Q8shc0 furcifer la	330	18	75.0	10	2	Q958L5	Q958l5 rana sylvat
258	19	79.2	10	2	Q8SHC3	Q8shc3 furcifer la	331	18	75.0	10	2	Q958L8	Q958l8 rana catesb
259	19	79.2	10	2	Q8SHC6	Q8shc6 furcifer be	332	18	75.0	10	2	Q6UJH3	Q6ujh3 lialis jica
260	19	79.2	10	2	Q8SHC9	Q8shc9 furcifer ba	333	18	75.0	10	2	Q6UJH6	Q6ujh6 pseudotheca
261	19	79.2	10	2	Q8SHD2	Q8shd2 chamaeleo w	334	18	75.0	10	2	Q6UJH9	Q6ujh9 phyllurus c
262	19	79.2	10	2	Q8SHD5	Q8shd5 chamaeleo s	335	18	75.0	10	2	Q6UJH12	Q6ujh12 nephurus m
263	19	79.2	10	2	Q8SHD8	Q8shd8 chamaeleo r	336	18	75.0	10	2	Q6UJH18	Q6ujh18 nephurus l
264	19	79.2	10	2	Q8SHE1	Q8she1 chamaeleo q	337	18	75.0	10	2	Q6UJH1	Q6ujh1 nephurus v
265	19	79.2	10	2	Q8SHE4	Q8she4 chamaeleo q	338	18	75.0	10	2	Q6UJH7	Q6ujh7 carphodacty
266	19	79.2	10	2	Q8SHE7	Q8she7 chamaeleo p	339	18	75.0	10	2	Q6UJK0	Q6ujk0 crenadactyl
267	19	79.2	10	2	Q8SHEF3	Q8shef3 chamaeleo m	340	18	75.0	10	2	Q6UJL8	Q6ujl8 strophurus
268	19	79.2	10	2	Q8SHF6	Q8shf6 chamaeleo m	341	18	75.0	10	2	Q6UJL1	Q6ujl1 strophurus
269	19	79.2	10	2	Q8SHF9	Q8shf9 chamaeleo j	342	18	75.0	10	2	Q9B0Z6	Q9b0z6 salamandra
270	19	79.2	10	2	Q8SHG2	Q8shg2 chamaeleo j	343	18	75.0	10	2	Q9B1W9	Q9b1w9 mertensiell
271	19	79.2	10	2	Q8SHG5	Q8shg5 chamaeleo h	344	18	75.0	10	2	Q9B1X0	Q9b1x0 mertensiell
272	19	79.2	10	2	Q8SHG8	Q8shg8 chamaeleo g	345	18	75.0	10	2	Q9B4S0	Q9b4s0 mertensiell
273	19	79.2	10	2	Q8SHH1	Q8shh1 chamaeleo f	346	18	75.0	10	2	Q9B4S5	Q9b4s5 mertensiell
274	19	79.2	10	2	Q8SHH4	Q8shh4 chamaeleo f	347	18	75.0	10	2	Q9B4S8	Q9b4s8 mertensiell
275	19	79.2	10	2	Q8SHH7	Q8shh7 chamaeleo e	348	18	75.0	10	2	Q9B4T1	Q9b4t1 mertensiell
276	19	79.2	10	2	Q8SHI0	Q8shio chamaeleo d	349	18	75.0	10	2	Q9B4U2	Q9b4u2 mertensiell
277	19	79.2	10	2	Q8SHI3	Q8shi3 chamaeleo c	350	18	75.0	10	2	Q9B4U5	Q9b4u5 mertensiell
278	19	79.2	10	2	Q8SHI6	Q8shi6 chamaeleo c	351	18	75.0	10	2	Q9B4U8	Q9b4u8 salamandra
279	19	79.2	10	2	Q8SHI9	Q8shi9 chamaeleo c	352	18	75.0	10	2	Q9B4V5	Q9b4v5 mertensiell
280	19	79.2	10	2	Q8SHJ2	Q8shj2 chamaeleo a	353	18	75.0	10	2	Q9B4V8	Q9b4v8 chiloglossa
281	19	79.2	10	2	Q8SHJ5	Q8shj5 calumma par	354	18	75.0	10	2	Q9B4W1	Q9b4w1 triturus vu
282	19	79.2	10	2	Q8SHJ8	Q8shj8 calumma osh	355	18	75.0	10	2	Q9B4W4	Q9b4w4 pachytriton
283	19	79.2	10	2	Q8SHK1	Q8shk1 calumma nas	356	18	75.0	10	2	Q9B4W7	Q9b4w7 tylotriton
284	19	79.2	10	2	Q8SHK4	Q8shk4 calumma hil	357	18	75.0	10	2	Q9B4X0	Q9b4x0 notophthalm
285	19	79.2	10	2	Q8SHK7	Q8shk7 calumma glo	358	18	75.0	10	2	Q9MJQ5	Q9mjQ5 potospora c
286	19	79.2	10	2	Q8SHL0	Q8shl0 calumma gas	359	18	75.0	10	2	Q9TFV2	Q9tfv2 teratoscinc
287	19	79.2	10	2	Q8SHL3	Q8shl3 calumma fur	360	18	75.0	11	2	Q94V15	Q94v15 varanus exa
288	19	79.2	10	2	Q8SHL6	Q8shl6 calumma cuc	361	18	75.0	11	2	Q9G637	Q9g637 calotes lio
289	19	79.2	10	2	Q8SHL9	Q8shl9 calumma bre	362	18	75.0	11	2	Q9G691	Q9g691 lophognathu
290	19	79.2	10	2	Q8SHM2	Q8shm2 calumma boe	363	18	75.0	11	2	Q83410	Q83410 mouse mamma
291	19	79.2	10	2	Q8SHM5	Q8shm5 bradypodion	364	18	75.0	12	2	Q6KEF1	Q6kef1 homo sapien
292	19	79.2	10	2	Q8SHM8	Q8shm8 bradypodion	365	18	75.0	12	2	Q9BZ49	Q9bz49 homo sapien
293	19	79.2	10	2	Q8SHN1	Q8shn1 bradypodion	366	18	75.0	12	2	Q6WR40	Q6wr40 burhinus se
294	19	79.2	10	2	Q8SHN4	Q8shn4 bradypodion	367	18	75.0	12	2	Q6WR46	Q6wr46 treron sieb
295	19	79.2	10	2	Q8SHN7	Q8shn7 bradypodion	368	18	75.0	12	2	Q6WR76	Q6wr76 centropus c
296	19	79.2	10	2	Q8SHP0	Q8shp0 bradypodion	369	18	75.0	12	2	Q6WR85	Q6wr85 collus stri
297	19	79.2	10	2	Q9G697	Q9g697 chamaeleo d	370	18	75.0	12	2	Q80Y04	Q80y04 rattus sp.
298	19	79.2	11	2	Q6DW13	Q6dw13 bos taurus	371	18	75.0	13	1	BML1_BOMVA	B4212 bombina var
299	19	79.2	11	2	Q77894	Q77894 oreochromis	372	18	75.0	13	2	Q99783	Q99783 caprimulgus
300	19	79.2	11	2	Q77895	Q77895 oreochromis	373	18	75.0	13	2	P92460	P92460 taxus bacca
301	19	79.2	11	2	Q77896	Q77896 oreochromis	374	18	75.0	13	2	Q36622	Q36622 picea abies
302	19	79.2	11	2	Q77898	Q77898 oreochromis	375	18	75.0	13	2	Q7M059	Q7m059 mus musculu
303	19	79.2	12	2	Q77915	Q77915 oreochromis	376	18	75.0	13	2	Q85645	Q85645 mouse mamma
304	19	79.2	13	2	Q9THR8	Q9thr8 bryopsis sp	377	18	75.0	14	1	ALYT_ALYOB	Q85645 alytes obst
305	19	79.2	13	2	Q718T2	Q718t2 newcastle d	378	18	75.0	14	1	BOMB_BOMBO	P08944 alberta bom
306	19	79.2	15	1	GLN2_P1NPS	P81107 pinus pinas	379	18	75.0	14	1	LPW_CITFR	P84214 bombina bom
307	19	79.2	15	2	Q7M110	Q7m110 bacillus ci	380	18	75.0	14	1	LPW_ECOLI	P03056 citrobacter
308	19	79.2	16	2	Q8HUM0	Q8hum0 uncultured	381	18	75.0	14	1	LPW_RHIME	P03053 escherichia
309	19	79.2	16	2	Q8HUM1	Q8hum1 uncultured	382	18	75.0	14	1	LPW_SALTY	P18854 rhizobium m
310	19	79.2	17	2	Q06800	Q06800 saccharomyc	383	18	75.0	14	2	Q7S6V5	P03054 salmonella
311	19	79.2	17	2	Q9TR22	Q9tr22 bos taurus	384	18	75.0	14	2	Q9BRY8	Q9bry8 homo sapien
312	19	79.2	20	2	Q7REE5	Q7ree5 plasmodium	385	18	75.0	14	2	Q7RLM6	Q7rlm6 plasmodium
313	18	75.0	18	1	AKH_GEOST	P84241 geotrupes s	386	18	75.0	14	2	Q9MJQ3	Q9mjQ3 podospora c
314	18	75.0	18	1	AKH_MELML	P84240 melolontha	387	18	75.0	14	2	Q7M1G6	Q7m1G6 avena sativ
315	18	75.0	18	1	AKH_PACMA	P84242 pachnoda ma	388	18	75.0	14	2	Q7M1G7	Q7m1G7 avena sativ
316	18	75.0	8	2	Q62721	Q62721 rattus norv	389	18	75.0	15	1	MUP_CAVPO	P83507 cavia porce
317	18	75.0	9	2	Q94XE6	Q94xe6 tectocoris	390	18	75.0	15	2	Q9TWD5	Q9twd5 locusta mig
318	18	75.0	19	2	Q85DB0	Q85db0 lepitemur s	391	18	75.0	15	2	P92076	P92076 euhadra her
319	18	75.0	10	2	Q7M3E8	Q7m3e8 sus scrofa	392	18	75.0	15	2	Q8SJ19	Q8sj19 phalacrocor
320	18	75.0	10	2	Q7TR47	Q7tr47 bos taurus	393	18	75.0	15	2	Q68PI7	Q68pi7 vasdavidus
321	18	75.0	10	2	P92733	P92733 fejeriarya	394	18	75.0	15	2	Q6JCR8	Q6jcr8 bemisia arg
322	18	75.0	10	2	P92762	P92762 uromastix a	395	18	75.0	15	2	Q76MK4	Q76mk4 eurypharynx
323	18	75.0	10	2	Q94NH4	Q94nh4 rana muscos	396	18	75.0	15	2	Q76MM0	Q76mm0 eurypharynx

397	18	75.0	15	2	P93515	P93515 arabidopsis	470	18	75.0	19	2	O99772	O99772 mycteria am
398	18	75.0	15	2	O9S8M8	O9S8M8 nicotiana a	471	18	75.0	19	2	O99773	O99773 nyctanassa
399	18	75.0	15	2	O9S8W9	O9S8W9 nicotiana a	472	18	75.0	19	2	O99776	O99776 pandion hal
400	18	75.0	15	2	O9S8X0	O9S8X0 nicotiana a	473	18	75.0	19	2	O99777	O99777 phasianus c
401	18	75.0	15	2	O6LCK0	O6LCK0 mus musculus	474	18	75.0	19	2	O99778	O99778 phalacrocor
402	18	75.0	15	2	O9QUT7	O9QUT7 mus sp. . g	475	18	75.0	19	2	O99779	O99779 phoenicopte
403	18	75.0	15	2	O9S8C0	O9S8C0 lupinus alb	476	18	75.0	19	2	O99780	O99780 podilymbus
404	18	75.0	16	2	O7MAY7	O7MAY7 pseudomonas	477	18	75.0	19	2	O99781	O99781 sphrapicus
405	18	75.0	16	2	O9R5K1	O9R5K1 pseudomonas	478	18	75.0	19	2	O99782	O99782 gavia pacif
406	18	75.0	16	2	O9CWF0	O9CWF0 mus musculus	479	18	75.0	19	2	O99784	O99784 urocolius m
407	18	75.0	16	2	O9PT90	O9PT90 gallus gall	480	18	75.0	19	2	O99785	O99785 tauraco har
408	18	75.0	17	1	LPW_AZOB	P50871 azospirillum	481	18	75.0	19	2	O99786	O99786 podiceps ni
409	18	75.0	17	1	O7M4W7	O7M4W7 flamulina	482	18	75.0	19	2	O99787	O99787 cathartes a
410	18	75.0	17	2	O7S179	O7S179 neurospora	483	18	75.0	19	2	O99788	O99788 toctus eryt
411	18	75.0	17	2	O81VK5	O81VK5 homo sapien	484	18	75.0	19	2	O99789	O99789 trogon curu
412	18	75.0	17	2	O7RDV1	O7RDV1 plasmodium	485	18	75.0	19	2	O99790	O99790 zenaida mac
413	18	75.0	17	2	O7RQU2	O7RQU2 plasmodium	486	18	75.0	19	2	O99791	O99791 zenaida mac
414	18	75.0	17	2	Q12862	Q12862 homo sapien	487	18	75.0	19	2	O99792	O99792 trogon curu
415	18	75.0	17	2	O9ZYW0	O9ZYW0 betylobraco	488	18	75.0	19	2	O99793	O99793 trogon curu
416	18	75.0	17	2	O9S8J2	O9S8J2 trichosanth	489	18	75.0	19	2	O99794	O99794 trogon curu
417	18	75.0	17	2	O9S919	O9S919 petunia hyb	490	18	75.0	19	2	O99795	O99795 trogon curu
418	18	75.0	17	2	O7M0G9	P46155 klebsiella	491	18	75.0	19	2	O99796	O99796 trogon curu
419	18	75.0	18	1	TOPI_KLEAE	O6uz65 littorina s	492	18	75.0	19	2	O99797	O99797 trogon curu
420	18	75.0	18	2	O6UZ65	O6uz65 littorina s	493	18	75.0	19	2	O99798	O99798 trogon curu
421	18	75.0	18	2	O9ZY78	O9ZY78 gryon sp. c	494	18	75.0	19	2	O99799	O99799 trogon curu
422	18	75.0	18	2	O9ZY79	O9ZY79 idris sp. c	495	18	75.0	19	2	O99800	O99800 trogon curu
423	18	75.0	18	2	O9ZY83	O9ZY83 xylocopa vi	496	18	75.0	19	2	O99801	O99801 trogon curu
424	18	75.0	18	2	O9ZYV8	O9ZYV8 aspilota sp	497	18	75.0	19	2	O99802	O99802 trogon curu
425	18	75.0	18	2	O9ZYV9	O9ZYV9 opius kraus	498	18	75.0	19	2	O99803	O99803 trogon curu
426	18	75.0	18	2	O8Z675	O8Z675 cryptoglena	499	18	75.0	19	2	O99804	O99804 trogon curu
427	18	75.0	18	2	O30588	O30588 streptomyce	500	18	75.0	19	2	O99805	O99805 trogon curu
428	18	75.0	18	2	O8R170	O8R170 mus musculus	501	18	75.0	19	2	O99806	O99806 trogon curu
429	18	75.0	18	2	O69185	O69185 human cytom	502	18	75.0	19	2	O99807	O99807 trogon curu
430	18	75.0	19	1	UC31_MAIZE	P80637 zea mays (m	503	18	75.0	19	2	O99808	O99808 trogon curu
431	18	75.0	19	2	Q16184	Q16184 homo sapien	504	18	75.0	19	2	O99809	O99809 trogon curu
432	18	75.0	19	2	O81VK8	O81VK8 homo sapien	505	18	75.0	19	2	O99810	O99810 trogon curu
433	18	75.0	19	2	O8NPL2	O8NPL2 homo sapien	506	18	75.0	19	2	O99811	O99811 trogon curu
434	18	75.0	19	2	O97584	O97584 macaca mula	507	18	75.0	19	2	O99812	O99812 trogon curu
435	18	75.0	19	2	O9BDG4	O9BDG4 bos taurus	508	18	75.0	19	2	O99813	O99813 trogon curu
436	18	75.0	19	2	O99724	O99724 dryoscopus	509	18	75.0	19	2	O99814	O99814 trogon curu
437	18	75.0	19	2	O99726	O99726 geococcyx c	510	18	75.0	19	2	O99815	O99815 trogon curu
438	18	75.0	19	2	O99728	O99728 buteo jama	511	18	75.0	19	2	O99816	O99816 trogon curu
439	18	75.0	19	2	O99730	O99730 chaetura ci	512	18	75.0	19	2	O99817	O99817 trogon curu
440	18	75.0	19	2	O99732	O99732 corvus brac	513	18	75.0	19	2	O99818	O99818 trogon curu
441	18	75.0	19	2	O99734	O99734 dendrocygna	514	18	75.0	19	2	O99819	O99819 trogon curu
442	18	75.0	19	2	O99736	O99736 lanius coll	515	18	75.0	19	2	O99820	O99820 trogon curu
443	18	75.0	19	2	O99738	O99738 sayornis ph	516	18	75.0	19	2	O99821	O99821 trogon curu
444	18	75.0	19	2	O99740	O99740 scolopax mi	517	18	75.0	19	2	O99822	O99822 trogon curu
445	18	75.0	19	2	O99742	O99742 sturnus vul	518	18	75.0	19	2	O99823	O99823 trogon curu
446	18	75.0	19	2	O99744	O99744 certhia fam	519	18	75.0	19	2	O99824	O99824 trogon curu
447	18	75.0	19	2	O99746	O99746 crocodylus	520	18	75.0	19	2	O99825	O99825 trogon curu
448	18	75.0	19	2	O99750	O99750 neophema el	521	18	75.0	19	2	O99826	O99826 trogon curu
449	18	75.0	19	2	O99751	O99751 alcedo cris	522	18	75.0	19	2	O99827	O99827 trogon curu
450	18	75.0	19	2	O99752	O99752 coracias sp	523	18	75.0	19	2	O99828	O99828 trogon curu
451	18	75.0	19	2	O99753	O99753 acryllium v	524	18	75.0	19	2	O99829	O99829 trogon curu
452	18	75.0	19	2	O99754	O99754 anseranas s	525	18	75.0	19	2	O99830	O99830 trogon curu
453	18	75.0	19	2	O99755	O99755 aptenodytes	526	18	75.0	19	2	O99831	O99831 trogon curu
454	18	75.0	19	2	O99756	O99756 bonasa umbe	527	18	75.0	19	2	O99832	O99832 trogon curu
455	18	75.0	19	2	O99757	O99757 burhinus oe	528	18	75.0	19	2	O99833	O99833 trogon curu
456	18	75.0	19	2	O99758	O99758 cactatus gof	529	18	75.0	19	2	O99834	O99834 trogon curu
457	18	75.0	19	2	O99759	O99759 cathartes m	530	18	75.0	19	2	O99835	O99835 trogon curu
458	18	75.0	19	2	O99760	O99760 cephus col	531	18	75.0	19	2	O99836	O99836 trogon curu
459	18	75.0	19	2	O99761	O99761 chordelles	532	18	75.0	19	2	O99837	O99837 trogon curu
460	18	75.0	19	2	O99762	O99762 colaptes au	533	18	75.0	19	2	O99838	O99838 trogon curu
461	18	75.0	19	2	O99763	O99763 coccyzus er	534	18	75.0	19	2	O99839	O99839 trogon curu
462	18	75.0	19	2	O99764	O99764 colius stri	535	18	75.0	19	2	O99840	O99840 trogon curu
463	18	75.0	19	2	O99765	O99765 diomedea ni	536	18	75.0	19	2	O99841	O99841 trogon curu
464	18	75.0	19	2	O99766	O99766 eudromia el	537	18	75.0	19	2	O99842	O99842 trogon curu
465	18	75.0	19	2	O99767	O99767 fulica amer	538	18	75.0	19	2	O99843	O99843 trogon curu
466	18	75.0	19	2	O99768	O99768 gavia immer	539	18	75.0	19	2	O99844	O99844 trogon curu
467	18	75.0	19	2	O99769	O99769 grus canade	540	18	75.0	19	2	O99845	O99845 trogon curu
468	18	75.0	19	2	O99770	O99770 gyps fulvus	541	17	70.8	7	1	O99846	O99846 trogon curu
469	18	75.0	19	2	O99771	O99771 meleagris g	542	17	70.8	7	2	O99847	O99847 trogon curu

543	17	70.8	7	2	O49223	O49223 glycine max	616	17	70.8	10	2	O79891	O79891 crotaphytus
544	17	70.8	8	1	CCKN_DASVI	P68125 dasyurus vi	617	17	70.8	10	2	O79894	O79894 gambelia wi
545	17	70.8	8	1	CCKN_MACEU	P68126 macropus eu	618	17	70.8	10	2	O79900	O79900 liaeomus p
546	17	70.8	8	1	VAM6_MOUSE	P83853 mus musculus	619	17	70.8	10	2	O79909	O79909 sauromalus
547	17	70.8	8	2	O9TR3	O9TRY3 sus sp. ins	620	17	70.8	10	2	O79915	O79915 leirolepis b
548	17	70.8	8	2	O8WGD7	O8WGD7 lomus hirta	621	17	70.8	10	2	O79924	O79924 elgaria pan
549	17	70.8	8	2	O94V82	O94V82 varanus yuw	622	17	70.8	10	2	P92616	P92616 aspidosceli
550	17	70.8	8	2	O94V88	O94V88 varanus tri	623	17	70.8	10	2	P92632	P92632 eremias gra
551	17	70.8	8	2	O94V91	O94V91 varanus tim	624	17	70.8	10	2	P92648	P92648 lialis jica
552	17	70.8	8	2	O94VA7	O94VA7 varanus sal	625	17	70.8	10	2	P92654	P92654 euprepis au
553	17	70.8	8	2	O94VB2	O94VB2 varanus sal	626	17	70.8	10	2	P92758	P92758 teratoscinc
554	17	70.8	8	2	O94VB5	O94VB5 varanus sal	627	17	70.8	10	2	P92766	P92766 varanus gri
555	17	70.8	8	2	O94VC1	O94VC1 varanus rud	628	17	70.8	10	2	P92771	P92771 xenosaurus
556	17	70.8	8	2	O94VE4	O94VE4 varanus mel	629	17	70.8	10	2	P92774	P92774 xantusia vi
557	17	70.8	8	2	O94VF6	O94VF6 varanus job	630	17	70.8	10	2	O8SH93	O8SH93 brookesia p
558	17	70.8	8	2	O94VF9	O94VF9 varanus ind	631	17	70.8	10	2	O8SHA8	O8SHA8 rhampholeon
559	17	70.8	8	2	O94VJ4	O94VJ4 varanus ben	632	17	70.8	10	2	O8SIT8	O8SIT8 xantusia ar
560	17	70.8	8	2	O70Y57	O70Y57 fuerstia af	633	17	70.8	10	2	O8SIU1	O8SIU1 xantusia be
561	17	70.8	8	2	O715L5	O715L5 varanus dum	634	17	70.8	10	2	O8SIU4	O8SIU4 xantusia he
562	17	70.8	8	2	O9TD02	O9TD02 terranatos	635	17	70.8	10	2	O8W916	O8W916 liaeomus m
563	17	70.8	8	2	O85406	O85406 coxiella bu	636	17	70.8	10	2	O8WDG8	O8WDG8 anolis line
564	17	70.8	8	2	O7M124	O7M124 kluyvera ci	637	17	70.8	10	2	O8WDI0	O8WDI0 anolis sagr
565	17	70.8	8	2	P79940	P79940 xenopus lae	638	17	70.8	10	2	O94PD8	O94PD8 varanus sca
566	17	70.8	8	2	O7L227	O7L227 najia oxiana	639	17	70.8	10	2	O94V85	O94V85 varanus var
567	17	70.8	9	1	CAER_PHYSA	O71ZC4 phyllomedus	640	17	70.8	10	2	O94V97	O94V97 varanus spe
568	17	70.8	9	1	COW_CONVE	P83047 conus ventr	641	17	70.8	10	2	O94VC9	O94VC9 varanus pan
569	17	70.8	9	1	NEF_HV128	P12481 human immu	642	17	70.8	10	2	O94VD2	O94VD2 varanus pan
570	17	70.8	9	2	O9H326	O9H326 homo sapien	643	17	70.8	10	2	O94VD5	O94VD5 varanus oll
571	17	70.8	9	2	O9UK44	O9UK44 homo sapien	644	17	70.8	10	2	O94VF0	O94VF0 varanus kin
572	17	70.8	9	2	O9UNAO	O9UNAO homo sapien	645	17	70.8	10	2	O94VG5	O94VG5 varanus gri
573	17	70.8	9	2	O7M4D5	O7M4D5 diadema set	646	17	70.8	10	2	O94VH1	O94VH1 varanus gle
574	17	70.8	9	2	O8SHF0	O8SHF0 chamaeleo n	647	17	70.8	10	2	O6UJG7	O6UJG7 heterototia
575	17	70.8	9	2	O94NA9	O94NA9 daubentonia	648	17	70.8	10	2	O6UJH0	O6UJH0 gehyra vari
576	17	70.8	9	2	O94NB0	O94NB0 microcebus	649	17	70.8	10	2	O6UJH5	O6UJH5 nephurus w
577	17	70.8	9	2	O94NB1	O94NB1 microcebus	650	17	70.8	10	2	O6UJH4	O6UJH4 nephurus l
578	17	70.8	9	2	O94NB2	O94NB2 microcebus	651	17	70.8	10	2	O6UJK3	O6UJK3 oedura marm
579	17	70.8	9	2	O94VC6	O94VC6 varanus pil	652	17	70.8	10	2	O6UJK6	O6UJK6 rhynchoedur
580	17	70.8	9	2	O94VD8	O94VD8 varanus nil	653	17	70.8	10	2	O6UJK9	O6UJK9 diplodactyl
581	17	70.8	9	2	O94VE1	O94VE1 varanus mer	654	17	70.8	10	2	O6UJM4	O6UJM4 diplodactyl
582	17	70.8	9	2	O94VG2	O94VG2 varanus ind	655	17	70.8	10	2	O6UJM7	O6UJM7 strophurus
583	17	70.8	9	2	O94VH4	O94VH4 varanus gla	656	17	70.8	10	2	O6UJN0	O6UJN0 diplodactyl
584	17	70.8	9	2	O94VI0	O94VI0 varanus gig	657	17	70.8	10	2	O6UJN3	O6UJN3 diplodactyl
585	17	70.8	9	2	O94VJ8	O94VJ8 varanus ere	658	17	70.8	10	2	O6UJN6	O6UJN6 diplodactyl
586	17	70.8	9	2	O94VJ1	O94VJ1 varanus dor	659	17	70.8	10	2	O6UJN9	O6UJN9 diplodactyl
587	17	70.8	9	2	O69ID6	O69ID6 anolis sagr	660	17	70.8	10	2	O6UJP2	O6UJP2 diplodactyl
588	17	70.8	9	2	O71DX2	O71DX2 urostrophus	661	17	70.8	10	2	O6UJP5	O6UJP5 diplodactyl
589	17	70.8	9	2	O85DB8	O85DB8 leplemur e	662	17	70.8	10	2	O6UJP8	O6UJP8 diplodactyl
590	17	70.8	9	2	O9T688	O9T688 gecko gecko	663	17	70.8	10	2	O6UJQ1	O6UJQ1 diplodactyl
591	17	70.8	9	2	O38366	O38366 bacterioph	664	17	70.8	10	2	O6UJQ4	O6UJQ4 strophurus
592	17	70.8	9	2	O62200	O62200 silene rotu	665	17	70.8	10	2	O6UJQ7	O6UJQ7 strophurus
593	17	70.8	9	2	O6VCX0	O6VCX0 streptomyce	666	17	70.8	10	2	O6UJF0	O6UJF0 strophurus
594	17	70.8	9	2	O9RSM1	O9RSM1 staphylococ	667	17	70.8	10	2	O6WBG8	O6WBG8 liaeomus c
595	17	70.8	9	2	O6LAQ1	O6LAQ1 rattus norv	668	17	70.8	10	2	O6WBH1	O6WBH1 liaeomus x
596	17	70.8	9	2	O80X07	O80X07 mus sp. thr	669	17	70.8	10	2	O6WBH4	O6WBH4 liaeomus r
597	17	70.8	9	2	O89491	O89491 murine minu	670	17	70.8	10	2	O6WBH7	O6WBH7 liaeomus h
598	17	70.8	9	2	O78DU2	O78DU2 gallus gall	671	17	70.8	10	2	O6WB10	O6WB10 liaeomus s
599	17	70.8	9	2	O9PRJ4	O9PRJ4 lepisosteus	672	17	70.8	10	2	O6WB13	O6WB13 liaeomus p
600	17	70.8	9	2	O85723	O85723 simian sarc	673	17	70.8	10	2	O6WB16	O6WB16 liaeomus k
601	17	70.8	10	1	AEGL_AGRAE	P83465 agrocypae ae	674	17	70.8	10	2	O6WB19	O6WB19 liaeomus h
602	17	70.8	10	1	APE_CAPGI	P80474 capnocytoph	675	17	70.8	10	2	O6WBJ2	O6WBJ2 liaeomus p
603	17	70.8	10	1	BRK_ONCMY	O9PRZ1 oncorhynch	676	17	70.8	10	2	O6WBJ5	O6WBJ5 liaeomus g
604	17	70.8	10	1	CA12_LITCI	P62540 litoria cit	677	17	70.8	10	2	O6WBJ8	O6WBJ8 liaeomus n
605	17	70.8	10	1	CA12_LITSP	P62541 litoria spl	678	17	70.8	10	2	O6WBK1	O6WBK1 scelopor
606	17	70.8	10	1	CAER_LITXA	P56264 litoria xan	679	17	70.8	10	2	O6WBK4	O6WBK4 scelopor
607	17	70.8	10	1	GRP_RANKI	P23260 rana ridibu	680	17	70.8	10	2	O6WBK7	O6WBK7 scelopor
608	17	70.8	10	1	LABA_JATMU	P13270 jatrophia mu	681	17	70.8	10	2	O6WBL0	O6WBL0 scelopor
609	17	70.8	10	1	MP2_MICOC	P81533 microplitis	682	17	70.8	10	2	O6WBL3	O6WBL3 scelopor
610	17	70.8	10	2	O7M530	O7M530 pyrococtus	683	17	70.8	10	2	O6WBL6	O6WBL6 scelopor
611	17	70.8	10	2	O15342	O15342 homo sapien	684	17	70.8	10	2	O6WBL9	O6WBL9 scelopor
612	17	70.8	10	2	O8WTT4	O8WTT4 homo sapien	685	17	70.8	10	2	O6WBM2	O6WBM2 scelopor
613	17	70.8	10	2	O6LA62	O6LA62 homo sapien	686	17	70.8	10	2	O6WBM5	O6WBM5 scelopor
614	17	70.8	10	2	O7M228	O7M228 bos taurus	687	17	70.8	10	2	O6WBM8	O6WBM8 scelopor
615	17	70.8	10	2	O79888	O79888 basiliscus	688	17	70.8	10	2	O6WBN1	O6WBN1 scelopor

689	17	70.8	10	2	Q6WBN4	Q6wbn4 scelopor	762	17	70.8	10	2	Q9T8P9	Q9t8p9 liolaemus m
690	17	70.8	10	2	Q6WBP0	Q6wbp0 scelopor	763	17	70.8	10	2	Q9T8Q2	Q9t8q2 liolaemus s
691	17	70.8	10	2	Q6WBP3	Q6wbp3 scelopor	764	17	70.8	10	2	Q9T8Q5	Q9t8q5 liolaemus l
692	17	70.8	10	2	Q6WBP6	Q6wbp6 scelopor	765	17	70.8	10	2	Q9T8Q8	Q9t8q8 liolaemus e
693	17	70.8	10	2	Q6WBP9	Q6wbp9 scelopor	766	17	70.8	10	2	Q9T8R1	Q9t8r1 liolaemus a
694	17	70.8	10	2	Q6WBQ2	Q6wbq2 scelopor	767	17	70.8	10	2	Q9T8R4	Q9t8r4 liolaemus p
695	17	70.8	10	2	Q6WBQ5	Q6wbq5 scelopor	768	17	70.8	10	2	Q9T8R7	Q9t8r7 liolaemus c
696	17	70.8	10	2	Q6WBQ8	Q6wbq8 scelopor	769	17	70.8	10	2	Q9T8R9	Q9t8r9 liolaemus b
697	17	70.8	10	2	Q6WBR7	Q6wbr7 scelopor	770	17	70.8	10	2	Q9T8S1	Q9t8s1 liolaemus l
698	17	70.8	10	2	Q6WBS0	Q6wbs0 scelopor	771	17	70.8	10	2	Q9T8S4	Q9t8s4 liolaemus c
699	17	70.8	10	2	Q6WBS6	Q6wbs6 scelopor	772	17	70.8	10	2	Q9T8S7	Q9t8s7 liolaemus n
700	17	70.8	10	2	Q6WBS9	Q6wbs9 scelopor	773	17	70.8	10	2	Q9T8T0	Q9t8t0 liolaemus f
701	17	70.8	10	2	Q6WBT2	Q6wbt2 scelopor	774	17	70.8	10	2	Q9T8T3	Q9t8t3 liolaemus n
702	17	70.8	10	2	Q6WBT5	Q6wbt5 scelopor	775	17	70.8	10	2	Q9T8T6	Q9t8t6 liolaemus m
703	17	70.8	10	2	Q6WBV0	Q6wbv0 urosaur	776	17	70.8	10	2	Q9T8T9	Q9t8t9 liolaemus l
704	17	70.8	10	2	Q6WBV7	Q6wbv7 callisaur	777	17	70.8	10	2	Q9T8U2	Q9t8u2 liolaemus t
705	17	70.8	10	2	Q6WBV3	Q6wbv3 holbrookia	778	17	70.8	10	2	Q9T8U5	Q9t8u5 liolaemus z
706	17	70.8	10	2	Q6WBV6	Q6wbv6 holbrookia	779	17	70.8	10	2	Q9T8V0	Q9t8v0 liolaemus c
707	17	70.8	10	2	Q6WBV9	Q6wbv9 cophosaur	780	17	70.8	10	2	Q9T8V3	Q9t8v3 liolaemus c
708	17	70.8	10	2	Q71DS1	Q71ds1 microloph	781	17	70.8	10	2	Q9T8V6	Q9t8v6 liolaemus b
709	17	70.8	10	2	Q71DV1	Q71dv1 scelopor	782	17	70.8	10	2	Q9T8V9	Q9t8v9 liolaemus g
710	17	70.8	10	2	Q71DV4	Q71dv4 scelopor	783	17	70.8	10	2	Q9T8W2	Q9t8w2 liolaemus b
711	17	70.8	10	2	Q71DV7	Q71dv7 scelopor	784	17	70.8	10	2	Q9T8W5	Q9t8w5 liolaemus r
712	17	70.8	10	2	Q71E02	Q71e02 anolis dist	785	17	70.8	10	2	Q9T8W8	Q9t8w8 liolaemus b
713	17	70.8	10	2	Q71E05	Q71e05 anolis crisi	786	17	70.8	10	2	Q9T8X4	Q9t8x4 liolaemus c
714	17	70.8	10	2	Q71E14	Q71e14 brachylophu	787	17	70.8	10	2	Q9T8X7	Q9t8x7 phymaturus
715	17	70.8	10	2	Q71E26	Q71e26 corytophane	788	17	70.8	10	2	Q9TFU6	Q9tfu6 teratoscinc
716	17	70.8	10	2	Q71E29	Q71e29 laemantus	789	17	70.8	10	2	Q9TFU9	Q9tfu9 teratoscinc
717	17	70.8	10	2	Q71E32	Q71e32 basiliscus	790	17	70.8	10	2	Q9TFV5	Q9tfv5 eublepharus
718	17	70.8	10	2	Q71ESB8	Q71esb8 liolaemus r	791	17	70.8	10	2	Q9TG32	Q9tg32 ophisaurus
719	17	70.8	10	2	Q71ISC1	Q71isc1 liolaemus f	792	17	70.8	10	2	Q9TG35	Q9tg35 ophisaurus
720	17	70.8	10	2	Q71ISC4	Q71isc4 liolaemus a	793	17	70.8	10	2	Q9TG38	Q9tg38 ophisaurus
721	17	70.8	10	2	Q71ISC7	Q71isc7 liolaemus s	794	17	70.8	10	2	Q9TG41	Q9tg41 ophisaurus
722	17	70.8	10	2	Q71ISD6	Q71isd6 liolaemus a	795	17	70.8	10	2	Q9TG44	Q9tg44 anguis frag
723	17	70.8	10	2	Q71ISD9	Q71isd9 liolaemus a	796	17	70.8	10	2	Q9TG47	Q9tg47 ophisaurus
724	17	70.8	10	2	Q71SE2	Q71se2 phymaturus	797	17	70.8	10	2	Q9TG50	Q9tg50 elgaria mul
725	17	70.8	10	2	Q71SE5	Q71se5 phymaturus	798	17	70.8	10	2	Q9TG53	Q9tg53 elgaria pau
726	17	70.8	10	2	Q71SE8	Q71se8 ctenoblepha	799	17	70.8	10	2	Q9TG56	Q9tg56 elgaria kin
727	17	70.8	10	2	Q76ML6	Q76ml6 eurypharynx	800	17	70.8	10	2	Q9TG59	Q9tg59 elgaria coe
728	17	70.8	10	2	Q85J75	Q85j75 varanus bre	801	17	70.8	10	2	Q9TG62	Q9tg62 mesaspis mo
729	17	70.8	10	2	Q9G362	Q9g362 acanthosaur	802	17	70.8	10	2	Q9TG65	Q9tg65 abronia oax
730	17	70.8	10	2	Q9G694	Q9g694 leiolepis g	803	17	70.8	10	2	Q9TG68	Q9tg68 gerhonorus
731	17	70.8	10	2	Q9T4P9	Q9t4p9 liolaemus d	804	17	70.8	10	2	Q9TG71	Q9tg71 barisia imb
732	17	70.8	10	2	Q9T8P5	Q9t8p5 liolaemus b	805	17	70.8	10	2	Q9TG74	Q9tg74 wetmorena h
733	17	70.8	10	2	Q9T8G0	Q9t8g0 liolaemus l	806	17	70.8	10	2	Q9TG77	Q9tg77 sauresia ag
734	17	70.8	10	2	Q9T8G5	Q9t8g5 liolaemus o	807	17	70.8	10	2	Q9TG80	Q9tg80 ophiodes at
735	17	70.8	10	2	Q9T8G8	Q9t8g8 liolaemus c	808	17	70.8	10	2	Q9TG83	Q9tg83 diploglossu
736	17	70.8	10	2	Q9T8H1	Q9t8h1 liolaemus u	809	17	70.8	10	2	Q9TG86	Q9tg86 diploglossu
737	17	70.8	10	2	Q9T8H4	Q9t8h4 liolaemus i	810	17	70.8	10	2	Q9TG89	Q9tg89 celestus en
738	17	70.8	10	2	Q9T8H7	Q9t8h7 liolaemus a	811	17	70.8	10	2	Q9TG92	Q9tg92 annielia pu
739	17	70.8	10	2	Q9T8I0	Q9t8i0 liolaemus o	812	17	70.8	10	2	Q9TG95	Q9tg95 annielia ge
740	17	70.8	10	2	Q9T8I3	Q9t8i3 liolaemus q	813	17	70.8	10	2	Q9TG98	Q9tg98 shinisaur
741	17	70.8	10	2	Q9T8I6	Q9t8i6 liolaemus k	814	17	70.8	10	2	Q9TGA1	Q9tga1 heloderma s
742	17	70.8	10	2	Q9T8I9	Q9t8i9 liolaemus a	815	17	70.8	10	2	Q9ZY89	Q9zy89 phymaturus
743	17	70.8	10	2	Q9T8J2	Q9t8j2 liolaemus x	816	17	70.8	10	2	Q9ZVT5	Q9zvt5 uta stanebu
744	17	70.8	10	2	Q9T8J5	Q9t8j5 liolaemus m	817	17	70.8	10	2	Q9ZVT8	Q9zvt8 urosaurus g
745	17	70.8	10	2	Q9T8J8	Q9t8j8 liolaemus w	818	17	70.8	10	2	Q9ZYU1	Q9zyu1 uma scopari
746	17	70.8	10	2	Q9T8K1	Q9t8k1 liolaemus s	819	17	70.8	10	2	Q9ZYU7	Q9zyu7 sator angus
747	17	70.8	10	2	Q9T8K4	Q9t8k4 liolaemus s	820	17	70.8	10	2	Q9ZYV0	Q9zyv0 petrosaurus
748	17	70.8	10	2	Q9T8K7	Q9t8k7 liolaemus m	821	17	70.8	10	2	Q9ZYV3	Q9zyv3 diposaurus
749	17	70.8	10	2	Q9T8L0	Q9t8l0 liolaemus o	822	17	70.8	10	2	Q9ZV13	Q9zv13 aegilops ta
750	17	70.8	10	2	Q9T8L3	Q9t8l3 liolaemus l	823	17	70.8	10	2	Q8KH9	Q8khn9 clostridium
751	17	70.8	10	2	Q9T8L6	Q9t8l6 liolaemus p	824	17	70.8	10	2	Q9J3J5	Q9j3j5 acinetobact
752	17	70.8	10	2	Q9T8L9	Q9t8l9 liolaemus f	825	17	70.8	10	2	Q6JL97	Q6jl97 neisseria g
753	17	70.8	10	2	Q9T8M2	Q9t8m2 liolaemus c	826	17	70.8	10	2	Q6RI01	Q6ri01 clostridium
754	17	70.8	10	2	Q9T8M5	Q9t8m5 liolaemus a	827	17	70.8	10	2	Q79AV7	Q79av7 klebsiella
755	17	70.8	10	2	Q9T8M8	Q9t8m8 liolaemus m	828	17	70.8	10	2	Q8G8W5	Q8g8w5 borrelia bu
756	17	70.8	10	2	Q9T8N1	Q9t8n1 liolaemus p	829	17	70.8	10	2	Q9F9H5	Q9f9h5 helicobacte
757	17	70.8	10	2	Q9T8N4	Q9t8n4 liolaemus d	830	17	70.8	10	2	Q9R5N2	Q9r5n2 clostridium
758	17	70.8	10	2	Q9T8N7	Q9t8n7 liolaemus o	831	17	70.8	10	2	Q7O580	Q7o580 mus musculu
759	17	70.8	10	2	Q9T8P0	Q9t8p0 liolaemus f	832	17	70.8	10	2	Q7ESU5	Q7esu5 mus musculu
760	17	70.8	10	2	Q9T8P3	Q9t8p3 liolaemus a	833	17	70.8	10	2	Q7LZC5	Q7lzc5 kassina mac
761	17	70.8	10	2	Q9T8P6	Q9t8p6 liolaemus r	834	17	70.8	10	2	Q9PRU9	Q9pru9 sparus aura

835	17	70.8	10	2	Q8UT83	Q8ut83 human immun	908	17	70.8	11	2	Q7Y9F2	Q7y9f2 pogona henr
836	17	70.8	11	1	CEP1_ACHFU	P22790 achatina fu	909	17	70.8	11	2	Q7Y9F5	Q7y9f5 pogona brev
837	17	70.8	11	1	LPW_THETH	P05624 thermus the	910	17	70.8	11	2	Q7Y9F8	Q7y9f8 lophognathu
838	17	70.8	11	1	MLG_THETS	P41989 thermozon	911	17	70.8	11	2	Q7Y9G1	Q7y9g1 hypsilurus
839	17	70.8	11	1	OATF_SARBU	P83188 sarcophaga	912	17	70.8	11	2	Q7Y9G4	Q7y9g4 hypsilurus
840	17	70.8	11	1	RANC_RANPI	P08951 rana pipien	913	17	70.8	11	2	Q7Y9G7	Q7y9g7 hypsilurus
841	17	70.8	11	1	RR2_CONAM	P42341 conopholis	914	17	70.8	11	2	Q7Y9H0	Q7y9h0 hypsilurus
842	17	70.8	11	2	Q9C1R7	Q9c1r7 saccharomyc	915	17	70.8	11	2	Q7Y9H3	Q7y9h3 hypsilurus
843	17	70.8	11	2	Q8TDA8	Q8tda8 homo sapien	916	17	70.8	11	2	Q7Y9H6	Q7y9h6 hypsilurus
844	17	70.8	11	2	Q9UCR1	Q9ucr1 homo sapien	917	17	70.8	11	2	Q7Y9H9	Q7y9h9 diporiphora
845	17	70.8	11	2	Q9UE69	Q9ue69 homo sapien	918	17	70.8	11	2	Q7Y9I2	Q7y9i2 diporiphora
846	17	70.8	11	2	Q9UEL0	Q9uel0 homo sapien	919	17	70.8	11	2	Q7Y9I5	Q7y9i5 diporiphora
847	17	70.8	11	2	Q6UZ55	Q6uz55 littorina s	920	17	70.8	11	2	Q7Y9I8	Q7y9i8 diporiphora
848	17	70.8	11	2	Q7RH63	Q7rh63 plasmodium	921	17	70.8	11	2	Q7Y9J1	Q7y9j1 diporiphora
849	17	70.8	11	2	Q77908	Q77908 oreochromis	922	17	70.8	11	2	Q7Y9J4	Q7y9j4 diporiphora
850	17	70.8	11	2	Q77914	Q77914 oreochromis	923	17	70.8	11	2	Q7Y9J7	Q7y9j7 diporiphora
851	17	70.8	11	2	Q78118	Q78118 oreochromis	924	17	70.8	11	2	Q7Y9K0	Q7y9k0 diporiphora
852	17	70.8	11	2	Q78120	Q78120 oreochromis	925	17	70.8	11	2	Q7Y9K3	Q7y9k3 diporiphora
853	17	70.8	11	2	Q79636	Q79636 laudakia hi	926	17	70.8	11	2	Q7Y9K6	Q7y9k6 diporiphora
854	17	70.8	11	2	Q79639	Q79639 laudakia le	927	17	70.8	11	2	Q7Y9K9	Q7y9k9 amphiboluru
855	17	70.8	11	2	Q79642	Q79642 laudakia mi	928	17	70.8	11	2	Q7Y9L3	Q7y9l3 amphiboluru
856	17	70.8	11	2	Q79918	Q79918 physignathu	929	17	70.8	11	2	Q7Y9L5	Q7y9l5 amphiboluru
857	17	70.8	11	2	Q79921	Q79921 phrynoceph	930	17	70.8	11	2	Q8G2N4	Q8g2n4 chlamydosau
858	17	70.8	11	2	Q79985	Q79985 laudakia ca	931	17	70.8	11	2	Q8G350	Q8g350 laudakia sa
859	17	70.8	11	2	Q79986	Q79986 laudakia er	932	17	70.8	11	2	Q8G353	Q8g353 trapelus sa
860	17	70.8	11	2	Q8SKN0	Q8skn0 ctenophorus	933	17	70.8	11	2	Q8G356	Q8g356 agama atra
861	17	70.8	11	2	Q8SKN3	Q8skn3 ctenophorus	934	17	70.8	11	2	Q8G371	Q8g371 pogona barb
862	17	70.8	11	2	Q8SKN6	Q8skn6 ctenophorus	935	17	70.8	11	2	Q8G374	Q8g374 moloch horr
863	17	70.8	11	2	Q8SKN9	Q8skn9 ctenophorus	936	17	70.8	11	2	Q8G5V0	Q8g5v0 laudakia st
864	17	70.8	11	2	Q8SKP2	Q8skp2 ctenophorus	937	17	70.8	11	2	Q8G5V3	Q8g5v3 phrynoceph
865	17	70.8	11	2	Q8SKP5	Q8skp5 ctenophorus	938	17	70.8	11	2	Q8G5V6	Q8g5v6 phrynoceph
866	17	70.8	11	2	Q8SKP8	Q8skp8 ctenophorus	939	17	70.8	11	2	Q8G5V9	Q8g5v9 laudakia st
867	17	70.8	11	2	Q8SKQ1	Q8skq1 ctenophorus	940	17	70.8	11	2	Q8G5W2	Q8g5w2 laudakia tu
868	17	70.8	11	2	Q8SKQ4	Q8skq4 ctenophorus	941	17	70.8	11	2	Q8G5W5	Q8g5w5 laudakia nu
869	17	70.8	11	2	Q8SKQ7	Q8skq7 ctenophorus	942	17	70.8	11	2	Q8G5W8	Q8g5w8 trapelus sa
870	17	70.8	11	2	Q8SKR0	Q8skr0 rankinia di	943	17	70.8	11	2	Q8G5X1	Q8g5x1 trapelus pe
871	17	70.8	11	2	Q8WCZ9	Q8wcz9 ctenophorus	944	17	70.8	11	2	Q8G5X4	Q8g5x4 trapelus ag
872	17	70.8	11	2	Q8WD02	Q8wd02 ctenophorus	945	17	70.8	11	2	Q8G5X7	Q8g5x7 trapelus ru
873	17	70.8	11	2	Q8WD05	Q8wd05 ctenophorus	946	17	70.8	11	2	Q8G5Y0	Q8g5y0 pseudotraper
874	17	70.8	11	2	Q8WD08	Q8wd08 ctenophorus	947	17	70.8	11	2	Q8G5Y3	Q8g5y3 agama impal
875	17	70.8	11	2	Q8WD11	Q8wd11 ctenophorus	948	17	70.8	11	2	Q8G5Y6	Q8g5y6 agama agama
876	17	70.8	11	2	Q8WD14	Q8wd14 ctenophorus	949	17	70.8	11	2	Q8G5Z5	Q8g5z5 japalura ep
877	17	70.8	11	2	Q8WD17	Q8wd17 ctenophorus	950	17	70.8	11	2	Q8G5Z8	Q8g5z8 acanthosaur
878	17	70.8	11	2	Q8WD20	Q8wd20 ctenophorus	951	17	70.8	11	2	Q8G604	Q8g604 gonoccephalu
879	17	70.8	11	2	Q8WD23	Q8wd23 ctenophorus	952	17	70.8	11	2	Q8G610	Q8g610 lyriocephal
880	17	70.8	11	2	Q8WD26	Q8wd26 ctenophorus	953	17	70.8	11	2	Q8G613	Q8g613 cophotis ce
881	17	70.8	11	2	Q8WD29	Q8wd29 ctenophorus	954	17	70.8	11	2	Q8G616	Q8g616 ceratophora
882	17	70.8	11	2	Q8WD50	Q8wd50 ceratophora	955	17	70.8	11	2	Q8G619	Q8g619 ceratophora
883	17	70.8	11	2	Q8WER4	Q8wer4 ceratophora	956	17	70.8	11	2	Q8G622	Q8g622 salea horsf
884	17	70.8	11	2	Q8WER7	Q8wer7 ceratophora	957	17	70.8	11	2	Q8G652	Q8g652 japalura va
885	17	70.8	11	2	Q94V74	Q94v74 lathanotus	958	17	70.8	11	2	Q8G655	Q8g655 japalura tr
886	17	70.8	11	2	Q94V77	Q94v77 heloderma s	959	17	70.8	11	2	Q8G658	Q8g658 hydrosaurus
887	17	70.8	11	2	Q94V94	Q94v94 varanus sto	960	17	70.8	11	2	Q8G661	Q8g661 typanocryp
888	17	70.8	11	2	Q94VB8	Q94vb8 varanus sal	961	17	70.8	11	2	Q8G664	Q8g664 diporiphora
889	17	70.8	11	2	Q94VE7	Q94ve7 varanus kom	962	17	70.8	11	2	Q8G667	Q8g667 calmanops a
890	17	70.8	11	2	Q94VG8	Q94vg8 varanus gou	963	17	70.8	11	2	Q8G670	Q8g670 rankinia ad
891	17	70.8	11	2	Q94VH7	Q94vh7 varanus gil	964	17	70.8	11	2	Q8G673	Q8g673 ctenophorus
892	17	70.8	11	2	Q94VK1	Q94vk1 varanus aca	965	17	70.8	11	2	Q8G676	Q8g676 amphiboluru
893	17	70.8	11	2	Q6ESN1	Q6esn1 ptyctolaemu	966	17	70.8	11	2	Q8G679	Q8g679 hypsilurus
894	17	70.8	11	2	Q6WR61	Q6wr61 nandayus ne	967	17	70.8	11	2	Q8G682	Q8g682 chelosania
895	17	70.8	11	2	Q6WR64	Q6wr64 neophena el	968	17	70.8	11	2	Q8G685	Q8g685 arua modest
896	17	70.8	11	2	Q7Y9B6	Q7y9b6 amphiboluru	969	17	70.8	11	2	Q8G688	Q8g688 physignathu
897	17	70.8	11	2	Q7Y9B9	Q7y9b9 typanocryp	970	17	70.8	11	2	Q8G688	Q8g688 elaeis guin
898	17	70.8	11	2	Q7Y9C2	Q7y9c2 typanocryp	971	17	70.8	11	2	Q7M1U2	Q7m1u2 cryza sativ
899	17	70.8	11	2	Q7Y9C5	Q7y9c5 typanocryp	972	17	70.8	11	2	Q7M1W2	Q7m1w2 canavalia e
900	17	70.8	11	2	Q7Y9C8	Q7y9c8 typanocryp	973	17	70.8	11	2	Q8GL19	Q8gl19 borrelia bu
901	17	70.8	11	2	Q7Y9D1	Q7y9d1 typanocryp	974	17	70.8	11	2	Q8GL24	Q8gl24 borrelia bu
902	17	70.8	11	2	Q7Y9D4	Q7y9d4 typanocryp	975	17	70.8	11	2	Q8K432	Q8k432 spalax juda
903	17	70.8	11	2	Q7Y9D7	Q7y9d7 pogona vilt	976	17	70.8	11	2	Q8K433	Q8k433 spalax gali
904	17	70.8	11	2	Q7Y9E0	Q7y9e0 pogona null	977	17	70.8	11	2	Q6LD68	Q6ld68 mus sp. acu
905	17	70.8	11	2	Q7Y9E3	Q7y9e3 pogona mitc	978	17	70.8	11	2	Q9QVH3	Q9qv h3 rattus sp.
906	17	70.8	11	2	Q7Y9E6	Q7y9e6 pogona mino	979	17	70.8	11	2	Q65CG7	Q65cg7 sinaloa tom
907	17	70.8	11	2	Q7Y9E9	Q7y9e9 pogona mini	980	17	70.8	11	2	Q90735	Q90735 gallus gall

981 17 70.8 11 2 Q8AD18
 982 17 70.8 12 1 LICA_BACSU
 983 17 70.8 12 1 NO40_LOTJA
 984 17 70.8 12 1 NO40_SESRO
 985 17 70.8 12 1 NO40_SOYBN
 986 17 70.8 12 1 RFI_CONSP
 987 17 70.8 12 1 UP01_CAEL
 988 17 70.8 12 1 UR2A_CATCO
 989 17 70.8 12 1 UR2B_CATCO
 990 17 70.8 12 1 UR2B_CYPCA
 991 17 70.8 12 1 UR2_GILMI
 992 17 70.8 12 1 UR2_POLSP
 993 17 70.8 12 1 UR2_SCVCA
 994 17 70.8 12 2 Q8J0A7
 995 17 70.8 12 2 Q7RZ24
 996 17 70.8 12 2 Q16405
 997 17 70.8 12 2 Q6YBQ9
 998 17 70.8 12 2 Q86CU1
 999 17 70.8 12 2 Q86FU4
 1000 17 70.8 12 2 Q90XU4

Q8ad18 human immun
 P83878 bacillus su
 O22426 lotus japon
 O24369 sebania ro
 P55960 glycine max
 P58805 conus spuri
 P55954 caenorhabdi
 P04558 catostomus
 P04559 catostomus
 P04561 cyprinus ca
 P01147 gillichthys
 P81022 polyodon sp
 P35490 scyliorhinu
 Q8j0a7 saccharomyc
 Q7r2z4 neurospora
 Q16405 homo sapien
 Q6ybg9 homo sapien
 Q86cu1 drosophila
 Q86fu4 drosophila
 Q90xu4 phalacrocor

ALIGNMENTS

RESULT 1

Q70F01 ID Q70F01 PRELIMINARY; PRT; 10 AA.
 AC Q70F01;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Calpastatin type 2 (Fragment).
 GN Name=CAS1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Rutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21531263; PubMed=11673859; DOI=10.1006/abbi.2001.2546;
 RA Parr T., Sensky P.L., Bardsley R.G., Buttery P.J.;
 RT "Calpastatin expression in porcine cardiac and skeletal muscle and
 RT partial gene structure."
 RL Arch. Biochem. Biophys. 395:1-13(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Parr T.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ583410; CAE47431.1; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9

Db 2 AFASWYKT 10

RESULT 2

Q79885 ID Q79885 PRELIMINARY; PRT; 10 AA.
 AC Q79885;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Anolis paternus.
 OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=52189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT mitochondrial genome among iguanian lizards.";
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82679; AAC62266.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; OA3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;

Best Local Similarity 22.2%; Pred. No. 4.6e+03;

Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9

Db 1 MEINRWFFS 9

RESULT 3

O79897 ID O79897 PRELIMINARY; PRT; 10 AA.
 AC O79897;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Hoplocercus spinosus (Club-tail iguana).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
 OC Hoplocercus.
 OX NCBI_TaxID=52193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT mitochondrial genome among iguanian lizards.";
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82683; AAC62284.1; -.
 DR PIR; T17063; T17063
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1288 MW; OA3480C7336415B0 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9

Db 1 MEINRWFFS 9

RESULT 4

O79903 ID O79903 PRELIMINARY; PRT; 10 AA.
 AC O79903;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Oplurus cuvieri (Madagascan collared iguanid lizard).

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Oplurinae; Oplurus.
 OX NCBI_TaxID=44151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT mitochondrial genome among iguanian lizards.";
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82685; AAC62293.1; -;
 DR PIR; T17066; T17066.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

 QY 1 XFXXXWXXX 9
 Db :|::|::|::
 1 MFENRWFFS 9

 RESULT 5
 O79906 PRELIMINARY; PRT; 10 AA.
 AC O79906;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Names=COI;
 OS Phrynosoma douglassii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
 OC Phrynosoma.
 OX NCBI_TaxID=43611;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97315309; PubMed=9169559;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Evolutionary shifts in three major structural features of the
 RT mitochondrial genome among iguanian lizards.";
 RL J. Mol. Evol. 44:660-674(1997).
 DR EMBL; U82686; AAC62299.1; -;
 DR PIR; T17069; T17069.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

 QY 1 XFXXXWXXX 9
 Db :|::|::|::
 1 MFENRWFFS 9

 RESULT 6
 P92707 PRELIMINARY; PRT; 10 AA.
 AC P92707;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;
 OS Platysaurus capensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
 OC Cordylidae; Platysaurus.
 OX NCBI_TaxID=52175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 RT rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 RT structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 DR EMBL; U71329; AAB48286.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1322 MW; 0A3480C9D36415B0 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

 QY 1 XFXXXWXXX 9
 Db :|::|::|::
 1 MFENRWFFS 9

 RESULT 7
 Q8W7U4 PRELIMINARY; PRT; 10 AA.
 AC Q8W7U4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cytochrome oxidase subunit 1 (Fragment).
 GN Names=COI;
 OS Anolis nitens.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=174262;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Glor R.E., Vitt L.J., Larson A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF337800; AAL72083.1; -;
 DR EMBL; AF337801; AAL72085.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1349 MW; C9348E29D3640449 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

 QY 1 XFXXXWXXX 9
 Db :|::|::|::
 1 MFENRWFFS 9

 RESULT 8
 Q8W8Q2 PRELIMINARY; PRT; 10 AA.
 ID Q8W8Q2

AC	Q8W8Q2;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Cytochrome oxidase subunit 1 (Cytochrome c oxidase subunit I (Fragment)).
GN	Name=COI; Synonym=COI;
OS	Anolis punctatus (Amazon green anole).
OC	Mitochondrion.
OG	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauroidea; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX	NCBI_TaxID=174263;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Glor R.E., Vitt L.J., Larson A.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Schulte J.A. II, Valladares J.P., Larson A.;
RT	"Phylogenetic relationships within Iguanidae inferred using molecular
RT	and morphological data and a phylogenetic taxonomy of iguanian
RT	lizards";
RL	Herpetologica 59:399-419(2003).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Schulte J.A., Valladares J.P., Larson A.;
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF337775; AAL72033.1; -
DR	ENBL; AF337776; AAL72035.1; -
DR	ENBL; AF337777; AAL72037.1; -
DR	ENBL; AF528726; AAQ09140.1; -
DR	GO; GO:0005739; C:mitchondrion; IEA.
KW	Mitochondrion.
FT	NON TER 10 10
SQ	SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;
Query Match 100.0%; Score 24; DB 2; Length 10;	
Best Local Similarity 22.2%; Pred. No. 4.6e+03;	
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps	
QY	1 XFXXXXXXXX 9
	: :: :::
Db	1 MFLLNRWFSS 9
RESULT 9	
Q8W8Q3	
ID	Q8W8Q3 PRELIMINARY; PRT; 10 AA.
AC	Q8W8Q3;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Cytochrome oxidase subunit 1 (Fragment).
GN	Name=COI;
OS	Anolis niteus.
OC	Mitochondrion.
OG	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauroidea; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX	NCBI_TaxID=174262;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Glor R.E., Vitt L.J., Larson A.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR	ENBL; AF337802; AAL72087.1; -
DR	ENBL; AF337803; AAL72089.1; -
DR	ENBL; AF337804; AAL72091.1; -
DR	GO; GO:0005739; C:mitchondrion; IEA.
KW	Mitochondrion.
FT	NON TER 10 10
SQ	SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;
Query Match 100.0%; Score 24; DB 2; Length 10;	
Best Local Similarity 22.2%; Pred. No. 4.6e+03;	

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. NO. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 XFXXWXWXX 9
    :|::|:::
Db 1 MFINRWFFS 9
```

RESULT 12

Q8W970	PRELIMINARY;	PRT;	10 AA.
ID	Q8W970		
AC	Q8W970;		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	25-OCT-2004 (TReMBLrel. 28, Last annotation update)		
DE	Cytochrome oxidase subunit 1 (Fragment) (Fragment).		
DE	Cytochrome oxidase subunit 1 (Fragment) (Fragment).		
GN	Name=COL;		
OS	Anolis nitens.		
OS	Mitochondrion.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidodactylia; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis;		
OX	NCBI_TaxID=174262;		
RN	[1]_TaxID=174262;		
RP	SEQUENCE FROM N.A.		
RL	Glur R.E., Vitt L.J., Larson A.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF337805; AAL72093.1; -		
DR	EMBL; AF337806; AAL72095.1; -		
DR	EMBL; AF337807; AAL72097.1; -		
DR	GO; GO:0005739; C:mitochondrion; IEA.		
KW	Mitochondrion.		
FT	NON TER	10	
SQ	SEQUENCE	10 AA; 1349 MW;	0A3480C9D33640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred.No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels

Qy	1	XFXXWX	9
		: :: ::	
Db	1	MEINRWFFS	9

RESULT 13

Q8W971	PRELIMINARY;	PRT;	10 AA.
AD	Q8W971		
IC	Q8W971;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Cytochrome oxidase subunit 1 (Fragment) (fragment).		
DE	Name=COL;		
GN	Anolis fuscoauratus (Slender anole).		
OS	Mitochondrion.		
OG	Anolis fuscoauratus (Slender anole).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis;		
OX	NCBI_TaxID=43584;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RL	Glom R.E., Vitt L.J., Larson A.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL, AF337786; AAL72055.1; -		
DR	EMBL, AF337787; AAL72057.1; -		
DR	EMBL, AF337788; AAL72059.1; -		
DR	EMBL, AF337789; AAL72061.1; -		
DR	EMBL, AF337790; AAL72063.1; -		
DR	EMBL, AF337791; AAL72065.1; -		
DR	EMBL, AF337792; AAL72067.1; -		
DR	GO; GO:0005739; C:mitochondrion; IEA.		
FW	Mitochondrion.		
FT	NON TER		10

SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;
 Query Match 100.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2: Conservative 7: Mismatches 0: Indels 0: Caps 0:

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Qy 1 XFXXXXXXX 9
    :|::|:::
Db 1 MFINRWFFS 9
```

RESULT 14

Q8WDG6	PRELIMINARY;	PRT;	10 AA.
ID	Q8WDG6		
AC	Q8WDG6;		
QC	Q8WDG6;		
DT	01-NAR-2002 (TReMBLrel. 20, Created)		
DT	01-NAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	Cytochrome oxidase subunit 1 (Fragment).		
DE	Name=COL;		
GN	Anolis trachyderma.		
OS	Anolis trachyderma.		
OG	Mitochondrion.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis		
OX	NCBI_TaxID=141901;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	Glor R.E., Vitt L.J., Larson A.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AF377785; AAL72053.1; -;		
DR	GO; GO:0005739; C:mitochondrion; IEA.		
DR	Mitochondrion.		
KW	NON_TER	10	
FT	SEQUENCE	10 AA;	1349 MW; 0A3480C9D3640440 CRC64;
SQ			

Query Match 100.0%; Score 24; i DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels

Qy 1 XFXXXWXXX 9
: : : : :
Db 1 MFINRWFFS 9

RESULT 15

Q8WDHO	PRELIMINARY;	PRT;	10 AA.
ID	Q8WDHO		
AC	Q8WDHO;		
DT	01-WAR-2002 (TrEMBLrel. 20, Created)		
DT	01-WAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Cytochrome oxidase subunit 1 (Fragment).		
GN	Name=COL;		
OS	Anolis limifrons.		
OG	Mitochondrion.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis		
NCBI	NCBI_TaxID=38897;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Glor R.E., Vitt L.J., Larson A.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF337783; AAL72049.1; -		
DR	GO; GO:0005739; C:mitochondrion; IEA.		
FT	Mitochondrion.		
KW	NON TER	10	
SQ	SEQUENCE 10 AA; 1315 MW; 0A3480C733640440	CRC64;	
	Query Match	100.0%;	Score 24; DB 2; Length 10;
	Best Local Similarity	22.2%;	Pred. No. 4.6e+03;
	Matches 2; Conservative	7; Mismatches 0;	Indels 0; Gaps 0;
OV	1	XXXXXXXXX	9

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Db      1 MFINRWLFS 9
:|::|::|

RESULT 16
Q8WDH2
ID      Q8WDH2      PRELIMINARY;      PRT;      10 AA.
AC      Q8WDH2;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Cytochrome oxidase subunit 1 (Fragment).
GN      Name=COL;
OS      Anolis lemuring.
OS      Mitochondrion.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodossa; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX      NCBI_TaxID=141898;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Glor R.E., Vitt L.J., Larson A.;
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF337782; AAL72047.1; -.
DR      GO; GO:0005739; C:mitochondrion; IEA.
KW      Mitochondrion.
FT      NON_TER      10      10
SQ      SEQUENCE      10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. NO. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
:|::|::|
Db      1 MFINRWLFS 9

RESULT 17
Q8WDH4
ID      Q8WDH4      PRELIMINARY;      PRT;      10 AA.
AC      Q8WDH4;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Cytochrome oxidase subunit 1 (Fragment).
GN      Name=COL;
OS      Anolis carpenteri.
OS      Mitochondrion.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodossa; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX      NCBI_TaxID=141894;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Glor R.E., Vitt L.J., Larson A.;
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF337781; AAL72045.1; -.
DR      GO; GO:0005739; C:mitochondrion; IEA.
KW      Mitochondrion.
FT      NON_TER      10      10
SQ      SEQUENCE      10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. NO. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
:|::|::|
Db      1 MFINRWLFS 9

RESULT 18
Q8WDH6
ID      Q8WDH6      PRELIMINARY;      PRT;      10 AA.

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AC      Q8WDH6;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Cytochrome oxidase subunit 1 (Fragment).
GN      Name=COL;
OS      Anolis woodi.
OS      Mitochondrion.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodossa; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX      NCBI_TaxID=174265;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Glor R.E., Vitt L.J., Larson A.;
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF337780; AAL72043.1; -.
DR      GO; GO:0005739; C:mitochondrion; IEA.
KW      Mitochondrion.
FT      NON_TER      10      10
SQ      SEQUENCE      10 AA; 1315 MW; 0A3480C733640440 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. NO. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
:|::|::|
Db      1 MFINRWLFS 9

RESULT 19
Q8WDH8
ID      Q8WDH8      PRELIMINARY;      PRT;      10 AA.
AC      Q8WDH8;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Cytochrome oxidase subunit 1 (Fragment).
GN      Name=COL;
OS      Anolis mestrei.
OS      Mitochondrion.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidodossa; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX      NCBI_TaxID=174261;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Glor R.E., Vitt L.J., Larson A.;
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF337779; AAL72041.1; -.
DR      GO; GO:0005739; C:mitochondrion; IEA.
KW      Mitochondrion.
FT      NON_TER      10      10
SQ      SEQUENCE      10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. NO. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 XFXXXWXXX 9
:|::|::|
Db      1 MFINRWLFS 9

RESULT 20
Q8WDI8
ID      Q8WDI8      PRELIMINARY;      PRT;      10 AA.
AC      Q8WDI8;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Cytochrome oxidase subunit 1 (Fragment).
GN      Name=COL;
OS      Anolis transversalis (Banded tree anole).

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```
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174264;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF337769; AAL72021.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|::
Db 1 MFLNRWFFS 9

RESULT 21
Q6UJL5
ID Q6UJL5 PRELIMINARY; PRT; 10 AA.
AC Q6UJL5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Strophurus pulcher.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Strophurus.
OX NCBI_TaxID=255186;
RN [1]
RP SEQUENCE FROM N.A.
RA Melville J., Schulte J.A. II, Larson A.;
RT "A Molecular Study of Phylogenetic Relationships and Evolution of
RT Antipredator Strategies in Australian Dipodactylus Geckos, Subgenus
RT Strophurus.";
RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).
DR EMBL; AY369011; AAR18865.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|::
Db 1 MFLNRWFFS 9

RESULT 22
Q6WBN7
ID Q6WBN7 PRELIMINARY; PRT; 10 AA.
AC Q6WBN7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus woodi (Florida scrub lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
```

```
OX NCBI_TaxID=59726;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297513; AAP84510.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|::
Db 1 MFLNRWFFS 9

RESULT 23
Q6WBR1
ID Q6WBR1 PRELIMINARY; PRT; 10 AA.
AC Q6WBR1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus teapensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=235404;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AY297505; AAP84486.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|::
Db 1 MFLNRWFFS 9

RESULT 24
Q6WBR4
ID Q6WBR4 PRELIMINARY; PRT; 10 AA.
AC Q6WBR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus jalapae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=57316;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AV297504; AAP84483.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1315 MW; 0A3480C733640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:|:|:
Db 1 MFNRWFLS 9

RESULT 25
Q6WBS3 PRELIMINARY; PRT; 10 AA.
AC Q6WBS3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus maculosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59708;
RN [1]_TaxID=59708;
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AV297501; AAP84474.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:|:|:
Db 1 MFNRWFLS 9

RESULT 26
Q6WBT8 PRELIMINARY; PRT; 10 AA.
AC Q6WBT8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus carinatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=110853;
RN [1]_TaxID=110853;
RP SEQUENCE FROM N.A.
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RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AV297496; AAP84459.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:|:|:
Db 1 MFNRWFLS 9

RESULT 27
Q6WBUI PRELIMINARY; PRT; 10 AA.
AC Q6WBUI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus squamosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=110857;
RN [1]_TaxID=110857;
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).
DR EMBL; AV297495; AAP84456.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
:|:|:|:|:|:
Db 1 MFNRWFLS 9

RESULT 28
Q6WBUI PRELIMINARY; PRT; 10 AA.
AC Q6WBUI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus siniferus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59719;
RN [1]_TaxID=59719;
RP SEQUENCE FROM N.A.
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RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003)
DR ENBL; AY297487; AAP84432.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1303 MW; 933480C733640451 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|:::
Db 1 MFTNRWFS 9

RESULT 29
Q6WBW2 PRELIMINARY; PRT; 10 AA.
AC Q6WBW2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Phrynosoma platyrhinos (Desert horned lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=52577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003)
DR ENBL; AY297488; AAP84435.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
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Db 1 MFTNRWFS 9

RESULT 30
Q6WBW5 PRELIMINARY; PRT; 10 AA.
AC Q6WBW5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Phrynosoma cornutum (Texas horned lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=43610;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
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RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003)
DR ENBL; AY297487; AAP84432.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|:::
Db 1 MFTNRWFS 9

RESULT 31
Q6WBW8 PRELIMINARY; PRT; 10 AA.
AC Q6WBW8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Phrynosoma mcallii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=159094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003)
DR ENBL; AY297488; AAP84429.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1349 MW; 0A3480C9D3640440 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWXXX 9
   :|::|:::
Db 1 MFTNRWFS 9

RESULT 32
Q6WBX1 PRELIMINARY; PRT; 10 AA.
AC Q6WBX1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Phrynosoma coronatum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Phrynosoma.
OX NCBI_TaxID=159093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
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ID O6XOE7 PRELIMINARY; PRT; 10 AA.
AC O6XOE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Anolis marcanoi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=75264;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990428; PubMed=14628926;
RA Gior R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
RT "Phylogenetic analysis of ecological and morphological diversification
in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
RL Evolution 57:2383-2397(2003).
DR EMBL; AY263006; AAP94301.1; -.
DR EMBL; AY263005; AAP94298.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1370 MW; C93480C9D36411A9 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. NO. 4.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXXWXXX 9
Db 1 MFPTRWFFS 9

Search completed: October 19, 2005, 15:45:21
Job time : 119.059 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:30:14 ; Search time 24.8824 Seconds
(without alignments)
34.802 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFXXWXXX 9

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	10	2 C39191	hypothetical prote
2	24	100.0	10	2 T17063	cytochrome-c oxida
3	24	100.0	10	2 T12325	cytochrome-c oxida
4	24	100.0	10	2 T17066	cytochrome-c oxida
5	24	100.0	10	2 T17069	cytochrome-c oxida
6	24	100.0	10	2 T12329	cytochrome-c oxida
7	24	100.0	13	2 PC4391	cysteine proteinase
8	24	100.0	17	2 A34704	protein-tyrosine k
9	24	100.0	19	2 S32675	nitrogen fixation
10	24	100.0	20	2 S77981	cytochrome-c oxida
11	24	100.0	20	2 PN0171	peptidylprolyl iso
12	24	100.0	20	2 PC1240	calcium-binding pr
13	24	100.0	20	2 PH1380	alpha-amylase (EC
14	23	95.8	19	2 I46023	growth hormone rec
15	23	95.8	10	2 B33995	hypotrrehalosemic h
16	23	95.8	10	2 S08997	hypotrrehalosemic
17	23	95.8	10	2 A60421	hypotrrehalosemic
18	23	95.8	10	2 S08998	hypotrrehalosemic
19	23	95.8	10	2 A26381	hypotrrehalosemic
20	23	95.8	10	2 JC1416	hypotrrehalosemic
21	23	95.8	10	2 S09138	hypotrrehalosemic
22	23	95.8	10	2 A31571	hypotrrehalosemic
23	23	95.8	9	2 S53789	neuropeptide Pec-H
24	22	91.7	9	2 A24244	adipokinetic hormo
25	22	91.7	15	2 PH1613	Ig H chain V-D-J r
26	21	87.5	8	2 A33995	adipokinetic hormo
27	21	87.5	8	2 A44960	neuropeptide led-C
28	21	87.5	8	2 B44960	neuropeptide led-C
29	21	87.5	8	2 A58620	adipokinetic hormo

30	21	87.5	8	2 S11545	adipokinetic hormo
31	21	87.5	8	2 S55310	adipokinetic hormo
32	21	87.5	8	2 A61348	red pigment-concen
33	21	87.5	8	2 S10596	adipokinetic hormo
34	21	87.5	8	2 S08995	hypotrrehalosemic
35	21	87.5	8	2 S08996	hypotrrehalosemic
36	21	87.5	8	2 A49823	adipokinetic hormo
37	21	87.5	8	2 B49823	adipokinetic hormo
38	21	87.5	8	2 A28004	adipokinetic hormo
39	21	87.5	8	2 A43976	hypotrrehalosemic
40	21	87.5	8	2 B43976	hypotrrehalosemic
41	21	87.5	8	2 A05169	neuropeptide M-I -
42	21	87.5	9	2 D57444	neuropeptide Grb-A
43	21	87.5	10	1 RHLMGS	gonadoliberin - se
44	21	87.5	10	2 PT0322	Ig heavy chain CRD
45	21	87.5	10	2 T12312	cytochrome-c oxida
46	21	87.5	11	2 C53652	thlr protein - pse
47	21	87.5	12	2 PT0274	Ig heavy chain CRD
48	21	87.5	12	2 PH1308	Ig heavy chain DJ
49	21	87.5	13	2 PT0304	Ig heavy chain CRD
50	21	87.5	15	2 PH1319	Ig heavy chain DJ
51	21	87.5	15	2 PH1366	Ig heavy chain DJ
52	21	87.5	15	2 PH1318	Ig heavy chain DJ
53	21	87.5	16	2 A36300	T-cell receptor ga
54	21	87.5	16	2 PH1346	Ig heavy chain DJ
55	21	87.5	16	2 C37290	homeotic protein G
56	21	87.5	17	2 H49048	T-cell receptor be
57	21	87.5	17	2 I49048	T-cell receptor be
58	21	87.5	17	2 S26744	Ig heavy chain J r
59	21	87.5	17	2 PT0235	Ig heavy chain CRD
60	21	87.5	18	2 S03528	Ig heavy chain J1
61	21	87.5	18	2 A25941	Ig heavy chain J-H
62	21	87.5	18	2 S39009	oviductin - golden
63	21	87.5	18	2 C49254	TCR C gamma 1 chai
64	21	87.5	19	2 G49048	T-cell receptor be
65	21	87.5	19	2 S60110	hypothetical prote
66	21	87.5	20	2 F49048	T-cell receptor be
67	21	87.5	20	2 A49048	T-cell receptor be
68	20	83.3	8	2 T13818	cytochrome oxidase
69	20	83.3	10	2 E41946	T-cell receptor ga
70	20	83.3	10	2 C41946	T-cell receptor ga
71	20	83.3	11	2 D41946	T-cell receptor ga
72	20	83.3	11	2 B41946	T-cell receptor ga
73	20	83.3	11	2 S05002	corazonin - Americ
74	20	83.3	12	2 PH1324	Ig heavy chain DJ
75	20	83.3	15	2 PS0382	Ig heavy chain J r
76	20	83.3	15	2 S10388	Ig heavy chain J r
77	20	83.3	15	2 S10386	Ig heavy chain J r
78	20	83.3	20	2 A60372	pollen allergen Po
79	19	79.2	10	1 A61126	gonadoliberin - sp
80	19	79.2	10	1 RHAQ2	gonadoliberin II -
81	19	79.2	10	2 B46030	gonadoliberin II -
82	19	79.2	10	2 A49187	gonadotropin-relea
83	19	79.2	10	2 A46030	gonadoliberin I -
84	19	79.2	10	2 A21114	gonadoliberin - ch
85	19	79.2	10	2 T17075	cytochrome-c oxida
86	19	79.2	11	2 PT0302	Ig heavy chain CRD
87	19	79.2	14	2 PH1322	Ig heavy chain DJ
88	19	79.2	14	2 PH1757	T cell receptor al
89	19	79.2	14	2 PH1758	T cell receptor al
90	19	79.2	14	2 PH1759	T cell receptor al
91	19	79.2	14	2 PH1766	T cell receptor al
92	19	79.2	14	2 PH1767	T cell receptor al
93	19	79.2	14	2 PH1768	T cell receptor al
94	19	79.2	14	2 PH1769	T cell receptor al
95	19	79.2	15	2 B60763	endo-1,3-beta-gluc
96	19	79.2	16	2 S03532	Ig heavy chain J r
97	19	79.2	16	2 D49021	Ig heavy chain J7
98	19	79.2	16	2 PS0383	Ig heavy chain J r
99	19	79.2	16	2 S26746	Ig heavy chain J r
100	19	79.2	16	2 PT0282	Ig heavy chain CDR
101	19	79.2	18	2 PH1323	Ig heavy chain DJ
102	19	79.2	19	2 PH1339	Ig heavy chain DJ

103	18	75.0	6	2	F41946	T-cell receptor ga	176	17	70.8	9	2	A43848	cell surface adhes
104	18	75.0	8	2	S15422	adipokinetic hormo	177	17	70.8	9	2	A60522	sperm-activating p
105	18	75.0	8	2	A58641	adipokinetic hormo	178	17	70.8	10	2	JC1367	thyroliiberin poten
106	18	75.0	8	2	S21663	neuropeptide - flo	179	17	70.8	10	2	A60647	neuromedin C - bov
107	18	75.0	9	2	P02088	Ig heavy chain CRD	180	17	70.8	10	2	PQ0177	neuromedin C - lau
108	18	75.0	10	2	S71868	glutathione transf	181	17	70.8	10	2	A61337	caerulein - frog (
109	18	75.0	10	2	F49033	T-cell receptor ga	182	17	70.8	10	2	A13687	caerulein-like pep
110	18	75.0	10	2	T14212	cytochrome-c oxida	183	17	70.8	10	2	S59625	beta-galactosidase
111	18	75.0	12	2	B49033	T-cell receptor de	184	17	70.8	10	2	PQ0753	beta-fructofuranos
112	18	75.0	13	2	A57678	gene rPLP-A protei	185	17	70.8	10	2	S63696	DNA polymerase - Y
113	18	75.0	13	2	A61514	glutathione transf	186	17	70.8	10	2	P02089	Ig heavy chain CRD
114	18	75.0	13	2	S32551	glutathione transf	187	17	70.8	10	2	PT0310	Ig heavy chain CRD
115	18	75.0	14	1	BSTD	bombesin - fire-be	188	17	70.8	10	2	PH1344	Ig heavy chain DJ
116	18	75.0	14	1	LPBWC	trp operon leader	189	17	70.8	10	2	A49033	T-cell receptor ga
117	18	75.0	14	1	LPBWT	trp operon leader	190	17	70.8	10	2	PH0923	T-cell receptor be
118	18	75.0	14	1	LPBWC	trp operon leader	191	17	70.8	10	2	A40753	aldehyde ferredoxi
119	18	75.0	14	2	E90858	trp operon leader	192	17	70.8	10	2	S66248	processing enzyme,
120	18	75.0	14	2	B85761	trp operon leader	193	17	70.8	10	2	F33932	Ig mu chain J regi
121	18	75.0	14	2	PH1332	Ig heavy chain DJ	194	17	70.8	10	2	T17054	cytochrome-c oxida
122	18	75.0	14	2	S33801	chaperone, TCPI-re	195	17	70.8	10	2	T13976	cytochrome-c oxida
123	18	75.0	14	2	S33802	chaperone, TCPI-re	196	17	70.8	10	2	T17057	cytochrome-c oxida
124	18	75.0	14	2	A44515	trp EG leader pept	197	17	70.8	10	2	T12303	cytochrome-c oxida
125	18	75.0	15	2	PQ0195	Sfil1-glycoprotein	198	17	70.8	10	2	T14019	cytochrome-c oxida
126	18	75.0	15	2	PQ0174	stylar glycoprotei	199	17	70.8	10	2	T17060	cytochrome-c oxida
127	18	75.0	15	2	PQ0175	self-incompatibili	200	17	70.8	10	2	T14043	cytochrome-c oxida
128	18	75.0	15	2	PQ0750	Ig H chain V-D-J r	201	17	70.8	10	2	T14054	cytochrome-c oxida
129	18	75.0	15	2	PH1590	T-cell receptor al	202	17	70.8	10	2	T12308	cytochrome-c oxida
130	18	75.0	16	2	A48839	glutamate receptor	203	17	70.8	10	2	T17072	cytochrome-c oxida
131	18	75.0	17	2	A41053	carboxypeptidase 3	204	17	70.8	10	2	T12316	cytochrome-c oxida
132	18	75.0	17	2	B44923	CD33 antigen homol	205	17	70.8	10	2	T12321	cytochrome-c oxida
133	18	75.0	17	2	I67524	protein Ptd3 - gol	206	17	70.8	10	2	T14215	cytochrome-c oxida
134	18	75.0	17	2	ES9137	DNA topoisomerase	207	17	70.8	10	2	T14223	cytochrome-c oxida
135	18	75.0	18	2	S43834	IH-4-oxoquinoline	208	17	70.8	10	2	T14219	lysyl-bradykinin -
136	18	75.0	18	2	S21669	leader peptide trp	209	17	70.8	11	1	S39030	probable trpEG lea
137	18	75.0	18	2	T03799	Ig mu chain V regi	210	17	70.8	11	1	LPTWE	chromogranin-B - r
138	18	75.0	18	2	S43958	testin II - rat (f	211	17	70.8	11	2	B49164	ribosomal protein
139	18	75.0	19	2	PC1251	H+-transporting tw	212	17	70.8	11	2	S32575	Ig heavy chain CRD
140	18	75.0	19	2	S60633	amyloid protein -	213	17	70.8	11	2	PT0249	Ig heavy chain CRD
141	18	75.0	19	2	I53673	Ig H chain V-D-J r	214	17	70.8	11	2	PT0273	Ig heavy chain DJ
142	18	75.0	19	2	PH1624	nonstructural prot	215	17	70.8	11	2	PH1343	Ig heavy chain DJ
143	18	75.0	19	2	A48354	hemoglobin Cl beta	216	17	70.8	11	2	S68649	spermadhesin AQN-3
144	18	75.0	19	2	A60505	glutathione transf	217	17	70.8	11	2	A33571	follicistatin - bovl
145	18	75.0	20	2	B37520	glutathione transf	218	17	70.8	11	2	A49037	Tcr gamma V-J regi
146	18	75.0	20	2	S29100	glutathione transf	219	17	70.8	11	2	B49037	Tcr gamma V-J regi
147	18	75.0	20	2	S71869	glutathione transf	220	17	70.8	11	2	C49037	Tcr gamma V-J regi
148	18	75.0	20	2	PQ0751	self-incompatibili	221	17	70.8	11	2	C59151	protein-tyrosine k
149	18	75.0	20	2	PH0111	style glycoprotein	222	17	70.8	11	2	PQ0731	unidentified 5.7/3
150	18	75.0	20	2	PH0110	style glycoprotein	223	17	70.8	11	2	S45698	gamma-MSH-like pro
151	18	75.0	20	2	PC2347	base nonspecific a	224	17	70.8	11	2	A34662	Achatina cardio-ex
152	18	75.0	20	2	A44773	pollen allergen I	225	17	70.8	11	2	T12264	cytochrome-c oxida
153	18	75.0	20	2	I64036	hypothetical prote	226	17	70.8	11	2	T12253	cytochrome-c oxida
154	18	75.0	20	2	S10876	hypothetical prote	227	17	70.8	11	2	T12244	cytochrome-c oxida
155	18	75.0	20	2	PC3248	lambda 112 protein	228	17	70.8	11	2	T12248	cytochrome-c oxida
156	18	75.0	20	2	S56756	link protein - rat	229	17	70.8	11	2	T17081	cytochrome-c oxida
157	18	75.0	20	2	A44927	major outer membra	230	17	70.8	11	2	T17078	cytochrome-c oxida
158	18	75.0	20	2	S29636	jacalin beta-1 cha	231	17	70.8	12	1	UOGM2	urotensin II - lon
159	18	75.0	20	2	S29635	jacalin beta chain	232	17	70.8	12	2	JS0423	urotensin II-A pep
160	18	75.0	20	2	S03987	agglutinin beta-2	233	17	70.8	12	2	S42765	urotensin II - tel
161	18	75.0	20	2	AE0120	insertion element	234	17	70.8	12	2	PH1675	Ig heavy chain V r
162	18	75.0	20	2	AC0269	probable trp opero	235	17	70.8	12	2	S26548	T-cell receptor be
163	18	75.0	20	2	B60505	hemoglobin Al-2 be	236	17	70.8	12	2	S26553	T-cell receptor be
164	17	70.8	7	2	S21230	dermorphin (trp-4,	237	17	70.8	12	2	A26093	microbial collagen
165	17	70.8	7	2	S09652	hypothetical prote	238	17	70.8	12	2	G64003	hypothetical prote
166	17	70.8	8	2	PQ0012	cholecystokinin -	239	17	70.8	12	2	S69123	proton-translocati
167	17	70.8	8	2	A43001	cholecystokinin -	240	17	70.8	12	2	S43957	Ig mu chain V regi
168	17	70.8	8	2	A59495	Vesicle associated	241	17	70.8	12	2	S25039	Ig heavy chain V r
169	17	70.8	8	2	S19288	acylase - Kluyvera	242	17	70.8	12	2	I41235	glutamine-tRNA lig
170	17	70.8	8	2	A41117	acetylcholinestera	243	17	70.8	12	2	JS0424	urotensin II-B pep
171	17	70.8	9	2	A61357	phytoceutlein -	244	17	70.8	12	2	I77529	estrogen receptor
172	17	70.8	9	2	PT0299	Ig heavy chain CRD	245	17	70.8	12	2	PN0046	ATP synthase D cha
173	17	70.8	9	2	PT0634	T-cell receptor be	246	17	70.8	12	2	I58273	thyroglobulin - ra
174	17	70.8	9	2	I58350	gene c-mpl protein	247	17	70.8	13	1	XAVI9B	angiotensin-conver
175	17	70.8	9	2	S56004	glutamine 1,3-beta-gl	248	17	70.8	13	1	MTCMAD	melanotropin alpha

249	17	70.8	13	1	MTHOAD	melanotropin alpha	322	17	70.8	16	2	S28213	glutathione transf
250	17	70.8	13	2	PQ0445	urotensin II - lau	323	17	70.8	16	2	PT0237	Ig heavy chain CDR
251	17	70.8	13	2	PH1676	Ig heavy chain V r	324	17	70.8	16	2	PT0296	Ig heavy chain CDR
252	17	70.8	13	2	B28810	glutathione transf	325	17	70.8	16	2	PH1604	Ig H chain V-D-J r
253	17	70.8	13	2	PT0293	Ig heavy chain CRD	326	17	70.8	16	2	D49037	Tcr delta chain V-
254	17	70.8	13	2	S57567	T cell receptor V-	327	17	70.8	16	2	A46236	transforming prote
255	17	70.8	13	2	PH0138	T-cell-specific tr	328	17	70.8	16	2	PH1299	subtilisin (EC 3.4
256	17	70.8	13	2	S61798	diptidyl-peptida	329	17	70.8	16	2	A24099	crystal protein, 2
257	17	70.8	13	2	B56964	T-cell receptor be	330	17	70.8	16	2	T44936	calmodulin kinase
258	17	70.8	13	2	PH0928	collecting duct wa	331	17	70.8	16	2	A48630	bothrojaracin - ja
259	17	70.8	13	2	I51905	glyceraldehyde-3-p	332	17	70.8	16	2	I37452	protein kinase - h
260	17	70.8	13	2	S54344	aeg-46.5 protein -	333	17	70.8	16	2	S13898	alkaline phosphata
261	17	70.8	13	2	I54984	unidentified 85K p	334	17	70.8	16	2	B23692	transcription fact
262	17	70.8	13	2	PC2369	early nodulin 40 -	335	17	70.8	16	2	E37290	homeotic protein G
263	17	70.8	13	2	S60046	factor X activator	336	17	70.8	16	2	S05703	homeotic protein c
264	17	70.8	13	2	A60379	serine proteinase	337	17	70.8	17	1	GMSH	gastrin - sheep
265	17	70.8	13	2	S66558	bombesin-like pept	338	17	70.8	17	2	S66198	alcohol dehydrogen
266	17	70.8	13	2	A60409	tryptophyllin-l3 -	339	17	70.8	17	2	A60071	gastrin - rheus m
267	17	70.8	13	2	A05174	somatostatin - spo	340	17	70.8	17	2	S24570	Ig heavy chain J r
268	17	70.8	14	2	A60622	somatostatin I - E	341	17	70.8	17	2	S03531	Ig heavy chain J5
269	17	70.8	14	2	A60840	somatostatin - sli	342	17	70.8	17	2	S27477	Ig heavy chain J r
270	17	70.8	14	2	C60414	somatostatin I - c	343	17	70.8	17	2	I57941	beta 3-adrenergic
271	17	70.8	14	2	B60842	somatostatin I - s	344	17	70.8	17	2	E40442	integrase homolog
272	17	70.8	14	2	S00172	Ig heavy chain V r	345	17	70.8	17	2	S03533	Ig heavy chain J r
273	17	70.8	14	2	PH1677	Ig heavy chain V r	346	17	70.8	17	2	PT0234	Ig heavy chain CRD
274	17	70.8	14	2	PH1705	proteochondroitin c	347	17	70.8	17	2	PH1367	Ig heavy chain DJ
275	17	70.8	14	2	PT0077	hypothetical prote	348	17	70.8	17	2	PH1331	Ig heavy chain DJ
276	17	70.8	14	2	A35105	Ig heavy chain J r	349	17	70.8	17	2	PH1357	Ig heavy chain DJ
277	17	70.8	14	2	S03530	Ig heavy chain CDR	350	17	70.8	17	2	PS0384	Ig heavy chain J r
278	17	70.8	14	2	PT0223	Ig heavy chain DJ	351	17	70.8	17	2	A44560	terephthalate 1,2-
279	17	70.8	14	2	PH1348	Ig heavy chain DJ	352	17	70.8	17	2	S10786	enamelin, 26K - bo
280	17	70.8	14	2	PH1356	T cell receptor V-	353	17	70.8	17	2	I67526	CD33 antigen homol
281	17	70.8	14	2	S57572	Tcr delta chain V-	354	17	70.8	17	2	A61211	anantin - Streptom
282	17	70.8	14	2	F49037	L-2,4-diaminobuty	355	17	70.8	17	2	B48943	phage antigenic de
283	17	70.8	14	2	B44854	calotropin DI - mu	356	17	70.8	17	2	A29834	melanotropin beta
284	17	70.8	14	2	PT0026	karatatin - karata	357	17	70.8	18	1	MTDFBC	melanotropin beta
285	17	70.8	14	2	PT0029	mastoparan B - hor	358	17	70.8	18	1	MTDOB	sorbitol dehydroge
286	17	70.8	14	2	S14336	leukotriene B-4 12	359	17	70.8	18	2	S29179	protein-tyrosine k
287	17	70.8	14	2	A47421	S-allele-associate	360	17	70.8	18	2	S24780	proteasome chain L
288	17	70.8	14	2	S39931	unspecific monocly	361	17	70.8	18	2	G02018	N4-(beta-N-acetylgl
289	17	70.8	15	2	B26997	glucan 1,4-alpha-g	362	17	70.8	18	2	S04229	plasma membrane ca
290	17	70.8	15	2	A26997	alpha-1,6-glucosid	363	17	70.8	18	2	D49570	Ig heavy chain DJ
291	17	70.8	15	2	S21202	oligo-1,6-glucosid	364	17	70.8	18	2	PH1368	T-cell receptor de
292	17	70.8	15	2	S21241	leukocyte elastase	365	17	70.8	18	2	A32220	ovoheamerythrin - d
293	17	70.8	15	2	S21241	cystatin Ci-4a - m	366	17	70.8	18	2	S29264	thrombospondin pre
294	17	70.8	15	2	S24159	Ig heavy chain V r	367	17	70.8	18	2	S55501	gamma2-gliadin P25
295	17	70.8	15	2	PQ0232	proteinase - Therm	368	17	70.8	18	2	S52125	NTL1 protein - cur
296	17	70.8	15	2	S26791	hypothetical prote	369	17	70.8	18	2	C56211	shikimate 5-dehydr
297	17	70.8	15	2	S39012	hypothetical prote	370	17	70.8	18	2	S46418	choline O-acetyltr
298	17	70.8	15	2	T46625	gamma 2 gliadin -	371	17	70.8	18	2	I40062	hypothetical prote
299	17	70.8	15	2	S08209	Fc gamma receptor	372	17	70.8	18	2	I52623	Ig heavy chain CDR
300	17	70.8	15	2	B56891	Ig heavy chain DJ	373	17	70.8	18	2	PT0239	Ig heavy chain CDR
301	17	70.8	15	2	A47828	Ig heavy chain DJ	374	17	70.8	18	2	PT0286	Ig heavy chain DJ
302	17	70.8	15	2	PH1365	Ig mu chain V regi	375	17	70.8	18	2	PH1349	Ig heavy chain DJ
303	17	70.8	15	2	PH1320	T-cell receptor al	376	17	70.8	18	2	PH1350	Ig heavy chain DJ
304	17	70.8	15	2	S43956	T-cell receptor be	377	17	70.8	18	2	A40256	interleukin-7 rece
305	17	70.8	15	2	PH1762	T-cell receptor be	378	17	70.8	18	2	I35141	T-cell receptor de
306	17	70.8	15	2	G49655	Tcr delta chain V-	379	17	70.8	18	2	A61577	Tcr delta chain V-
307	17	70.8	15	2	PQ0073	complement factor	380	17	70.8	18	2	S20322	24k serine protein
308	17	70.8	15	2	E49037	probable membrane	381	17	70.8	18	2	A61577	gluten - wheat
309	17	70.8	15	2	PL0109	acetolactate synth	382	17	70.8	18	2	S20322	hypothetical prote
310	17	70.8	15	2	S02381	phenotypic variati	383	17	70.8	18	2	A35678	neuropeptide A - b
311	17	70.8	15	2	S33781	mixed lymphocyte r	384	17	70.8	18	2	S27141	ancovenin - Strept
312	17	70.8	15	2	PA0099	hypothetical prote	385	17	70.8	18	2	A24749	cytochrome P450-C-
313	17	70.8	15	2	FX0031	locustapryrokinin -	386	17	70.8	19	1	EWSMAN	L-lactate dehydrog
314	17	70.8	16	2	C84035	melanotropin beta	387	17	70.8	19	2	A28702	glutathione transf
315	17	70.8	16	1	A49761	cytochrome P450 IF	388	17	70.8	19	2	I49422	protein kinase (EC
316	17	70.8	16	1	MTDPBS	hydrogenase (EC 1.	389	17	70.8	19	2	S71871	Ig heavy chain DJ
317	17	70.8	16	2	E41425	leukocyte elastase	390	17	70.8	19	2	I45957	Ig heavy chain CDR
318	17	70.8	16	2	S03405	little gastrin - C	391	17	70.8	19	2	PH1304	Ig heavy chain DJ
319	17	70.8	16	2	A60551	protein p12E - Fri	392	17	70.8	19	2	PT0244	Ig heavy chain DJ
320	17	70.8	16	2	A29541		393	17	70.8	19	2	PH1307	Ig heavy chain DJ
321	17	70.8	16	2	S66613		394	17	70.8	19	2	A28814	Ig kappa chain V r

395	17	70.8	19	2	B61409	genome polypeptide	468	16	66.7	8	2	A39308	glycine reductase
396	17	70.8	19	2	PX0062	beta-galactoside-b	469	16	66.7	8	2	A31570	angiotensin-conver
397	17	70.8	19	2	S63489	dissimilatory sulf	470	16	66.7	9	2	S07205	litorin 2-Glu - Au
398	17	70.8	19	2	T50329	wd-repeat protein	471	16	66.7	9	2	S07204	litorin 1 - Austr
399	17	70.8	19	2	PH1352	Ig heavy chain DJ	472	16	66.7	9	2	S07241	litorin - Rohde's
400	17	70.8	19	2	PH1315	Ig heavy chain DJ	473	16	66.7	9	2	JS0302	xenopsin-related p
401	17	70.8	19	2	S57515	T cell receptor be	474	16	66.7	9	2	A60320	xenopsin-related p
402	17	70.8	19	2	S57516	T cell receptor be	475	16	66.7	9	2	PT0231	Ig heavy chain CRD
403	17	70.8	19	2	S03519	T-cell receptor ga	476	16	66.7	9	2	PT0272	Ig heavy chain CRD
404	17	70.8	19	2	PH0793	T-cell receptor al	477	16	66.7	9	2	PT0562	T-cell receptor be
405	17	70.8	19	2	I49037	TCR delta chain V-	478	16	66.7	9	2	XASNPC	angiotensin-conver
406	17	70.8	19	2	B46592	lactase-phlorizin	479	16	66.7	10	1	XAVI6B	angiotensin-conver
407	17	70.8	19	2	I40063	shikimate 5-dehydr	480	16	66.7	10	1	RHPGG	gonadoliberin - pi
408	17	70.8	19	2	A44854	L-2,4-diaminobuty	481	16	66.7	10	1	RHSHG	gonadoliberin - sh
409	17	70.8	19	2	S23212	protein C - oat (f	482	16	66.7	10	1	RHAQ1	gonadoliberin I -
410	17	70.8	19	2	S19532	globin - polychaet	483	16	66.7	10	2	A35556	hypothetical prote
411	17	70.8	19	2	S19613	globin - polychaet	484	16	66.7	10	2	S23370	T-cell receptor al
412	17	70.8	19	2	I52721	gene hMLH1 protein	485	16	66.7	10	2	B38887	T-cell receptor ga
413	17	70.8	19	2	S12268	Oa-2 antigen - mou	486	16	66.7	10	2	PH0916	T-cell receptor be
414	17	70.8	19	2	A58700	actagardine [valid	487	16	66.7	10	2	A59272	peptide-N4-(N-acet
415	17	70.8	19	4	I54264	rhodopsin single b	488	16	66.7	10	2	B37196	bradykinin-potent
416	17	70.8	20	2	S21176	testosterone beta	489	16	66.7	11	2	C38887	T-cell receptor ga
417	17	70.8	20	2	A60728	cytochrome P450 3A	490	16	66.7	11	2	I41946	T-cell receptor ga
418	17	70.8	20	2	B61080	5-carboxymethyl-2-	491	16	66.7	12	1	A53709	alpha-conotoxin im
419	17	70.8	20	2	S23099	glutathione transf	492	16	66.7	12	2	A29169	phospholipase A2 (
420	17	70.8	20	2	S30381	glutathione transf	493	16	66.7	12	2	I64829	gene HEXA protein
421	17	70.8	20	2	S33787	pancreatic elastas	494	16	66.7	12	2	A40763	sucrose-6-phosphat
422	17	70.8	20	2	A56900	chymotrypsin I (EC	495	16	66.7	12	2	A49033	T-cell receptor de
423	17	70.8	20	2	B61333	chymotrypsin (EC 3	496	16	66.7	12	2	H41946	T-cell receptor ga
424	17	70.8	20	2	I49423	cytotoxic T-lympho	497	16	66.7	12	2	A42324	cytochrome P450c27
425	17	70.8	20	2	S46205	comosain (EC 3.4.2	498	16	66.7	12	2	PO0776	NADH2 dehydrogenas
426	17	70.8	20	2	S46204	anapsin (EC 3.4.22	499	16	66.7	13	2	S23372	T-cell receptor al
427	17	70.8	20	2	C54052	phosphoribosyl-AMP	500	16	66.7	13	2	A86126	hypothetical prote
428	17	70.8	20	2	A37111	ribulose-bisphosph	501	16	66.7	14	1	QMVHXX	mastoparan X - hor
429	17	70.8	20	2	C49164	chromogranin-B - r	502	16	66.7	14	1	QMVHXX	polistes mastopara
430	17	70.8	20	2	PT0248	Ig heavy chain CDR	503	16	66.7	14	2	PH0801	T-cell receptor al
431	17	70.8	20	2	S39049	cytotoxin-binding	504	16	66.7	14	2	PH0747	T-cell receptor be
432	17	70.8	20	2	A05313	apolipoprotein A-I	505	16	66.7	14	2	JH0328	probursin tetradec
433	17	70.8	20	2	S03335	photosystem II pho	506	16	66.7	15	2	PH1342	Ig heavy chain DJ
434	17	70.8	20	2	FW0003	chlorophyll a/b-bi	507	16	66.7	15	2	A45103	Ig heavy chain DJ
435	17	70.8	20	2	S04988	gag core shell pro	508	16	66.7	15	2	PH0216	agarase (EC 3.2.1.1
436	17	70.8	20	2	T46626	hypothetical prote	509	16	66.7	16	2	I57530	gene c-fms protein
437	17	70.8	20	2	S16202	pyrrolidine-5-carbox	510	16	66.7	16	2	PH1637	Ig H chain V-D-J r
438	17	70.8	20	2	D25507	proteinase inhibit	511	16	66.7	16	2	PH1637	T-cell receptor be
439	17	70.8	20	2	S53882	hypothetical prote	512	16	66.7	16	2	PH0748	T-cell receptor be
440	17	70.8	20	2	PH1358	Ig heavy chain DJ	513	16	66.7	16	2	A20190	hypodermin B - ear
441	17	70.8	20	2	PH1341	Ig heavy chain DJ	514	16	66.7	17	2	B44873	caldesmon - rabbit
442	17	70.8	20	2	PH1326	Ig heavy chain DJ	515	16	66.7	17	2	PC1318	hypothetical prote
443	17	70.8	20	2	S60350	kallikrein, pankre	516	16	66.7	17	2	I53392	large granule L6 c
444	17	70.8	20	2	S15861	estrogen receptor	517	16	66.7	18	2	JU0124	CD33 antigen homol
445	17	70.8	20	2	A38689	1-phosphatidylinos	518	16	66.7	18	2	JU0125	polyphemusin I - A
446	17	70.8	20	2	PQ0071	T-cell receptor be	519	16	66.7	18	2	S02269	glycogen(starch) s
447	17	70.8	20	2	S66222	defensin AMP2 - Da	520	16	66.7	19	2	B56613	virion morphogenes
448	17	70.8	20	2	T44453	acetyl-CoA synthet	521	16	66.7	19	2	PH1330	Ig heavy chain DJ
449	17	70.8	20	2	S45637	oxidoreductase - p	522	16	66.7	20	2	PL0192	Ig lambda 2 chain
450	17	70.8	20	2	S63490	dissimilatory sulf	523	16	66.7	20	2	D37396	pollen allergen Fe
451	17	70.8	20	2	S35460	alliin lyase (EC 4	524	16	66.7	20	2	D84716	hypothetical prote
452	17	70.8	20	2	PC2084	serine proteinase	525	16	66.7	20	2	A85659	hypothetical prote
453	17	70.8	20	2	S87763	S-adenosyl-L-methi	526	15	62.5	5	2	A32516	cholecystokinin-5
454	17	70.8	20	2	A44817	collagenolytic pro	527	15	62.5	5	2	JH0253	gut pentapeptide -
455	17	70.8	20	2	A56899	serum heterodimer,	528	15	62.5	5	2	PT0281	Ig heavy chain CRD
456	17	70.8	20	2	A61506	alpha-1-antitrypsi	529	15	62.5	5	2	PT0308	Ig heavy chain CRD
457	17	70.8	20	2	S08605	hypothetical prote	530	15	62.5	5	2	PT0580	T-cell receptor be
458	17	70.8	20	2	S27142	hypothetical prote	531	15	62.5	5	2	G37196	bradykinin-potent
459	17	70.8	20	2	DIRT	dental fluid tra	532	15	62.5	6	2	S66195	alcohol dehydrogen
460	16	66.7	6	2	A31263	dihydrofolate redu	533	15	62.5	6	2	B35640	cerebellar degener
461	16	66.7	6	2	B31263	dihydrofolate redu	534	15	62.5	6	2	PT0629	T-cell receptor be
462	16	66.7	7	2	PT0642	T-cell receptor be	535	15	62.5	6	2	PT0519	T-cell receptor be
463	16	66.7	7	2	PT0586	T-cell receptor be	536	15	62.5	6	2	PT0637	T-cell receptor be
464	16	66.7	7	2	PT0728	T-cell receptor be	537	15	62.5	6	2	PT0641	T-cell receptor be
465	16	66.7	7	2	PN0649	pullulanase (EC 3.	538	15	62.5	6	2	PT0028	pev-kinin 2 - pena
466	16	66.7	7	2	A61081	tryptophyllin, bas	539	15	62.5	6	2	A61068	locustakinin - mig
467	16	66.7	8	2	A38887	T-cell receptor ga	540	15	62.5	6	4	I79564	hypothetical TCL3

541	15	62.5	7	2	PH1602	Ig H chain V-D-J r	614	15	62.5	19	2	S43960	Ig mu chain V regi
542	15	62.5	7	2	PT0526	T-cell receptor be	615	15	62.5	19	2	PH1353	Ig heavy chain DJ
543	15	62.5	7	2	PT0628	T-cell receptor be	616	15	62.5	19	2	E49048	T-cell receptor be
544	15	62.5	7	2	PT0722	T-cell receptor be	617	15	62.5	19	2	I46554	T-cell receptor de
545	15	62.5	7	2	PX0008	glucuronosyltransf	618	15	62.5	19	2	JX0124	tachyplesin I prec
546	15	62.5	7	2	PD0029	pev-kinin I - pena	619	15	62.5	20	2	A23739	cytochrome P450 MU
547	15	62.5	7	4	A58512	venom heptapeptide	620	15	62.5	20	2	A49164	chromogranin-B - r
548	15	62.5	7	4	A58725	virotaxin - destro	621	15	62.5	20	2	I70108	microsomal triglyc
549	15	62.5	8	2	PT0724	T-cell receptor be	622	15	62.5	20	2	PS0087	microbial serine p
550	15	62.5	8	2	JS0315	leucokinin V - Mad	623	15	62.5	20	2	S68341	procathepsin L - g
551	15	62.5	8	2	JS0316	leucokinin VI - Ma	624	15	62.5	20	2	C56894	intracrySTALLINE c
552	15	62.5	8	2	JS0317	leucokinin VII - M	625	15	62.5	20	2	A04451	dormancy-related p
553	15	62.5	8	2	JS0318	leucokinin VIII -	626	15	62.5	20	2	S77989	cytochrome-c oxida
554	15	62.5	9	1	AKLQIM	locustamyoinhibiti	627	15	62.5	20	2	S77992	cytochrome-c oxida
555	15	62.5	9	2	S78426	52.5K protein - sp	628	15	62.5	20	2	B53283	major cat allergen
556	15	62.5	9	2	A57444	neuropeptide Grb-A	629	15	62.5	20	2	A58894	intracrySTALLINE c
557	15	62.5	9	2	B57444	neuropeptide Grb-A	630	15	62.5	20	2	B56894	intracrySTALLINE c
558	15	62.5	9	2	C57444	neuropeptide Grb-A	631	15	58.3	4	2	A34626	RPCH-related neuro
559	15	62.5	10	2	H37196	bradykinin-potenti	632	14	58.3	4	2	B53284	T-cell receptor be
560	15	62.5	10	2	A24867	scylorhinin I - s	633	14	58.3	4	2	PT0661	T-cell receptor be
561	15	62.5	11	2	S66196	alcohol dehydrogen	634	14	58.3	5	2	A60803	neuropeptide - sea
562	15	62.5	11	2	JQ2307	hypothetical 1.5K	635	14	58.3	5	2	PT0729	T-cell receptor be
563	15	62.5	11	2	JQ2317	hypothetical 1.5K	636	14	58.3	6	2	B34835	dnaA protein - pse
564	15	62.5	12	2	S10824	lipovitelin - Afr	637	14	58.3	6	2	PT0532	T-cell receptor be
565	15	62.5	12	2	S23168	Z protein - guinea	638	14	58.3	6	2	PT0726	T-cell receptor be
566	15	62.5	12	2	PH1462	T-cell receptor be	639	14	58.3	7	2	PQ0727	H2 class I protein
567	15	62.5	12	2	PH1457	T-cell receptor be	640	14	58.3	7	2	E48394	glycoprotein compo
568	15	62.5	12	2	A49637	MHC class II histo	641	14	58.3	7	2	PT0688	T-cell receptor be
569	15	62.5	13	2	E60396	antigen 7H8/2 - ma	642	14	58.3	7	2	B48394	major fat-globule
570	15	62.5	13	2	PH1636	Ig H chain V-D-J r	643	14	58.3	7	2	S57274	triacylglycerol li
571	15	62.5	13	2	PH1620	Ig H chain V-D-J r	644	14	58.3	7	2	S33244	neuromodulatory pe
572	15	62.5	13	2	G37266	Ig heavy chain C r	645	14	58.3	7	2	S33245	neuromodulatory pe
573	15	62.5	13	2	D37267	Ig heavy chain C r	646	14	58.3	7	2	S33246	neuromodulatory pe
574	15	62.5	13	2	A59491	epithelial dog all	647	14	58.3	7	2	S33567	tubulin beta-3 cha
575	15	62.5	14	2	PC2373	probable IMP dehyd	648	14	58.3	7	4	IS5382	hypothetical pepti
576	15	62.5	14	2	S39932	S-allele-associate	649	14	58.3	8	2	C61512	variant surface gl
577	15	62.5	14	2	PC1215	homeotic protein E	650	14	58.3	8	2	D61512	variant surface gl
578	15	62.5	14	2	IS4284	Cl-inhibitor - hum	651	14	58.3	9	2	S39766	cardioactive pepti
579	15	62.5	14	2	PH1327	Ig heavy chain DJ	652	14	58.3	9	2	PT0270	Ig heavy chain CRD
580	15	62.5	14	2	S58426	spermadhesin AWW h	653	14	58.3	9	2	PT0324	Ig heavy chain CRD
581	15	62.5	14	2	PH1625	Ig H chain V-D-J r	654	14	58.3	9	2	S39767	cardioactive pepti
582	15	62.5	14	2	PH1626	Ig H chain V-D-J r	655	14	58.3	9	2	A26363	cardioactive pepti
583	15	62.5	14	2	PH1627	Ig H chain V-D-J r	656	14	58.3	9	2	S27233	cardioactive pepti
584	15	62.5	14	2	PH1594	Ig H chain V-D-J r	657	14	58.3	9	2	A37027	macrophage chemota
585	15	62.5	14	2	S39930	S-allele-associate	658	14	58.3	9	2	ODR8	delta sleep-induci
586	15	62.5	14	2	E81280	probable proteolys	659	14	58.3	10	2	A60410	beta-neoendorphin
587	15	62.5	15	2	A54397	ubiquitin-carrier	660	14	58.3	10	2	PT0245	Ig heavy chain CRD
588	15	62.5	15	2	E41383	23K variable histo	661	14	58.3	10	2	A27617	triose-phosphate i
589	15	62.5	15	2	S29485	GTP-binding protei	662	14	58.3	10	2	A59173	nuclease Bhl (EC 3
590	15	62.5	15	2	PH1616	Ig H chain V-D-J r	663	14	58.3	11	2	H54346	pyruvate synthase
591	15	62.5	15	2	PH1612	Ig H chain V-D-J r	664	14	58.3	11	2	S70338	napin small chain
592	15	62.5	15	2	PH0782	T-cell receptor al	665	14	58.3	11	2	A59146	conotoxin ausa - c
593	15	62.5	15	2	S21411	modulation protein	666	14	58.3	11	2	B59146	conotoxin ausb - c
594	15	62.5	15	2	A48372	benzoyl-CoA ligase	667	14	58.3	12	2	A28856	fructose-bisphosph
595	15	62.5	15	2	A61612	allatostatin - tob	668	14	58.3	12	2	A34858	proteinase E - bla
596	15	62.5	15	4	I38032	hypothetical MN1/T	669	14	58.3	12	2	S43170	kinase light chai
597	15	62.5	16	2	S51733	Ig H chain V-D-J r	670	14	58.3	12	2	A33208	calreticulin, hepa
598	15	62.5	16	2	PH1638	T-cell receptor al	671	14	58.3	13	2	B25448	Ig kappa-1 chain,
599	15	62.5	16	2	PH1588	Ig H chain V-D-J r	672	14	58.3	13	2	B26406	Ig kappa chain J r
600	15	62.5	16	2	S34889	beta-crystallin A4	673	14	58.3	13	2	A47630	Ig kappa chain J r
601	15	62.5	16	2	B48820	7K protein - Esche	674	14	58.3	13	2	LFECFS	pheST operon leade
602	15	62.5	16	4	I79565	hypothetical TGL3/	675	14	58.3	14	2	F90931	pheST operon leade
603	15	62.5	17	2	I51910	SP-A2 - human (fra	676	14	58.3	14	2	B85780	pheST operon leade
604	15	62.5	17	2	PH1630	Ig H chain V-D-J r	677	14	58.3	14	2	A37789	heat shock cognate
605	15	62.5	17	2	A46592	lactase-phlorizin	678	14	58.3	14	2	AG0705	phenylalanyl-tRNA
606	15	62.5	17	2	B31435	adherence lectin l	679	14	58.3	14	2	A41589	25K elastin-bindin
607	15	62.5	17	2	A38824	tachyplesin I - ho	680	14	58.3	14	2	S68095	calcium-binding pr
608	15	62.5	17	2	JX0125	tachyplesin III -	681	14	58.3	14	2	AF0296	phenylalanyl-tRNA
609	15	62.5	17	2	C85956	hypothetical prote	682	14	58.3	15	1	LFECF	phe operon leader
610	15	62.5	18	2	S74195	epoxide hydrolase	683	14	58.3	15	2	B33208	calreticulin, uter
611	15	62.5	18	2	PH1792	T cell receptor al	684	14	58.3	15	2	G60977	protein 425 - Cali
612	15	62.5	18	2	PH1794	T cell receptor al	685	14	58.3	15	2	PH1788	T cell receptor al
613	15	62.5	19	2	S20289	cytochrome-c oxida	686	14	58.3	15	2	C31409	protein 425 - rat

687	14	58.3	15	2	AF0832	phe leader peptide	760	12	50.0	19	2	PH1609	Ig H chain V-D-J r
688	14	58.3	15	2	E91061	hypothetical prote	761	12	50.0	20	2	A26380	cytochrome P450 4A
689	14	58.3	15	2	T03463	ribosomal protein	762	12	50.0	20	2	E60894	crystallin - Pacif
690	14	58.3	15	2	A28965	ribulose-bisphosph	763	12	50.0	20	2	D49215	urease (EC 3.5.1.5
691	14	58.3	15	2	PA0036	glycine cleavage s	764	12	50.0	20	2	S06466	T-cell receptor al
692	14	58.3	15	2	I46909	voltage-dependent	765	12	50.0	20	2	S02002	photosystem II pro
693	14	58.3	15	4	I52698	hypothetical THR1	766	12	50.0	20	2	H49034	nuclear antigen BB
694	14	58.3	16	2	A44908	chitinase (EC 3.2.	767	12	50.0	20	2	A61093	glue protein - Cal
695	14	58.3	16	2	S23184	redoxendonuclease	768	12	50.0	20	2	A85645	Amino terminal of
696	14	58.3	16	2	I40065	shikimate 5-dehydr	769	12	50.0	20	2	S43676	ubenimex (bestatin
697	14	58.3	16	2	C53113	lys-gingipain form	770	12	50.0	20	2	A37988	acid proteinase he
698	14	58.3	16	2	T09741	photosystem I chai	771	12	50.0	20	2	S46479	retinoid-X-recepto
699	14	58.3	17	2	S19614	globin - polychaet	772	12	50.0	20	2	A28495	conopressin G - co
700	14	58.3	17	2	A27636	cytotoxin B - Clos	773	11	45.8	9	2	D58503	translation elonga
701	14	58.3	18	2	S09731	photosystem I prot	774	11	45.8	9	2	S63491	peptidylglycine mo
702	14	58.3	18	2	B44995	alkanal monooxygen	775	11	45.8	9	2	A42266	inflammatory sulf
703	14	58.3	18	2	B35910	neurofibromatosis-	776	11	45.8	9	2	S39040	lysine-conopressin
704	14	58.3	18	2	B41589	40K elastin-bindin	777	11	45.8	9	2	SC2021	oxytocin-related p
705	14	58.3	19	2	A92058	pepsin-like protei	778	11	45.8	9	2	A28924	fructose-bisphosph
706	14	58.3	19	2	S13046	calreticulin - rab	779	11	45.8	9	2	I49406	bone gla protein -
707	14	58.3	19	2	S59486	cell wall protein,	780	11	45.8	9	2	S19329	sperm-activating p
708	14	58.3	19	2	A61144	probable flagellar	781	11	45.8	10	2	D37397	hypothetical prote
709	14	58.3	19	2	S43045	translation elonga	782	11	45.8	10	2	G58501	48K bile/gallblad
710	14	58.3	20	2	B60822	cytochrome P450 UT	783	11	45.8	10	2	D46285	formaldehyde dehyd
711	14	58.3	20	2	PN0115	insulin-like growt	784	11	45.8	10	2	A30823	bohrpotoxin - ja
712	14	58.3	20	2	A53875	creatine kinase (E	785	11	45.8	10	2	A60527	sperm-activating p
713	14	58.3	20	2	S33761	actin - Acanthamo	786	11	45.8	10	2	H60787	sperm-activating p
714	14	58.3	20	2	A36045	thrombospondin hom	787	11	45.8	10	2	G60787	sperm-activating p
715	14	58.3	20	2	PC1152	equinotoxin 1D - s	788	11	45.8	10	2	F60787	sperm-activating p
716	14	58.3	20	2	A38600	trypsin inhibitor	789	11	45.8	10	2	F60787	sperm-activating p
717	14	58.3	20	2	A37984	ADP-ATP carrier pr	790	11	45.8	10	2	C60787	sperm-activating p
718	14	58.3	20	2	A60295	apolipoprotein III	791	11	45.8	10	2	A60787	sperm-activating p
719	14	58.3	20	2	A47105	dystroglycan - chi	792	11	45.8	10	2	D60787	sperm-activating p
720	13	54.2	3	3	F37196	bradykinin-potent	793	11	45.8	10	2	D60787	sperm-activating p
721	13	54.2	11	2	PT0250	Ig heavy chain CRD	794	11	45.8	10	2	D60588	sperm-activating p
722	13	54.2	11	2	A32428	amine oxidase (cop	795	11	45.8	10	2	B60588	sperm-activating p
723	13	54.2	16	2	T14224	NADH2 dehydrogenas	796	11	45.8	10	2	C60588	sperm-activating p
724	13	54.2	18	2	S29166	quinidine oxidore	797	11	45.8	10	2	I60527	sperm-activating p
725	13	54.2	19	2	S43657	hsp90 protein homo	798	11	45.8	10	2	A60588	sperm-activating p
726	13	54.2	19	2	A42339	amine oxidase (cop	799	11	45.8	10	2	A60788	sperm-activating p
727	13	54.2	19	2	A05305	hemoglobin beta-2	800	11	45.8	10	2	D60527	sperm-activating p
728	13	54.2	9	2	PT0315	Ig heavy chain CRD	801	11	45.8	10	2	C39572	sperm-activating p
729	12	50.0	11	2	G42762	proteasome endopep	802	11	45.8	10	2	F60527	sperm-activating p
730	12	50.0	11	2	PT0301	Ig heavy chain CRD	803	11	45.8	10	2	C60527	sperm-activating p
731	12	50.0	12	2	S17869	glutathione transf	804	11	45.8	10	2	E60527	sperm-activating p
732	12	50.0	12	2	S25056	Ig heavy chain - m	805	11	45.8	10	2	G60527	sperm-activating p
733	12	50.0	12	2	S26547	T-cell receptor be	806	11	45.8	10	2	E39572	sperm-activating p
734	12	50.0	12	2	S26546	T-cell receptor be	807	11	45.8	10	2	D60788	sperm-activating p
735	12	50.0	12	2	PH1461	T-cell receptor be	808	11	45.8	10	2	E60788	sperm-activating p
736	12	50.0	12	2	PH1459	T-cell receptor be	809	11	45.8	10	2	C60788	sperm-activating p
737	12	50.0	12	2	B61497	seed protein ws-17	810	11	45.8	10	2	F60589	sperm-activating p
738	12	50.0	12	2	A61503	sterol carrier pro	811	11	45.8	10	2	C60589	sperm-activating p
739	12	50.0	13	2	B26093	microbial collagen	812	11	45.8	10	2	D60589	sperm-activating p
740	12	50.0	13	2	S29488	GTP-binding protei	813	11	45.8	10	2	I60588	sperm-activating p
741	12	50.0	13	2	PT0263	Ig heavy chain CRD	814	11	45.8	10	2	I60589	sperm-activating p
742	12	50.0	13	2	G83988	hypothetical prote	815	11	45.8	11	1	GMROL	leucosulfakinin -
743	12	50.0	13	2	A61361	bradykinin-like pe	816	11	45.8	11	2	C58501	42K bile stone pro
744	12	50.0	14	2	S22236	lipoxigenase (EC 1	817	11	45.8	11	2	PC2330	perisulfakinin - A
745	12	50.0	14	2	S21247	H+-transporting tw	818	11	45.8	11	2	A60656	perisulfakinin - A
746	12	50.0	14	2	S57574	T cell receptor V-	819	11	45.8	11	2	D42965	talain - chicken (f
747	12	50.0	15	2	PH1582	Ig H chain V-D-J r	820	11	45.8	12	2	S26554	T-cell receptor (f
748	12	50.0	15	2	S03353	plastocyanin - Mic	821	11	45.8	12	2	B46662	collagen alpha 2(V
749	12	50.0	15	2	I67525	CD33 antigen homol	822	11	45.8	12	2	S67528	napin - rape (frag
750	12	50.0	16	2	S28433	major outer membra	823	11	45.8	12	2	A09985	gamma-crystallin -
751	12	50.0	17	2	C37520	glutathione transf	824	11	45.8	12	2	A37933	Ig lambda chain J1
752	12	50.0	17	2	PH1607	Ig H chain V-D-J r	825	11	45.8	12	2	A20907	Ig kappa chain J1
753	12	50.0	17	2	S33609	extensin - maize (826	11	45.8	12	2	D20907	Ig kappa-1 chain J
754	12	50.0	17	2	A61019	17K basolateral pl	827	11	45.8	12	2	F20907	Ig kappa-2 chain J
755	12	50.0	17	2	PD0005	very-high-density	828	11	45.8	12	2	PH0785	T-cell receptor al
756	12	50.0	18	2	B49215	urease (EC 3.5.1.5	829	11	45.8	12	2	PH0771	T-cell receptor be
757	12	50.0	18	2	B49254	Tcr C gamma 1 chai	830	11	45.8	12	2	PH1454	T-cell receptor al
758	12	50.0	18	2	PH1629	Ig H chain V-D-J r	831	11	45.8	12	2	PH1469	T-cell receptor be
759	12	50.0	18	2	A59396	Tha p 1 - Thaumeto	832	11	45.8	12	2	PH1468	T-cell receptor be

833	11	45.8	13	2	848210	collagen alpha 1(V	906	11	45.8	15	2	PQ0193	stylar glycoprotei
834	11	45.8	13	2	S63492	dissimilatory sulf	907	11	45.8	15	2	PQ0194	Sz-glycoprotein -
835	11	45.8	13	2	PC2371	probable endopepti	908	11	45.8	15	2	PA0092	protein QF200011 -
836	11	45.8	13	2	PS0325	tetrahydroberberin	909	11	45.8	15	2	PA0097	starch phosphoryla
837	11	45.8	13	2	S23640	Ig kappa chain J s	910	11	45.8	15	2	B61457	alpha-glucosidase
838	11	45.8	13	2	B20907	Ig kappa-1 chain J	911	11	45.8	15	2	C61498	T-cell receptor be
839	11	45.8	13	2	E53275	Ig kappa-1 chain J	912	11	45.8	15	2	PH1807	T-cell receptor al
840	11	45.8	13	2	S22761	Ig lambda-2 chain	913	11	45.8	15	2	C24687	T-cell receptor be
841	11	45.8	13	2	PH0787	T-cell receptor al	914	11	45.8	15	2	D28587	T-cell receptor be
842	11	45.8	13	2	C47630	Ig kappa chain J r	915	11	45.8	15	2	F28587	T-cell receptor be
843	11	45.8	13	2	B47630	Ig kappa chain J r	916	11	45.8	15	2	E56978	collagen alpha 2(X
844	11	45.8	13	2	D47630	Ig kappa chain J r	917	11	45.8	15	2	PQ0074	T-cell receptor be
845	11	45.8	13	2	E47630	Ig kappa chain J r	918	11	45.8	15	2	S55312	TSH protein beta c
846	11	45.8	13	2	S03063	Ig lambda chain J	919	11	45.8	15	2	PN0662	dystrophin-associa
847	11	45.8	13	2	AB0764	his operon leader	920	11	45.8	15	2	I53284	T-cell receptor be
848	11	45.8	13	2	B19434	probable sex-speci	921	11	45.8	15	2	PH1619	Ig H chain V-D-J r
849	11	45.8	13	2	S23638	Ig kappa chain J s	922	11	45.8	15	2	PH0784	T-cell receptor al
850	11	45.8	13	2	H33932	Ig kappa chain J r	923	11	45.8	15	2	PH0784	T-cell receptor be
851	11	45.8	13	2	A33933	Ig kappa chain J r	924	11	45.8	15	2	C44101	calmodulin, vasoac
852	11	45.8	13	2	JH0460	corticostatic pept	925	11	45.8	15	2	PH1435	T-cell receptor al
853	11	45.8	14	2	A01250	angiotensin precu	926	11	45.8	15	2	PH1452	T-cell receptor al
854	11	45.8	14	2	S19803	ubiquitin - potato	927	11	45.8	15	2	PH1449	T-cell receptor al
855	11	45.8	14	2	S50900	chlorophyll a/b-bi	928	11	45.8	15	2	PH1436	T-cell receptor al
856	11	45.8	14	2	S13864	methyl coenzyme M	929	11	45.8	15	2	PH1443	T-cell receptor al
857	11	45.8	14	2	S17766	beta-glucosidase (930	11	45.8	15	2	PH1441	T-cell receptor al
858	11	45.8	14	2	S38307	DEB-A protein - fr	931	11	45.8	15	2	A35389	urease (EC 3.5.1.5
859	11	45.8	14	2	PH1347	Ig heavy chain DJ	932	11	45.8	15	2	B41868	hypothetical prote
860	11	45.8	14	2	S23639	Ig kappa chain J s	933	11	45.8	15	2	E56819	PS I complex subun
861	11	45.8	14	2	C48394	major fat-globule	934	11	45.8	15	2	PA0110	translation elonga
862	11	45.8	14	2	A17150	glucose 1-dehydrog	935	11	45.8	15	2	PA0005	lectin Al - Paopho
863	11	45.8	14	2	PH1448	T-cell receptor al	936	11	45.8	15	2	PA0093	ubiquitin - fungus
864	11	45.8	14	2	PH1450	T-cell receptor al	937	11	45.8	15	2	PA0063	hemoglobin (N-term
865	11	45.8	14	2	S29632	xylan 1,4-beta-xy	938	11	45.8	15	2	A46586	interphotorceptor
866	11	45.8	14	2	I39753	nitrogenase (EC 1	939	11	45.8	15	2	G24417	leukocyte chemotac
867	11	45.8	14	2	S07768	soluble hydrogenas	940	11	45.8	15	2	JT0610	his operon leader
868	11	45.8	14	2	S58862	botulinum neurotox	941	11	45.8	16	1	LFEC	casein kinase II (
869	11	45.8	14	2	S58866	botulinum neurotox	942	11	45.8	16	2	C45133	protein kinase C i
870	11	45.8	14	2	PQ0058	glycerol kinase (E	943	11	45.8	16	2	S10807	proteasome endopep
871	11	45.8	14	2	PQ0152	18K iron-sulfur pr	944	11	45.8	16	2	A44413	alpha-conotoxin Au
872	11	45.8	14	2	PA0007	lectin B1 - Paopho	945	11	45.8	16	2	C59045	alpha-conotoxin Au
873	11	45.8	14	2	PS0249	porin - rice (atra	946	11	45.8	16	2	A44101	calmodulin, vasoac
874	11	45.8	14	2	A56632	neofakinin-II -	947	11	45.8	16	2	A29501	fibrinopeptide A -
875	11	45.8	14	2	I56493	endothelial growth	948	11	45.8	16	2	B24180	fibrinogen alpha c
876	11	45.8	14	2	S36678	dodecenoyl-CoA Del	949	11	45.8	16	2	A24180	fibrinogen alpha c
877	11	45.8	14	2	PC4376	telomeric and tetr	950	11	45.8	16	2	B28854	fibrinopeptide A -
878	11	45.8	14	2	S27140	hypothetical prote	951	11	45.8	16	2	C28854	fibrinopeptide A -
879	11	45.8	14	2	A32654	fibrinopeptide A -	952	11	45.8	16	2	A28854	fibrinopeptide A -
880	11	45.8	15	2	A60834	angiotensin I prec	953	11	45.8	16	2	G29501	fibrinopeptide A -
881	11	45.8	15	2	B59045	alpha-conotoxin Au	954	11	45.8	16	2	H29501	fibrinopeptide A -
882	11	45.8	15	2	S26524	T-cell receptor al	955	11	45.8	16	2	S01669	rRNA N-glycosidase
883	11	45.8	15	2	S26527	T-cell receptor al	956	11	45.8	16	2	F41299	T-cell receptor al
884	11	45.8	15	2	S26532	T-cell receptor al	957	11	45.8	16	2	H41299	T-cell receptor al
885	11	45.8	15	2	S26535	T-cell receptor al	958	11	45.8	16	2	C49048	T-cell receptor be
886	11	45.8	15	2	S26515	T-cell receptor al	959	11	45.8	16	2	G24687	T-cell receptor be
887	11	45.8	15	2	S26523	T-cell receptor al	960	11	45.8	16	2	A28587	T-cell receptor be
888	11	45.8	15	2	S26525	T-cell receptor al	961	11	45.8	16	2	B28587	T-cell receptor be
889	11	45.8	15	2	S26531	T-cell receptor al	962	11	45.8	16	2	C28587	T-cell receptor be
890	11	45.8	15	2	S26518	T-cell receptor al	963	11	45.8	16	2	F53284	T-cell receptor be
891	11	45.8	15	2	S26516	T-cell receptor al	964	11	45.8	16	2	G53284	T-cell receptor be
892	11	45.8	15	2	S26534	T-cell receptor al	965	11	45.8	16	2	B60566	cytochrome P450m51
893	11	45.8	15	2	S26517	T-cell receptor al	966	11	45.8	16	2	PH1580	Ig H chain V-D-J r
894	11	45.8	15	2	S26528	T-cell receptor al	967	11	45.8	16	2	PH1580	triose-phosphate i
895	11	45.8	15	2	S26528	T-cell receptor al	968	11	45.8	16	2	PH1453	T-cell receptor al
896	11	45.8	15	2	I49407	placental calcium-	969	11	45.8	16	2	C90981	his operon leader
897	11	45.8	15	2	I29501	fibrinopeptide A -	970	11	45.8	16	2	S16376	L-serine dehydrata
898	11	45.8	15	2	F29501	fibrinopeptide A -	971	11	45.8	16	2	S42237	hypothetical prote
899	11	45.8	15	2	JPW001	fibrinogen alpha c	972	11	45.8	16	2	B44896	heat shock protein
900	11	45.8	15	2	JPW004	chlorophyll a/b-bi	973	11	45.8	16	2	S09732	photosystem I prot
901	11	45.8	15	2	S21238	hydrogensulfite re	974	11	45.8	16	2	F54226	light-harvesting p
902	11	45.8	15	2	PA0027	protein QA100006 -	975	11	45.8	16	2	A85827	his operon leader
903	11	45.8	15	2	PA0026	protein QA300027 -	976	11	45.8	16	2	A61268	cytochrome P450-th
904	11	45.8	15	2	S13973	chlorophyll a/b-bi	977	11	45.8	16	2	A36889	leu operon leader
905	11	45.8	15	2	PQ0192	stylar glycoprotei	978	11	45.8	16	2		

979	11	45..8	17	2	B49404	T-cell receptor be
980	11	45..8	17	2	E29501	fibrinopeptide A -
981	11	45..8	17	2	S05917	chorion class A pr
982	11	45..8	17	2	S05923	chorion class A pr
983	11	45..8	17	2	S05913	chorion class A pr
984	11	45..8	17	2	S05921	chorion class A pr
985	11	45..8	17	2	S05919	chorion class A pr
986	11	45..8	17	2	S05915	chorion class A pr
987	11	45..8	17	2	B23219	high-cysteine chor
988	11	45..8	17	2	S50901	chlorophyll a/b-bi
989	11	45..8	17	2	S63503	83K protein - Euba
990	11	45..8	17	2	A58946	formylmethanofuran
991	11	45..8	17	2	PH0082	neuroglial protein
992	11	45..8	17	2	I24687	T-cell receptor be
993	11	45..8	17	2	B31769	T-cell receptor de
994	11	45..8	17	2	S47201	T-cell receptor J-
995	11	45..8	17	2	D53284	T-cell receptor be
996	11	45..8	17	2	PH0769	T-cell receptor be
997	11	45..8	17	2	S09085	proteasome chain 4
998	11	45..8	17	2	S69164	ferredoxin al - Ja
999	11	45..8	17	2	B61491	seed protein ws-2
1000	11	45..8	17	2	JO2310	hypothetical 2.1K

ALIGNMENTS

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RESULT 1
C39191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C:Species: Bacteroides fragilis
C:Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C:Accession: C39191
R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A:Reference number: A39191; MUID:91100280; PMID:1846135
A:Accession: C39191
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <SPE>
A:Cross-references: GB:M37699

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Query Match      100.0%;   Score 24;   DB 2;   Length 10;
Best Local Similarity 22.2%;   Pred. NO. 8.8e+02;
Matches 2;   Conservative 7;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1  XFXXXWXXX 9
       :|::|::|::
Db      2  YFSPPTSTI 10

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RESULT 2
T17063
Cytochrome-c oxidase (EC 1.9.3.1) chain I - *Hoplocercus spinosus* mitochondrion (fragment
C;Species: mitochondrion *Hoplocercus spinosus*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17063
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: T17063
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>

C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 24; DB 2; Length 10;

```

Best Local Similarity 22.2%; Pred. No. 8.8e+02;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
   :|:|:|:|:
Db 1 MFISRWLFS 9

RESULT 3
T12325
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fragment)
C/Species: mitochondrion Leiocephalus carinatus
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12325
R/Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A/Title: Molecular tests of phylogenetic taxonomies: A general procedure and example using
A/Reference number: Z17488; MUID:99162288; PMID:10051389
A/Accession: T12325
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-10 <SCH>
A/Cross-references: UNIPROT:Q9ZYT2; EMBL:AF049864; NID:G4105754; PID:G4105757; PIDN:AADC
C/Genetics:
A/Genome: mitochondrion
A/Note: COI
C/Keywords: mitochondrion; oxidoreductase

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Query Match      100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 8.8e+02;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      1 XFXXXWXXX 9
      .|::|::
      .|::|::
Db      1 MFIIRWLFS 9

RESULT 4
TL7066
cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)
C/Species: Mitochondrion Oplurus cuvieri
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: TL7066
R/Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A/Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A/Reference number: Z18674; MUID:97315309; PMID:9169559
A/Accession: TL7066

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A;Residues: 1-10 <MAC>
A;Cross-references: UNIPROT:O79903; EMBL:U82685; NID:g3603136; PID:g3603139; PIDN:AAC622
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match	100.0%	Score 24;	DB 2;	Length 10;
Best Local Similarity	22.2%;	Pred. No. 8.8e+02;		
Matches 2;	Conservative	7;	Mismatches 0;	Indels 0;
				Gaps 0;

```

Qy      1 XPXXXXXX 9
      :|::|::
Db      1 MFNRWFFS 9

RESULT 5
T17069
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglassii mitochondrion (fragmen
C:Species: mitochondrion Phrynosoma douglassii
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17069
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

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Qy 1 XFXXWXXX 9
   :|::|::
Db 3 PFFDWRSG 11

RESULT 8
A34704
protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34704
R:Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A:Title: Identification of a novel neuronal C-SRC exon expressed in human brain
A:Reference number: A34704; MUID:90220588; PMID:1691439
A:Accession: A34704
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <PYP>
A:Cross-references: UNIPROT:Q14925
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 100.0%; Score 24; DB 2; Length 17;
Best Local Similarity 22.2%; Pred. No. 1.4e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
   :|::|::
Db 9 WFTFRWLQR 17

RESULT 9
S32675
nitrogen fixation protein nifB - Anabaena variabilis (fragment)
C:Species: Anabaena variabilis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32675
R:Monnerjahn, U.; Boehme, H.
submitted to the EMBL Data Library, December 1992
A:Description: Cloning and expression in E. coli of the Anabaena.
A:Reference number: S32675
A:Accession: S32675
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-19 <MON>
A:Cross-references: UNIPROT:Q44506; EMBL:X69898; NID:G296503; PIDN:CAA49521.1;
C:Genetics:
A:Gene: nifB
C:Superfamily: Rhizobium nifB protein

Query Match 100.0%; Score 24; DB 2; Length 19;
Best Local Similarity 22.2%; Pred. No. 1.5e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XFXXWXXX 9
   :|::|::
Db 11 EFVEQWNGK 19

RESULT 10
S77981
cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: S77981
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach,
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77981
A:Molecule type: protein
A:Residues: 1-20 <ARN>
A:Cross-references: UNIPROT:P80972
A:Experimental source: heart; liver

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C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Superfamily: mammalian cytochrome-c oxidase chain va
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match      100.0%; Score 24; DB 2; Length 20;
Best Local Similarity 22.2%; Pred. No. 1.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
   :|::|::|
Db 10 EFDARWTV 18

RESULT 11
PN0171
peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichioides)
N;Contains: cyclophilin
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000
C;Accession: PN0171
R;Fukaya, N.; Chow, L.P.; Sugitara, Y.; Taugita, A.; Ueno, Y.; Tabuchi, K.
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A;Reference number: PN0160
A;Accession: PN0171
A;Molecule type: protein
A;Residues: 1-20 <FUK>
A;Experimental source: strain M-1-1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match      100.0%; Score 24; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
   :|::|::|
Db 5 FPDITWEGX 13

RESULT 12
PC1240
calcium-binding protein, 53K - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1240; PC1241
R;Menegazzi, P.; Guzzo, F.; Baldan, B.; Mariani, P.; Treves, S.
Biochem. Biophys. Res. Commun. 190, 1130-1135, 1993
A;Title: Purification of calreticulin-like protein(s) from spinach leaves.
A;Reference number: PC1240; MUID:93176159; PMID:8439313
A;Accession: PC1240
A;Molecule type: protein
A;Residues: 1-20 <MEN>
A;Cross-references: UNIPROT:P30806
A;Experimental source: leaf
A;Note: 53K form
A;Accession: PC1241
A;Molecule type: protein
A;Residues: 1-20 <ME2>
A;Experimental source: leaf
A;Note: 55K form
C;Superfamily: calreticulin
C;Keywords: calcium binding; metal binding

Query Match      100.0%; Score 24; DB 2; Length 20;
Best Local Similarity 22.2%; Pred. No. 1.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
   :|::|::|
```

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Db 7 RFDGWNRR 15

RESULT 13
PH1380
alpha-amylase (EC 3.2.1.1) (Halm sensitive) - Bacillus sp. (fragment)
C;Species: Bacillus sp.
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1380
R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
A;Title: Purification and some properties of a Halm-sensitive alpha-amylase from newly
A;Reference number: PH1380; MUID:93113087; PMID:1369074
A;Accession: PH1380
A;Molecule type: protein
A;Residues: 1-20 <KAW>
A;Cross-references: UNIPROT:Q9R5E8
A;Experimental source: strain NO.195
C;Comment: This enzyme has an optimum pH of 7.0.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      100.0%; Score 24; DB 2; Length 20;
Best Local Similarity 22.2%; Pred. No. 1.6e+03;
Matches 2; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXWXXX 9
   :|::|::|
Db 12 MFSWTWNAI 20

RESULT 14
I46023
growth hormone receptor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46023
R;Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
Mol. Cell. Endocrinol. 72, 187-200, 1990
A;Title: Cloning and in vivo expression of bovine growth hormone receptor mRNA.
A;Reference number: I46023; MUID:91146804; PMID:2289631
A;Accession: I46023
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-9 <HAU>
A;Cross-references: UNIPROT:Q28121; EMBL:U24113; NID:g775221; PIDN:AAA91014.1; PID:g7752
C;Genetics:
A;Gene: GHR

Query Match      95.8%; Score 23; DB 2; Length 9;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 FXXXXWXXX 9
   |::|::|
Db 1 FQFPWFVI 8

RESULT 15
B33995
hypotrehalosemic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C;Accession: B33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neurotrophic hormones with adipokinetic and hypotrehal
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: B33995
A;Molecule type: protein
A;Residues: 1-10 <JAF>
```

Best Local Similarity 25.0%; Pred. No. i.3e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XEXXXWXX 8
Db 3 NFSFGWGT 10

RESULT 18

S08998

hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach

C/Species: Leucophaea maderae (Madeira cockroach)
C/Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C/Accession: S08998
R/Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A/Reference number: S08995; MUID:90253659; PMID:2340112
A/Accession: S08998
A/Molecule type: protein
A/Residues: 1-10 <GAE>
A/Cross-references: UNIPROT:P10939
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.8%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. i.3e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XEXXXWXX 8
Db 3 NFSFGWGT 10

RESULT 19

A26381

hypertrehalosemic hormone - gray cockroach

C/Species: Nauphoeta cinerea (gray cockroach)
C/Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C/Accession: A26381
R/Gade, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A/Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardiaca of the gray cockroach, Nauphoeta cinerea
A/Reference number: A26381; MUID:87100208; PMID:3801028
A/Accession: A26381
A/Molecule type: protein
A/Residues: 1-10 <GAD>
A/Cross-references: UNIPROT:P10939
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.8%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. i.3e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XEXXXWXX 8
Db 3 NFSFGWGT 10

RESULT 20

JC1416

hypertrehalosemic hormone I - stick insect (Carausius morosus)

N/Alternate names: neuropeptide Cam-HrTH-I
N/Contains: hypertrehalosemic factor II
C/Species: Carausius morosus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JCI1416; S07157
R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect
A:Reference number: JCI1416; MUID:93129188; PMID:1482345
A:Accession: JCI1416
A:Molecule type: protein
A:Residues: 1-10 <GAE1>
A:Cross-references: UNIPROT:P11385
R:Gaede, G.; Rinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A:Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiaca
A:Reference number: S07157; MUID:87157103; PMID:3828078
A:Accession: S07157
A:Molecule type: protein
A:Residues: '2', 2-10 <GAE2>
C:Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach periplaneta
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Binding site: carbohydrate (Trp) (covalent) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.8%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 6;

QY 1 XFXXWXX 8
:|::|::|
Db 3 TFTPNGWT 10

RESULT 21
S09138
Hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
N:Alternate names: Cam-HrTH-II
C:Species: Extatosoma tiaratum
C>Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S09138
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S09138
A:Molecule type: protein
A:Residues: 1-10 <GAE>
A:Cross-references: UNIPROT:P11385
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.8%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 6;

QY 1 XFXXWXX 8
:|::|::|
Db 3 TFTPNGWT 10

RESULT 22
A31571
Hypertrehalosemic/adipokinetic hormone - bollworm
N:Alternate names: Hez-HrTH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C>Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A31571
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S
Biochem. Biophys. Res. Commun. 155, 344-350, 1988

A:Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea w
A:Reference number: A31571; MUID:88326324; PMID:3415690
A:Accession: A31571
A:Molecule type: protein
A:Residues: 1-10 <JAF>
A:Cross-references: UNIPROT:P16353
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 95.8%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 6;

QY 1 XFXXWXX 8
:|::|::|
Db 3 TFPSSGWN 10

RESULT 23
S53789
Neuropeptide Pec-HrTH - Platypleura capensis
C:Species: Platypleura capensis
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S53789
R:Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A:Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehal
A:Reference number: S53789; MUID:95225985; PMID:7710694
A:Accession: S53789
A:Molecule type: protein
A:Residues: 1-10 <GAE>
A:Cross-references: UNIPROT:Q7M465
C:Keywords: blocked amino end; blocked carboxyl end

Query Match 95.8%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 6;

QY 1 XFXXWXX 8
:|::|::|
Db 3 NFSPSGWN 10

RESULT 24
A24244
Adipokinetic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C>Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A24244
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgwa
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic
A:Reference number: A24244; MUID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAF>
A:Cross-references: UNIPROT:P08901
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 91.7%; Score 22; DB 2; Length 9;
Best Local Similarity 28.6%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 5;

QY 1 XFXXWXX 7
:|::|::|
Db 3 TFTSSWG 9

RESULT 25

PH1613
IG H chain V-D-J region (clone B-less 17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1613
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 91.7%; Score 22; DB 2; Length 15;
Best Local Similarity 28.6%; Pred. No. 2.7e+03;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWX 7
:|::|
Db 9 YFTWLWT 15

RESULT 26

A33995
adipokinetic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuro peptide hormones with adipokinetic and hypotrehal
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: A33995
A;Molecule type: protein
A;Residues: 1-8 <JAP>
A;Cross-references: UNIPROT:P14595
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuro peptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWX 6
:|::|
Db 3 TTFPGW 8

RESULT 27

A44960
neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: A44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04548
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuro peptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWX 6
:|::|
Db 3 NFSPNW 8

RESULT 28

B44960
neuropeptide Led-CC-II - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: B44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04549
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuro peptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWX 6
:|::|
Db 3 TTFPGW 8

RESULT 29

A58620
adipokinetic hormone - damselfly (Ischnura senegalensis)
C;Species: Ischnura senegalensis
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C;Accession: A58620
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudegria inconspicua
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: A58620
A;Molecule type: protein
A;Residues: 1-8 <JAN>
A;Cross-references: UNIPROT:Q7M4H6
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuro peptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXWX 6
:|::|
Db 3 TTFPGW 8

RESULT 30

S11545
adipokinetic hormone - nestling-sucking blowfly
C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S11545
R;Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990

A:Title: Isolation and structure of a novel charged member of the red-pigment-concentrating erraenovae (Diptera).
A:Reference number: S11545; MUID:90351345; PMID:2386478
A:Accession: S11545
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P61856
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6
Db 3 TFSPDW 8
:|:|:|

RESULT 31
S55310
adipokinetic hormone - damselfly (Pseudagrion inconstipicum)
N:Alternate names: Psi-AKH
C:Species: Pseudagrion inconstipicum
C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconstipicum
A:Reference number: S55310; MUID:94379987; PMID:8093008
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
A:Cross-references: UNIPROT:Q7M4H7
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6
Db 3 NFTPWG 8
:|:|:|

RESULT 32
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: A61348; S07139
R:Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738; PMID:5041363
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FER1>
A:Cross-references: UNIPROT:P08939
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis
A:Reference number: S07139; MUID:75054965; PMID:4433569
A:Accession: S07139
A:Molecule type: protein
A:Residues: 'E', 2-8 <FER2>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in: zed pigment-containing cells.
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6
Db 3 NFSPGW 8
:|:|:|

RESULT 33
S10596
adipokinetic hormone - pond skimmer
C:Species: Libellula auripennis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S10596
R:Gaede, G.
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone
A:Reference number: S10596; MUID:90359055; PMID:2390213
A:Accession: S10596
A:Molecule type: protein
A:Residues: 1-8 <BIO>
A:Cross-references: UNIPROT:P25418
C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6
Db 3 NFTPWG 8
:|:|:|

RESULT 34
S08995
hypertrehalosemic hormone I - oriental cockroach
N:Alternate names: Pea-CAH-I
C:Species: Blatta orientalis (oriental cockroach)
C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S08995
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08995
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P04548
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6
Db 3 NFTPWG 8
:|:|:|

Db 3 NFSPNW 8

RESULT 35

S08996

hypertrehalosemic hormone II - oriental cockroach
N/Alternate names: Pea-CAH-II
C/Species: Blatta orientalis (oriental cockroach)
C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C/Accession: S08996

R/Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry of a peptide
A/Reference number: S08995; MUID:90253659; PMID:2340112
A/Accession: S08996
A/Molecule type: protein
A/Residues: 1-8 <GAE>
A/Cross-references: UNIPROT:P04549
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F1/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6

Db 3 TFTPWN 8

RESULT 36

A49823

adipokinetic hormone I - American cockroach
N/Alternate names: periplanetin CC-1
C/Species: Periplaneta americana (American cockroach)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: A49823
R/Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A/Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activity
A/Reference number: A49823; MUID:84298179; PMID:6591205
A/Accession: A49823
A/Molecule type: protein
A/Residues: 1-8 <SCA>
A/Cross-references: UNIPROT:P04548
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F1/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6

Db 3 NFSPNW 8

RESULT 37

B49823

adipokinetic hormone II - American cockroach
N/Alternate names: neuropeptide M-II; periplanetin CC-1
C/Species: Periplaneta americana (American cockroach)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: B49823; A05170
R/Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A/Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activity

A/Reference number: A49823; MUID:84298179; PMID:6591205

A/Accession: B49823
A/Molecule type: protein
A/Residues: 1-8 <SCA>
A/Cross-references: UNIPROT:P04549
R/Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A/Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry of a peptide
A/Reference number: A90118; MUID:85046530; PMID:6548628
A/Accession: A05170
A/Molecule type: protein
A/Residues: 'E', 2-8 <WIT>
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F1/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6

Db 3 TFTPWN 8

RESULT 38

A28004

adipokinetic hormone G - two-spotted cricket
N/Alternate names: AKH-G
C/Species: Gryllus bimaculatus (two-spotted cricket)
C/Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C/Accession: A28004
R/Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
A/Reference number: A28004; MUID:88106553; PMID:3426616
A/Accession: A28004
A/Molecule type: protein
A/Residues: 1-8 <GAE>
A/Cross-references: UNIPROT:P14086
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F1/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXW 6

Db 3 NFSTGW 8

RESULT 39

A43976

hypertrehalosemic hormone - yellow mealworm
C/Species: Tenebrio molitor (yellow mealworm)
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C/Accession: A43976
R/Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid b.

A/Accession: A43976

A/Residues: 1-8 <GAE>
A/Cross-references: UNIPROT:P25419
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXW 6
:|:|:
Db 3 NFSPNW 8

RESULT 40

B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: B43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A;Reference number: A43976; MUID:90341081; PMID:2381871
A;Accession: B43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P25419
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.5%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XFXXXW 6
:|:|:
Db 3 NFSPNW 8

Search completed: October 19, 2005, 15:41:35
Job time : 26.8824 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:30:14 ; Search time 22.1176 Seconds
(without alignments)
34.802 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 79:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	9	I46023	growth hormone rec
2	23	100.0	10	C39191	hypothetical prote
3	23	100.0	10	T17063	cytochrome-c oxida
4	23	100.0	10	T12325	cytochrome-c oxida
5	23	100.0	10	T17066	cytochrome-c oxida
6	23	100.0	10	T17069	cytochrome-c oxida
7	23	100.0	10	T12329	cytochrome-c oxida
8	23	100.0	13	PC4391	cysteine proteinas
9	23	100.0	17	A34704	protein-tyrosine k
10	23	100.0	19	S32675	nitrogen fixation
11	23	100.0	20	S77981	peptidylprolyl iso
12	23	100.0	20	PN0171	calcium-binding pr
13	23	100.0	20	PC1240	alpha-amylase JEC
14	23	100.0	20	PH1380	hypotrrehalosemic h
15	22	95.7	10	B33995	hypotrrehalosemic
16	22	95.7	10	S08997	hypotrrehalosemic
17	22	95.7	10	A60421	hypotrrehalosemic
18	22	95.7	10	S08998	hypotrrehalosemic
19	22	95.7	10	A26381	hypotrrehalosemic
20	22	95.7	10	JC1416	hypotrrehalosemic
21	22	95.7	10	S09138	hypotrrehalosemic
22	22	95.7	10	A31571	hypotrrehalosemic
23	22	95.7	10	S53789	neuropeptide Pec-H
24	21	91.3	9	A24244	adipokinetic hormo
25	21	91.3	15	PH1613	Ig H chain V-D-J r
26	20	87.0	8	A33995	adipokinetic hormo
27	20	87.0	8	A44960	neuropeptide led-C
28	20	87.0	8	B44960	neuropeptide led-C
29	20	87.0	8	A58620	adipokinetic hormo

30	20	87.0	8	2	S11545	adipokinetic hormo
31	20	87.0	8	2	S55310	adipokinetic hormo
32	20	87.0	8	2	A61348	red pigment-concen
33	20	87.0	8	2	S10596	adipokinetic hormo
34	20	87.0	8	2	S08995	hypotrrehalosemic
35	20	87.0	8	2	S08996	hypotrrehalosemic
36	20	87.0	8	2	A49823	adipokinetic hormo
37	20	87.0	8	2	B49823	adipokinetic hormo
38	20	87.0	8	2	A28004	adipokinetic hormo
39	20	87.0	8	2	A43976	hypotrrehalosemic
40	20	87.0	8	2	B43976	hypotrrehalosemic
41	20	87.0	8	2	A05169	neuropeptide M-I -
42	20	87.0	8	2	D57444	neuropeptide Grb-A
43	20	87.0	10	1	RHLMS	gonadoliberein - se
44	20	87.0	10	2	PT0322	Ig heavy chain CRD
45	20	87.0	10	2	E41946	T-cell receptor ga
46	20	87.0	10	2	C41946	T-cell receptor ga
47	20	87.0	10	2	T12312	cytochrome-c oxida
48	20	87.0	11	2	C53652	rhlR protein - Pse
49	20	87.0	11	2	D41946	T-cell receptor ga
50	20	87.0	11	2	B41946	T-cell receptor ga
51	20	87.0	12	2	PT0274	Ig heavy chain CRD
52	20	87.0	12	2	PH1324	Ig heavy chain DJ
53	20	87.0	12	2	PH1308	Ig heavy chain DJ
54	20	87.0	13	2	PT0304	Ig heavy chain CRD
55	20	87.0	15	2	PH1319	Ig heavy chain DJ
56	20	87.0	15	2	PS0382	Ig heavy chain J r
57	20	87.0	15	2	S10388	Ig heavy chain J r
58	20	87.0	15	2	S10386	Ig heavy chain J r
59	20	87.0	15	2	PH1366	Ig heavy chain DJ
60	20	87.0	15	2	PH1318	Ig heavy chain DJ
61	20	87.0	16	2	A36300	T-cell receptor ga
62	20	87.0	16	2	PH1346	Ig heavy chain DJ
63	20	87.0	16	2	C37290	homotetic protein G
64	20	87.0	17	2	H49048	T-cell receptor be
65	20	87.0	17	2	I49048	T-cell receptor be
66	20	87.0	17	2	S26744	Ig heavy chain J r
67	20	87.0	17	2	PT0235	Ig heavy chain CRD
68	20	87.0	18	2	S03528	Ig heavy chain J1
69	20	87.0	18	2	A25941	Ig heavy chain J-H
70	20	87.0	18	2	S39009	oviductin - golden
71	20	87.0	18	2	C49254	Tcr C gamma 1 chai
72	20	87.0	19	2	G49048	T-cell receptor be
73	20	87.0	19	2	S60110	hypothetical prote
74	20	87.0	20	2	F49048	T-cell receptor be
75	20	87.0	20	2	A49048	T-cell receptor be
76	19	82.6	8	2	T13818	cytochrome oxidase
77	19	82.6	11	2	S05002	corazonin - Americ
78	19	82.6	20	2	A60372	pollen allergen Po
79	18	78.3	6	2	F41946	T-cell receptor ga
80	18	78.3	10	1	A61126	gonadoliberein - sp
81	18	78.3	10	1	RHAQ2	gonadoliberein II -
82	18	78.3	10	2	B46030	gonadoliberein II -
83	18	78.3	10	2	A49187	gonadotropin-relea
84	18	78.3	10	2	A46030	gonadoliberein I -
85	18	78.3	10	2	A21114	gonadoliberein - ch
86	18	78.3	10	2	T17075	cytochrome-c oxida
87	18	78.3	11	2	PT0302	Ig heavy chain CRD
88	18	78.3	14	2	PH1322	Ig heavy chain DJ
89	18	78.3	14	2	PH1757	T cell receptor al
90	18	78.3	14	2	PH1758	T cell receptor al
91	18	78.3	14	2	PH1759	T cell receptor al
92	18	78.3	14	2	PH1766	T cell receptor al
93	18	78.3	14	2	PH1767	T cell receptor al
94	18	78.3	14	2	PH1768	T cell receptor al
95	18	78.3	14	2	PH1769	T cell receptor al
96	18	78.3	15	2	B60763	endo-1,3-beta-gluc
97	18	78.3	16	2	S03532	Ig heavy chain J r
98	18	78.3	16	2	D49021	Ig heavy chain J7
99	18	78.3	16	2	PS0383	Ig heavy chain J r
100	18	78.3	16	2	S26746	Ig heavy chain J r
101	18	78.3	16	2	PT0282	Ig heavy chain CDR
102	18	78.3	18	2	PH1323	Ig heavy chain DJ

103	18	78.3	19	2	PH1339	Ig heavy chain DJ	176	17	73.9	11	2	TI7081	cytochrome-c oxida
104	17	73.9	7	2	S21230	dermorphin (trp-4,	177	17	73.9	11	2	TI7078	cytochrome-c oxida
105	17	73.9	7	2	S09652	hypothetical prote	178	17	73.9	12	1	UOQM2	urotensin II - lon
106	17	73.9	8	2	S15422	adipokinetic hormo	179	17	73.9	12	2	USQ423	urotensin II-A pep
107	17	73.9	8	2	A58641	adipokinetic hormo	180	17	73.9	12	2	S42765	urotensin II - tel
108	17	73.9	8	2	PQ0012	cholecystokinin -	181	17	73.9	12	2	PH1675	Ig heavy chain V r
109	17	73.9	8	2	A43001	cholecystokinin -	182	17	73.9	12	2	PH1675	Ig heavy chain V r
110	17	73.9	8	2	A59495	Vesicle associated	183	17	73.9	12	2	S26548	T-cell receptor be
111	17	73.9	8	2	S19288	acylase - Kluuyvera	184	17	73.9	12	2	A26093	microbial collagen
112	17	73.9	8	2	S21663	neuropeptide - flo	185	17	73.9	12	2	G64003	hypothetical prote
113	17	73.9	8	2	A41117	acetylcholinestera	186	17	73.9	12	2	S69123	proton-translocat
114	17	73.9	9	2	A61357	phylocaerulein -	187	17	73.9	12	2	S43957	Ig mu chain V regi
115	17	73.9	9	2	PT0288	Ig heavy chain CRD	188	17	73.9	12	2	B49033	T-cell receptor de
116	17	73.9	9	2	PT0299	Ig heavy chain CRD	189	17	73.9	12	2	S25039	Ig heavy chain V r
117	17	73.9	9	2	PT0634	T-cell receptor be	190	17	73.9	12	2	I57678	gene rPLP-A protei
118	17	73.9	9	2	I58350	gene c-mpl protein	191	17	73.9	12	2	I41235	glutamine-tRNA lig
119	17	73.9	9	2	S56004	glucan 1,3-beta-gl	192	17	73.9	12	2	JS0424	urotensin II-B pep
120	17	73.9	9	2	A43848	cell surface adhes	193	17	73.9	12	2	I77529	estrogen receptor
121	17	73.9	9	2	A60522	sperm-activating p	194	17	73.9	12	2	PN0046	ATP synthase D cha
122	17	73.9	10	2	S71868	glutathione transf	195	17	73.9	12	2	I58273	thyroglobulin - ra
123	17	73.9	10	2	JC1367	thyloliberin poten	196	17	73.9	13	1	XAVI9B	angiotensin-conver
124	17	73.9	10	2	A60647	neuromedin C - bov	197	17	73.9	13	1	MTCMAD	melanotropin alpha
125	17	73.9	10	2	PQ0177	neuromedin C - lau	198	17	73.9	13	1	MTHEAD	melanotropin alpha
126	17	73.9	10	2	A61337	caerulein - frog (199	17	73.9	13	2	PQ0445	urotensin II - lau
127	17	73.9	10	2	A13687	caerulein-like pep	200	17	73.9	13	2	PH1676	Ig heavy chain V r
128	17	73.9	10	2	S58625	beta-galactosidase	201	17	73.9	13	2	B28810	glutathione transf
129	17	73.9	10	2	PQ0753	beta-fructofuranos	202	17	73.9	13	2	PT0293	Ig heavy chain CRD
130	17	73.9	10	2	S63696	DNA polymerase - Y	203	17	73.9	13	2	S57567	T cell receptor V-
131	17	73.9	10	2	PT0289	Ig heavy chain CRD	204	17	73.9	13	2	PH0138	T-cell receptor be
132	17	73.9	10	2	PT0310	Ig heavy chain CRD	205	17	73.9	13	2	S61798	T-cell-specific tr
133	17	73.9	10	2	PH1344	Ig heavy chain CRD	206	17	73.9	13	2	B56864	dipeptidyl-peptida
134	17	73.9	10	2	E49033	Ig heavy chain DJ	207	17	73.9	13	2	PH1676	T-cell receptor be
135	17	73.9	10	2	F49033	T-cell receptor ga	208	17	73.9	13	2	PH0928	collecting duct wa
136	17	73.9	10	2	PH0923	T-cell receptor be	209	17	73.9	13	2	I51905	glyceraldehyde-3-p
137	17	73.9	10	2	A40753	aldehyde ferredoxi	210	17	73.9	13	2	I54984	aeg-46.5 protein -
138	17	73.9	10	2	S66248	processing enzyme,	211	17	73.9	13	2	PC2369	unidentified 85K p
139	17	73.9	10	2	F33932	Ig mu chain J regi	212	17	73.9	13	2	S60046	early nodulin 40 -
140	17	73.9	10	2	TI7054	cytochrome-c oxida	213	17	73.9	13	2	A61514	glutathione transf
141	17	73.9	10	2	TI3976	cytochrome-c oxida	214	17	73.9	13	2	A60379	factor X activator
142	17	73.9	10	2	TI7057	cytochrome-c oxida	215	17	73.9	13	2	S32551	glutathione transf
143	17	73.9	10	2	TI2303	cytochrome-c oxida	216	17	73.9	13	2	S66558	serine proteinase
144	17	73.9	10	2	TI4019	cytochrome-c oxida	217	17	73.9	13	2	A60409	bombesin-like pept
145	17	73.9	10	2	TI7060	cytochrome-c oxida	218	17	73.9	13	2	A05174	cryptophyllin-13 -
146	17	73.9	10	2	TI4043	cytochrome-c oxida	219	17	73.9	14	1	BSTD	bombesin - fire-be
147	17	73.9	10	2	TI4054	cytochrome-c oxida	220	17	73.9	14	1	LFEBWC	trp operon leader
148	17	73.9	10	2	TI2308	cytochrome-c oxida	221	17	73.9	14	1	LFEBWT	trp operon leader
149	17	73.9	10	2	TI7072	cytochrome-c oxida	222	17	73.9	14	1	LFECW	trp operon leader
150	17	73.9	10	2	TI2316	cytochrome-c oxida	223	17	73.9	14	2	A60622	somatostatin - spo
151	17	73.9	10	2	TI4212	cytochrome-c oxida	224	17	73.9	14	2	A60840	somatostatin I - E
152	17	73.9	10	2	TI2321	cytochrome-c oxida	225	17	73.9	14	2	C60414	somatostatin - sll
153	17	73.9	10	2	TI4215	cytochrome-c oxida	226	17	73.9	14	2	B60842	somatostatin I - C
154	17	73.9	10	2	TI4223	cytochrome-c oxida	227	17	73.9	14	2	S00172	somatostatin I - s
155	17	73.9	10	2	TI4219	cytochrome-c oxida	228	17	73.9	14	2	PH1677	Ig heavy chain V r
156	17	73.9	10	2	S39030	lysyl-bradykinin -	229	17	73.9	14	2	PH1705	Ig heavy chain V r
157	17	73.9	11	1	LPTWWE	probable trpEG lea	230	17	73.9	14	2	PT0077	proteochondotin c
158	17	73.9	11	2	B41664	chromogranin-B - r	231	17	73.9	14	2	E90858	trp operon leader
159	17	73.9	11	2	S35755	ribosomal protein	232	17	73.9	14	2	B85761	trp operon leader
160	17	73.9	11	2	PT0249	Ig heavy chain CRD	233	17	73.9	14	2	A35105	hypothetical prote
161	17	73.9	11	2	PT0273	Ig heavy chain CRD	234	17	73.9	14	2	S03530	Ig heavy chain J r
162	17	73.9	11	2	PH1343	Ig heavy chain DJ	235	17	73.9	14	2	PT0223	Ig heavy chain CRD
163	17	73.9	11	2	S68649	spermadhesin AQN-3	236	17	73.9	14	2	PH1348	Ig heavy chain DJ
164	17	73.9	11	2	A33571	follicultatin - bovi	237	17	73.9	14	2	PH1356	Ig heavy chain DJ
165	17	73.9	11	2	A49037	Tcr gamma V-J regi	238	17	73.9	14	2	PH1332	Ig heavy chain DJ
166	17	73.9	11	2	B49037	Tcr gamma V-J regi	239	17	73.9	14	2	S57572	Ig heavy chain DJ
167	17	73.9	11	2	C49037	Tcr gamma V-J regi	240	17	73.9	14	2	F49037	T cell receptor V-
168	17	73.9	11	2	C59151	protein-tyrosine k	241	17	73.9	14	2	B44854	L-2, 4-diaminobuty
169	17	73.9	11	2	PQ0731	unidentified 5.7/3	242	17	73.9	14	2	PT0026	calotropin DI - mu
170	17	73.9	11	2	S45698	gamma-MSH-like pro	243	17	73.9	14	2	S33801	chaperone, TCP1-re
171	17	73.9	11	2	A34662	Achathina cardio-ex	244	17	73.9	14	2	S33802	chaperone, TCP1-re
172	17	73.9	11	2	TI2264	cytochrome-c oxida	245	17	73.9	14	2	PT0029	karatasin - karata
173	17	73.9	11	2	TI2253	cytochrome-c oxida	246	17	73.9	14	2	S14336	mastoparan B - hor
174	17	73.9	11	2	TI2244	cytochrome-c oxida	247	17	73.9	14	2	A47421	leukotriene B-4 12
175	17	73.9	11	2	TI2248	cytochrome-c oxida	248	17	73.9	14	2	S39931	S-allele-associate

249	17	73.9	14	2	A44515	Trp EG leader pept	322	17	73.9	17	2	I67526	CD33 antigen homol
250	17	73.9	15	2	A26997	unspecific monooxy	323	17	73.9	17	2	A61211	anantin - Streptom
251	17	73.9	15	2	B26997	unspecific monooxy	324	17	73.9	17	2	B48943	phage antigenic de
252	17	73.9	15	2	PQ0195	Sfil-glycoprotein	325	17	73.9	17	2	E59137	protein pfd3 - gol
253	17	73.9	15	2	PQ0174	styiar glycoprotei	326	17	73.9	17	2	A29834	trp leader peptide
254	17	73.9	15	2	PQ0175	styiar glycoprotei	327	17	73.9	18	1	MTDFBC	melanotropin beta
255	17	73.9	15	2	S21202	glucan 1,4-alpha-g	328	17	73.9	18	1	MTDOB	melanotropin beta
256	17	73.9	15	2	S21240	alpha-glucosidase	329	17	73.9	18	2	S29379	sorbitol dehydroge
257	17	73.9	15	2	S21241	oligo-1,6-glucosid	330	17	73.9	18	2	S24780	protein-tyrosine k
258	17	73.9	15	2	S24159	leukocyte elastase	331	17	73.9	18	2	G02018	proteasome chain L
259	17	73.9	15	2	PQ0232	cystatin Ci-4a - m	332	17	73.9	18	2	S04229	N4-(beta-N-acetylgl
260	17	73.9	15	2	S26791	Ig heavy chain V r	333	17	73.9	18	2	D49570	plasma membrane ca
261	17	73.9	15	2	S39012	proteinase - Therm	334	17	73.9	18	2	S43834	DNA topoisomerase
262	17	73.9	15	2	S08209	hypothetical prote	335	17	73.9	18	2	PHI368	Ig heavy chain DJ
263	17	73.9	15	2	PQ0750	self-incompatibili	336	17	73.9	18	2	A32220	T-cell receptor de
264	17	73.9	15	2	B56891	gamma 2 gliadin -	337	17	73.9	18	2	S29264	ovoheemerythrin - d
265	17	73.9	15	2	A47628	Pc gamma receptor	338	17	73.9	18	2	S55501	thrombospondin pre
266	17	73.9	15	2	PHI1365	Ig heavy chain DJ	339	17	73.9	18	2	S52125	gamma2-gliadin P25
267	17	73.9	15	2	PHI1320	Ig heavy chain DJ	340	17	73.9	18	2	C56211	progesterone recep
268	17	73.9	15	2	S43956	Ig mu chain V regi	341	17	73.9	18	2	S46418	NTLI protein - cur
269	17	73.9	15	2	PHI1762	T cell receptor al	342	17	73.9	18	2	I40062	shikimate 5-dehydr
270	17	73.9	15	2	G49655	T-cell-receptor be	343	17	73.9	18	2	S21669	1H-4-oxoquinoline
271	17	73.9	15	2	PQ0073	T-cell receptor be	344	17	73.9	18	2	T03799	leader peptide trp
272	17	73.9	15	2	PHI590	Ig H chain V-D-J r	345	17	73.9	18	2	S19914	choline O-acetyltr
273	17	73.9	15	2	E49037	TcR delta chain V-	346	17	73.9	18	2	I52623	hypothetical prote
274	17	73.9	15	2	PL0109	complement factor	347	17	73.9	18	2	PT0239	Ig heavy chain CDR
275	17	73.9	15	2	S02381	probable membrane	348	17	73.9	18	2	PT0286	Ig heavy chain CDR
276	17	73.9	15	2	S33781	acetolactate synth	349	17	73.9	18	2	PHI1349	Ig heavy chain DJ
277	17	73.9	15	2	PA0099	phenotypic variati	350	17	73.9	18	2	PHI1350	Ig heavy chain DJ
278	17	73.9	15	2	FX0031	mixed lymphocyte r	351	17	73.9	18	2	S43958	Ig mu chain V regi
279	17	73.9	15	2	C84035	hypothetical prote	352	17	73.9	18	2	A40256	interleukin-7 rece
280	17	73.9	16	1	A49761	locustapyrokinin -	353	17	73.9	18	2	I35141	T-cell receptor de
281	17	73.9	16	1	MTDFBS	melanotropin beta	354	17	73.9	18	2	G49037	TcR delta chain V-
282	17	73.9	16	2	B41425	cytochrome P450 IF	355	17	73.9	18	2	A61577	24k serine protein
283	17	73.9	16	2	S03405	hydrogenase (EC 1.	356	17	73.9	18	2	S20322	gluten - wheat
284	17	73.9	16	2	A60551	leukocyte elastase	357	17	73.9	18	2	A35678	hypothetical prote
285	17	73.9	16	2	A29541	little gastrin - C	358	17	73.9	18	2	S27141	hypothetical prote
286	17	73.9	16	2	S66613	protein p12E - Fri	359	17	73.9	18	2	A24749	neuropeptide A - b
287	17	73.9	16	2	S28213	glutathione transf	360	17	73.9	19	1	EWSMAN	ancovenin - Strept
288	17	73.9	16	2	PT0237	Ig heavy chain CDR	361	17	73.9	19	2	A28702	Cytochrome P450-C-
289	17	73.9	16	2	PT0296	Ig heavy chain CDR	362	17	73.9	19	2	I49422	L-lactate dehydrog
290	17	73.9	16	2	PHI604	Ig H chain V-D-J r	363	17	73.9	19	2	S71871	glutathione transf
291	17	73.9	16	2	A48839	T-cell receptor al	364	17	73.9	19	2	I45957	protein kinase (EC
292	17	73.9	16	2	D49037	TcR delta chain V-	365	17	73.9	19	2	PC1251	tesin II - rat (f
293	17	73.9	16	2	A46236	transforming prote	366	17	73.9	19	2	S06633	H+-transporting tw
294	17	73.9	16	2	PC1299	subtilisin (EC 3.4	367	17	73.9	19	2	PHI1304	Ig heavy chain DJ
295	17	73.9	16	2	A24099	crystal protein, 2	368	17	73.9	19	2	PT0244	Ig heavy chain CDR
296	17	73.9	16	2	T44936	calmodulin kinase	369	17	73.9	19	2	PHI1307	Ig heavy chain DJ
297	17	73.9	16	2	A48630	bothrojaracin - ja	370	17	73.9	19	2	A28814	Ig kappa chain V r
298	17	73.9	16	2	I37452	protein kinase - h	371	17	73.9	19	2	I53673	amyloid protein -
299	17	73.9	16	2	S13898	alkaline phosphata	372	17	73.9	19	2	B61409	genome polyprotein
300	17	73.9	16	2	B23692	transcription fact	373	17	73.9	19	2	PX0062	beta-galactoside-b
301	17	73.9	16	2	E37290	homeotic protein G	374	17	73.9	19	2	S63489	wd-repeat protein
302	17	73.9	16	2	S05703	homeotic protein c	375	17	73.9	19	2	T50329	disinflammatory sulf
303	17	73.9	17	1	GMSH	gastrin - sheep	376	17	73.9	19	2	PHI1352	Ig heavy chain DJ
304	17	73.9	17	2	S66198	alcohol dehydrogen	377	17	73.9	19	2	PHI1315	Ig heavy chain DJ
305	17	73.9	17	2	A60071	gastrin - rhesus m	378	17	73.9	19	2	S57515	T cell receptor be
306	17	73.9	17	2	S24570	Ig heavy chain J r	379	17	73.9	19	2	S57516	T cell receptor be
307	17	73.9	17	2	S03531	Ig heavy chain J5	380	17	73.9	19	2	S03519	T-cell receptor ga
308	17	73.9	17	2	S26747	Ig heavy chain J r	381	17	73.9	19	2	PHI624	Ig H chain V-D-J r
309	17	73.9	17	2	I57941	beta 3-adrenergic	382	17	73.9	19	2	PH0793	T-cell receptor al
310	17	73.9	17	2	A41053	glutamate receptor	383	17	73.9	19	2	I49037	TcR delta chain V-
311	17	73.9	17	2	B40442	integrase homolog	384	17	73.9	19	2	B46592	lactase-phlorizin
312	17	73.9	17	2	B44923	carboxypeptidase 3	385	17	73.9	19	2	A48354	nonstructural prot
313	17	73.9	17	2	S03533	Ig heavy chain J r	386	17	73.9	19	2	I40063	shikimate 5-dehydr
314	17	73.9	17	2	PT0234	Ig heavy chain CRD	387	17	73.9	19	2	A44854	L-2,4-diaminobuty
315	17	73.9	17	2	PHI1367	Ig heavy chain DJ	388	17	73.9	19	2	S29212	protein C - oat (f
316	17	73.9	17	2	PHI1331	Ig heavy chain DJ	389	17	73.9	19	2	S19532	globin - polychaet
317	17	73.9	17	2	PHI1357	Ig heavy chain DJ	390	17	73.9	19	2	I52721	globin - polychaet
318	17	73.9	17	2	PS0384	Ig heavy chain J r	391	17	73.9	19	2	I52721	Gene hMLH1 protein
319	17	73.9	17	2	A44560	terephthalate 1,2-	392	17	73.9	19	2	S12268	Ca-2 antigen - mou
320	17	73.9	17	2	S10786	enamelin, 26K - bo	393	17	73.9	19	2	A60505	hemoglobin Ci beta
321	17	73.9	17	2	I67524	CD33 antigen homol	394	17	73.9	19	2	A58700	actagardine [valid

395	17	73.9	19	4	I54264	rhodopsin single b	468	16	69.6	9	2	S07205	litorin 2-Glu - Au
396	17	73.9	20	2	S21176	testosterone beta	469	16	69.6	9	2	S07204	litorin I - Austr
397	17	73.9	20	2	A60728	cytochrome P450 3A	470	16	69.6	9	2	S07241	xenopsin - Rohde's
398	17	73.9	20	2	B61080	5-carboxymethyl-2-	471	16	69.6	9	2	JS0302	xenopsin-related p
399	17	73.9	20	2	B37520	glutathione transf	472	16	69.6	9	2	A60320	ig heavy chain CDR
400	17	73.9	20	2	S29099	glutathione transf	473	16	69.6	9	2	PT0231	ig heavy chain CDR
401	17	73.9	20	2	S29100	glutathione transf	474	16	69.6	9	2	PT0272	ig heavy chain CDR
402	17	73.9	20	2	S71869	glutathione transf	475	16	69.6	9	2	PT0562	T-cell receptor be
403	17	73.9	20	2	S30381	glutathione transf	476	16	69.6	10	1	XASNPC	angiotensin-conver
404	17	73.9	20	2	PQ0751	self-incompatibili	477	16	69.6	10	1	XAVI6B	angiotensin-conver
405	17	73.9	20	2	PH0111	style glycoprotein	478	16	69.6	10	1	RHPGG	gonadoliberin - pi
406	17	73.9	20	2	PH0110	style glycoprotein	479	16	69.6	10	1	RHSHG	gonadoliberin - sh
407	17	73.9	20	2	PC2347	base nonspecific a	480	16	69.6	10	1	RUAQ1	gonadoliberin I -
408	17	73.9	20	2	S33787	pancreatic elastas	481	16	69.6	10	2	A35556	hypothetical prote
409	17	73.9	20	2	A56900	chymotrypsin I (EC	482	16	69.6	10	2	S23370	T-cell receptor al
410	17	73.9	20	2	B61333	chymotrypsin (8C 3	483	16	69.6	10	2	B38887	T-cell receptor ga
411	17	73.9	20	2	I49423	cytotoxic T-lympho	484	16	69.6	10	2	PH0916	T-cell receptor be
412	17	73.9	20	2	S46205	comosain (EC 3.4.2	485	16	69.6	10	2	A59272	peptide-N4-(N-acet
413	17	73.9	20	2	S46204	anaphorin (EC 3.4.22	486	16	69.6	10	2	B37196	bradykinin-potenti
414	17	73.9	20	2	C54052	phosphoribosyl-AMP	487	16	69.6	11	2	C38887	T-cell receptor ga
415	17	73.9	20	2	A37111	ribulose-bisphosph	488	16	69.6	11	2	I41946	T-cell receptor ga
416	17	73.9	20	2	C09164	chromogranin-B - r	489	16	69.6	12	1	A53709	alpha-conotoxin im
417	17	73.9	20	2	PT0248	Ig heavy chain CDR	490	16	69.6	12	2	A29169	phospholipase A2 (
418	17	73.9	20	2	S39049	cytotoxin-binding	491	16	69.6	12	2	A40763	sucrose-6-phosphat
419	17	73.9	20	2	A05313	apolipoprotein A-I	492	16	69.6	12	2	A49033	T-cell receptor de
420	17	73.9	20	2	S03335	photosystem II pho	493	16	69.6	12	2	H41946	T-cell receptor ga
421	17	73.9	20	2	PM0003	chlorophyll a/b-bi	494	16	69.6	12	2	PQ0776	NADH2 dehydrogenas
422	17	73.9	20	2	S04988	gag core shell pro	495	16	69.6	13	2	S23372	T-cell receptor al
423	17	73.9	20	2	A44773	pollen allergen I	496	16	69.6	13	2	A86126	hypothetical prote
424	17	73.9	20	2	I64036	hypothetical prote	497	16	69.6	14	1	QMVHXX	masoparan X - hor
425	17	73.9	20	2	T46626	hypothetical prote	498	16	69.6	14	1	QMWAPP	polistes mastopara
426	17	73.9	20	2	S16202	pyrroline-5-carbox	499	16	69.6	14	2	PH0801	T-cell receptor al
427	17	73.9	20	2	D25507	proteinase inhibit	500	16	69.6	14	2	PH0747	T-cell receptor be
428	17	73.9	20	2	S10876	hypothetical prote	501	16	69.6	14	2	JH0328	probursin tetracac
429	17	73.9	20	2	S58382	hypothetical prote	502	16	69.6	15	2	T46625	hypothetical prote
430	17	73.9	20	2	PH1358	Ig heavy chain DJ	503	16	69.6	15	2	PH1342	Ig heavy chain DJ
431	17	73.9	20	2	PH1341	Ig heavy chain DJ	504	16	69.6	15	2	A45103	7 alpha-hydroxy-4-
432	17	73.9	20	2	PH1326	Ig heavy chain DJ	505	16	69.6	15	2	PH0216	agarase (EC 3.2.1.
433	17	73.9	20	2	PC2248	lambda I12 protein	506	16	69.6	16	2	PH0748	T-cell receptor be
434	17	73.9	20	2	S60350	kallikrein, pankre	507	16	69.6	16	2	A20190	hypodermin B - ear
435	17	73.9	20	2	S15861	estrogen receptor	508	16	69.6	17	2	B44873	caldesmon - rabbit
436	17	73.9	20	2	A38689	1-phosphatidylinos	509	16	69.6	17	2	S18534	hypothetical prote
437	17	73.9	20	2	PQ0071	T-cell receptor be	510	16	69.6	17	2	PC1318	large granule L6 c
438	17	73.9	20	2	S56756	link protein - rat	511	16	69.6	17	2	I53392	CD33 antigen homol
439	17	73.9	20	2	S66222	defensin AMP2 - Da	512	16	69.6	18	2	JU0124	polyphemusin I - A
440	17	73.9	20	2	T44453	acetyl-CoA synthet	513	16	69.6	18	2	JU0125	polyphemusin II -
441	17	73.9	20	2	A44927	major outer membra	514	16	69.6	19	2	S02269	glycogen(starch) s
442	17	73.9	20	2	S45637	oxidoreductase - P	515	16	69.6	19	2	B56613	virion morphogenes
443	17	73.9	20	2	S63490	disimilatory sulf	516	16	69.6	19	2	PH1330	Ig heavy chain DJ
444	17	73.9	20	2	S29636	jacalin beta-1 cha	517	16	69.6	20	2	PL0192	Ig lambda 2 chain
445	17	73.9	20	2	S29635	jacalin beta chain	518	16	69.6	20	2	D84716	hypothetical prote
446	17	73.9	20	2	S03987	agglutinin beta-2	519	16	69.6	20	2	A85659	hypothetical prote
447	17	73.9	20	2	S35460	alliin lyase (EC 4	520	15	65.2	5	2	A32516	cholecystokinin-5
448	17	73.9	20	2	PC2084	serine proteinase	521	15	65.2	5	2	JH0253	gut pentapeptide -
449	17	73.9	20	2	S38763	S-adenosyl-L-methi	522	15	65.2	5	2	PT0281	Ig heavy chain CDR
450	17	73.9	20	2	A34817	collagenolytic pro	523	15	65.2	5	2	PT0308	Ig heavy chain CDR
451	17	73.9	20	2	A56899	serum heterodimer,	524	15	65.2	5	2	PT0580	T-cell receptor be
452	17	73.9	20	2	A61506	alpha-1-antitrypsi	525	15	65.2	5	2	G37196	bradykinin-potenti
453	17	73.9	20	2	AE0120	insertion element	526	15	65.2	6	2	S66195	alcohol dehydrogen
454	17	73.9	20	2	AC0269	probable trp opero	527	15	65.2	6	2	B35640	cerebellar degener
455	17	73.9	20	2	B60505	hemoglobin A1-2 be	528	15	65.2	6	2	PT0629	T-cell receptor be
456	17	73.9	20	2	S08505	hypothetical prote	529	15	65.2	6	2	PT0519	T-cell receptor be
457	17	73.9	20	2	S27142	hypothetical prote	530	15	65.2	6	2	PT0637	T-cell receptor be
458	17	73.9	20	2	D1RT	dendinal fluid tra	531	15	65.2	6	2	PT0641	T-cell receptor be
459	16	69.6	6	2	A31263	dihydrofolate redu	532	15	65.2	6	2	PD0028	locustakinin - mig
460	16	69.6	6	2	B31263	dihydrofolate redu	533	15	65.2	6	2	A61068	pev-kinin 2 - pena
461	16	69.6	7	2	PT0642	T-cell receptor be	534	15	65.2	6	4	I79564	hypothetical TcL3
462	16	69.6	7	2	PT0586	T-cell receptor be	535	15	65.2	7	2	PH1602	Ig H chain V-D-J r
463	16	69.6	7	2	PT0728	T-cell receptor be	536	15	65.2	7	2	PT0526	T-cell receptor be
464	16	69.6	7	2	A61081	tryptophyllin, bas	537	15	65.2	7	2	PT0628	T-cell receptor be
465	16	69.6	8	2	A38887	T-cell receptor ga	538	15	65.2	7	2	PT0722	T-cell receptor be
466	16	69.6	8	2	A39308	glycine reductase	539	15	65.2	7	2	PK0008	glucuronosyltransf
467	16	69.6	8	2	A31570	angiotensin-conver	540	15	65.2	7	2	PD0029	pev-kinin 1 - pena

541	15	65.2	7	2	PN0649	pullulanase (EC 3.1.1.1)	614	14	60.9	7	2	B48394	major fat-globule
542	15	65.2	7	2	A58512	venom heptapeptide	615	14	60.9	7	2	S57274	triacylglycerol li
543	15	65.2	7	4	A58725	virotoxin - destro	616	14	60.9	7	2	S33244	neuromodulatory pe
544	15	65.2	8	2	PT0724	T-cell receptor be	617	14	60.9	7	2	S33245	neuromodulatory pe
545	15	65.2	8	2	JS0315	leucokinin V - Mad	618	14	60.9	7	2	S33246	tubulin beta-3 cha
546	15	65.2	8	2	JS0316	leucokinin VI - Ma	619	14	60.9	7	2	S33567	hypothetical pepti
547	15	65.2	8	2	JS0317	leucokinin VII - M	620	14	60.9	7	4	I55382	hypothetical pepti
548	15	65.2	8	2	JS0318	leucokinin VIII -	621	14	60.9	8	2	C61512	variant surface gl
549	15	65.2	9	1	AKLQIM	locustamyoinhibiti	622	14	60.9	8	2	D61512	variant surface gl
550	15	65.2	9	2	S78426	52.5K protein - sp	623	14	60.9	9	2	PT0270	Ig heavy chain CRD
551	15	65.2	9	2	A57444	neuropeptide Grb-A	624	14	60.9	9	2	PT0324	Ig heavy chain CRD
552	15	65.2	9	2	B57444	neuropeptide Grb-A	625	14	60.9	9	2	A37027	macrophage chemota
553	15	65.2	9	2	C57444	neuropeptide Grb-A	626	14	60.9	9	2	QDRB	delta sleep-induci
554	15	65.2	10	2	H37196	bradykinin-potent	627	14	60.9	10	2	PT0245	Ig heavy chain CRD
555	15	65.2	11	2	S66196	alcohol dehydrogen	628	14	60.9	10	2	A27617	triose-phosphate i
556	15	65.2	11	2	QJ2307	hypothetical 1.5K	629	14	60.9	10	2	A59173	nuclease Bhl (EC 3
557	15	65.2	11	2	QJ2317	hypothetical 1.5K	630	14	60.9	10	2	A59173	scyllorhizin I - s
558	15	65.2	12	2	I64829	gene HEXA protein	631	14	60.9	11	2	A24867	pyruvate synthase
559	15	65.2	12	2	A42324	cytochrome P450c27	632	14	60.9	11	2	H54346	napin small chain
560	15	65.2	12	2	A49637	MHC class II histo	633	14	60.9	11	2	S70338	conotoxin au5a - c
561	15	65.2	13	2	PH1636	Ig H chain V-D-J r	634	14	60.9	11	2	A59146	conotoxin au5b - c
562	15	65.2	13	2	PH1620	Ig H chain V-D-J r	635	14	60.9	11	2	B59146	lipovitellin - Afr
563	15	65.2	13	2	G37266	Ig heavy chain C r	636	14	60.9	12	2	S10624	z protein - guinea
564	15	65.2	13	2	D37267	Ig heavy chain C r	637	14	60.9	12	2	PH1462	T-cell receptor be
565	15	65.2	13	2	A59491	epithelial dog all	638	14	60.9	12	2	PH1457	T-cell receptor be
566	15	65.2	14	2	PC2373	probable IMP dehyd	639	14	60.9	12	2	A34858	proteinase E - bla
567	15	65.2	14	2	PC1215	homeotic protein E	640	14	60.9	12	2	A34858	kinase light chai
568	15	65.2	14	2	I54284	Cl-inhibitor - hum	641	14	60.9	12	2	E60396	antigen 7H8/2 - ma
569	15	65.2	14	2	PH1327	Ig heavy chain DJ	642	14	60.9	13	2	B25448	Ig kappa-1 chain,
570	15	65.2	14	2	S58426	spermadhesin AMN h	643	14	60.9	13	2	B25448	Ig kappa chain J r
571	15	65.2	14	2	PH1625	Ig H chain V-D-J r	644	14	60.9	13	2	A47630	Ig kappa chain J r
572	15	65.2	14	2	PH1626	Ig H chain V-D-J r	645	14	60.9	13	2	A39932	S-allele-associate
573	15	65.2	14	2	PH1627	Ig H chain V-D-J r	646	14	60.9	14	2	S68095	calcium-binding pr
574	15	65.2	14	2	PH1594	Ig H chain V-D-J r	647	14	60.9	14	2	S39930	S-allele-associate
575	15	65.2	15	2	PH1616	Ig H chain V-D-J r	648	14	60.9	14	2	E81280	probable proteolys
576	15	65.2	15	2	PH1612	Ig H chain V-D-J r	649	14	60.9	15	2	A54397	ubiquitin-carrier
577	15	65.2	15	2	PH0782	T-cell receptor al	650	14	60.9	15	2	E41383	23K variable histo
578	15	65.2	15	2	S21411	nodulation protein	651	14	60.9	15	2	S29485	GTP-binding protei
579	15	65.2	15	2	A48372	benzoyl-CoA ligase	652	14	60.9	15	2	PH1788	T cell receptor al
580	15	65.2	15	4	I38032	hypothetical Wbl/T	653	14	60.9	15	2	T09463	ribosomal protein
581	15	65.2	16	2	I57530	gene c-fms protein	654	14	60.9	15	2	PA0036	glycine cleavage s
582	15	65.2	16	2	PH1637	Ig H chain V-D-J r	655	14	60.9	15	2	A61612	allatostatin - tob
583	15	65.2	16	2	PH1638	Ig H chain V-D-J r	656	14	60.9	16	2	S51733	T-cell receptor al
584	15	65.2	16	2	S33589	beta-crystallin A4	657	14	60.9	16	2	S23184	redoxendonuclease
585	15	65.2	16	2	B4820	7K protein - Esche	658	14	60.9	16	2	PH1588	Ig H chain V-D-J r
586	15	65.2	16	4	I79565	hypothetical TGL3/	659	14	60.9	17	2	S19614	Globin - polychaet
587	15	65.2	17	2	I51910	SP-A2 - human (fra	660	14	60.9	17	2	A27636	cytoxin B - Clos
588	15	65.2	17	2	PH1630	Ig H chain V-D-J r	661	14	60.9	17	2	B31435	adherence lectin l
589	15	65.2	17	2	A46592	lactase-phlorizin	662	14	60.9	17	2	C85956	hypothetical prote
590	15	65.2	17	2	A38824	tachyplesin I - ho	663	14	60.9	18	2	PH1792	T cell receptor al
591	15	65.2	18	2	JS0125	tachyplesin III -	664	14	60.9	18	2	PH1794	T cell receptor al
592	15	65.2	18	2	S74195	epoxide hydrolase	665	14	60.9	19	2	S20289	cytochrome-c oxida
593	15	65.2	19	2	S43960	Ig mu chain V regi	666	14	60.9	19	2	A23739	cytochrome P450 MU
594	15	65.2	19	2	PH1353	Ig heavy chain DJ	667	14	60.9	20	2	A49164	chromogranin-B - r
595	15	65.2	19	2	I46654	T-cell receptor de	668	14	60.9	20	2	A31761	actin - Acanthamo
596	15	65.2	19	2	JX0124	tachyplesin I prec	669	14	60.9	20	2	A36045	thrombospondin hom
597	15	65.2	20	2	D37396	pollen allergen Fe	670	14	60.9	20	2	I70108	microsomal triglyc
598	15	65.2	20	2	S68341	prothapsin L - g	671	14	60.9	20	2	PS0087	microbial serine p
599	15	65.2	20	2	C56894	intracystalline c	672	14	60.9	20	2	SC1152	equinotoxin 1D - s
600	15	65.2	20	2	A40451	dormancy-related p	673	14	60.9	20	2	S77989	cytochrome-c oxida
601	15	65.2	20	2	A56894	intracystalline c	674	14	60.9	20	2	S77992	cytochrome-c oxida
602	15	65.2	20	2	B56894	RPCH-related neuro	675	14	60.9	20	2	A47105	dysglycan - chl
603	14	60.9	4	2	A34626	T-cell receptor be	676	14	60.9	20	2	B53283	major cat allergen
604	14	60.9	4	2	B53284	T-cell receptor be	677	14	60.9	20	2	S37196	bradykinin-potent
605	14	60.9	4	2	PT0661	neuropeptide - sea	678	13	56.5	3	3	S39766	cardioactive pepti
606	14	60.9	5	2	A60803	T-cell receptor be	679	13	56.5	9	2	S39767	cardioactive pepti
607	14	60.9	5	2	PT0729	T-cell receptor be	680	13	56.5	9	2	A26363	cardioactive pepti
608	14	60.9	6	2	B34835	dnaA protein - Pse	681	13	56.5	9	2	S27233	cardioactive pepti
609	14	60.9	6	2	PT0532	T-cell receptor be	682	13	56.5	10	2	A60410	beta-neoendorphin
610	14	60.9	6	2	PT0726	T-cell receptor be	683	13	56.5	12	2	A28856	fructose-bisphosph
611	14	60.9	7	2	PQ0727	H2 class I protein	684	13	56.5	13	2	A33208	calreticulin, hepa
612	14	60.9	7	2	I48394	glycoprotein compo	685	13	56.5	14	1	LFECFS	pheT operon leade
613	14	60.9	7	2	PT0688	T-cell receptor be	686	13	56.5	14	1	LFECFS	

687	13	56.5	14	2	F90931	pheST operon leader	760	11	47.8	18	2	B49254	TcR C gamma 1 chain
688	13	56.5	14	2	B85780	pheST operon leader	761	11	47.8	18	2	B32473	histidine-rich protein
689	13	56.5	14	2	A37789	heat shock cognate	762	11	47.8	18	2	PH1629	Ig H chain V-D-J r
690	13	56.5	14	2	AG0705	phenylalanyl-tRNA	763	11	47.8	18	2	A59396	Tha p 1 - Thaumeto
691	13	56.5	14	2	A41589	25K elastin-binding	764	11	47.8	19	2	PH1609	Ig H chain V-D-J r
692	13	56.5	14	2	AF0296	phenylalanyl-tRNA	765	11	47.8	20	2	A26380	cytochrome P450 4A
693	13	56.5	15	1	LPSCF	phe operon leader	766	11	47.8	20	2	E60894	crystallin - Pacific
694	13	56.5	15	2	B32008	calreticulin, uter	767	11	47.8	20	2	D49215	urease (EC 3.5.1.5
695	13	56.5	15	2	G60977	protein 425 - Cal	768	11	47.8	20	2	S06466	T-cell receptor al
696	13	56.5	15	2	C31409	protein 425 - rat	769	11	47.8	20	2	I59073	MHC class II histo
697	13	56.5	15	2	AF0832	phe leader peptide	770	11	47.8	20	2	S02002	photosystem II pro
698	13	56.5	15	2	E91061	hypothetical prote	771	11	47.8	20	2	H49034	nuclear antigen EB
699	13	56.5	15	2	A28965	ribulose-bisphosph	772	11	47.8	20	2	A61093	gluc protein - Cal
700	13	56.5	15	2	I48909	voltage-dependent	773	11	47.8	20	2	A85645	Amino terminal of
701	13	56.5	15	4	IS2698	hypothetical THR1	774	11	47.8	20	2	S43676	ubeninex (Beastatin
702	13	56.5	16	2	F44908	chitinase (EC 3.2.	775	11	47.8	20	2	A37988	acid proteinase he
703	13	56.5	16	2	I40065	shikimate 5-dehydr	776	11	47.8	20	2	S46479	retinoid-X-recepto
704	13	56.5	16	2	C53113	Lys-gingipain form	777	11	43.5	7	1	A61324	dermorphin - Rohde
705	13	56.5	16	2	T09741	photosystem I chai	778	10	43.5	7	2	S36662	dermorphin (Lys-7)
706	13	56.5	16	2	T14224	NADH2 dehydrogenas	779	10	43.5	8	2	PH1407	Ig heavy chain V r
707	13	56.5	18	2	S09731	photosystem I prot	780	10	43.5	8	2	PT0030	inulinase (EC 3.2.
708	13	56.5	18	2	B44995	alkanal monooxygen	781	10	43.5	8	2	S43972	tumor-associated a
709	13	56.5	18	2	S29166	quinoline oxidore	782	10	43.5	8	2	S43971	tumor-associated a
710	13	56.5	18	2	B35910	neurofibromatosis-	783	10	43.5	9	2	A28495	conopressin G - co
711	13	56.5	18	2	B41589	40K elastin-binding	784	10	43.5	9	2	D58503	translation elonga
712	13	56.5	19	2	A92058	pepsin-like protei	785	10	43.5	9	2	S63491	dissimulatory sulf
713	13	56.5	19	2	S13046	calreticulin - rab	786	10	43.5	9	2	A42266	peptidylglycine mo
714	13	56.5	19	2	S59486	cell wall protein,	787	10	43.5	9	2	S39040	lysine-conopressin
715	13	56.5	19	2	A61144	probable flagellar	788	10	43.5	9	2	PC2021	oxotocin-related p
716	13	56.5	19	2	S43045	translation elonga	789	10	43.5	9	2	S10784	emamelin i - bovin
717	13	56.5	19	2	A05305	hemoglobin beta-2	790	10	43.5	9	2	A28924	fructose-bisphosph
718	13	56.5	19	2	B60822	cytochrome P450 U	791	10	43.5	9	2	S19329	sperm-activating p
719	13	56.5	20	2	PN0115	insulin-like growt	792	10	43.5	10	2	D37397	hypothetical prote
720	13	56.5	20	2	A53875	creatine kinase (E	793	10	43.5	10	2	G58501	48K bile/gallblad
721	13	56.5	20	2	A38600	trypsin inhibitor	794	10	43.5	10	2	D46285	formaldehyde dehyd
722	13	56.5	20	2	A37984	ADP ATP carrier pr	795	10	43.5	10	2	A30823	bohrpoxotoxin - ja
723	13	56.5	20	2	A60295	apolipoprotein III	796	10	43.5	10	2	A60527	sperm-activating p
724	12	52.2	11	2	PT0250	Ig heavy chain CRD	797	10	43.5	10	2	H60787	sperm-activating p
725	12	52.2	11	2	A34428	amine oxidase (cop	798	10	43.5	10	2	G60787	sperm-activating p
726	12	52.2	19	2	S43657	hsp90 protein homo	799	10	43.5	10	2	F60787	sperm-activating p
727	12	52.2	19	2	A44239	amine oxidase (cop	800	10	43.5	10	2	E60787	sperm-activating p
728	11	47.8	9	2	PT0315	Ig heavy chain CRD	801	10	43.5	10	2	C60787	sperm-activating p
729	11	47.8	9	2	I49406	bone gla protein -	802	10	43.5	10	2	A60787	sperm-activating p
730	11	47.8	11	2	G42762	proteasome endopep	803	10	43.5	10	2	D60787	sperm-activating p
731	11	47.8	11	2	PT0301	Ig heavy chain CRD	804	10	43.5	10	2	B60787	sperm-activating p
732	11	47.8	11	2	PC2330	cycloinulooligosac	805	10	43.5	10	2	D60588	sperm-activating p
733	11	47.8	12	2	S17869	glutathione transf	806	10	43.5	10	2	B60588	sperm-activating p
734	11	47.8	12	2	S25056	Ig heavy chain - m	807	10	43.5	10	2	C60588	sperm-activating p
735	11	47.8	12	2	S25457	T-cell receptor be	808	10	43.5	10	2	I60527	sperm-activating p
736	11	47.8	12	2	S25446	T-cell receptor be	809	10	43.5	10	2	C60527	sperm-activating p
737	11	47.8	12	2	PH1461	T-cell receptor be	810	10	43.5	10	2	A60788	sperm-activating p
738	11	47.8	12	2	PH1459	T-cell receptor be	811	10	43.5	10	2	D60527	sperm-activating p
739	11	47.8	12	2	B61497	seed protein ws-17	812	10	43.5	10	2	C39572	sperm-activating p
740	11	47.8	12	2	A61503	sterol carrier pro	813	10	43.5	10	2	F60527	sperm-activating p
741	11	47.8	13	2	B26093	microbial collagen	814	10	43.5	10	2	C60527	sperm-activating p
742	11	47.8	13	2	S29488	GIP-binding protei	815	10	43.5	10	2	E60527	sperm-activating p
743	11	47.8	13	2	PT0263	Ig heavy chain CRD	816	10	43.5	10	2	G60527	sperm-activating p
744	11	47.8	13	2	G83988	hypothetical prote	817	10	43.5	10	2	E39572	sperm-activating p
745	11	47.8	13	2	A61361	bradykinin-like pe	818	10	43.5	10	2	D60788	sperm-activating p
746	11	47.8	14	2	S22336	lipoxigenase (EC 1	819	10	43.5	10	2	E60788	sperm-activating p
747	11	47.8	14	2	S21247	H+-transporting tw	820	10	43.5	10	2	C60788	sperm-activating p
748	11	47.8	14	2	S57574	T cell receptor V-	821	10	43.5	10	2	F60589	sperm-activating p
749	11	47.8	14	2	S36678	dodecenoyl-CoA Del	822	10	43.5	10	2	C60589	sperm-activating p
750	11	47.8	15	2	PH1582	Ig H chain V-D-J r	823	10	43.5	10	2	D60589	sperm-activating p
751	11	47.8	15	2	S03353	plastocyanin - Mic	824	10	43.5	10	2	I60588	sperm-activating p
752	11	47.8	15	2	I67525	CD33 antigen homol	825	10	43.5	10	2	B60589	sperm-activating p
753	11	47.8	16	2	S28433	major outer membra	826	10	43.5	11	1	GMROL	leucosulfakinin -
754	11	47.8	17	2	C37520	glutathione transf	827	10	43.5	11	2	C58501	42K bile stone pro
755	11	47.8	17	2	PH1607	Ig H chain V-D-J r	828	10	43.5	11	2	A60656	perisulfakinin - A
756	11	47.8	17	2	S33609	extensin - maize (829	10	43.5	11	2	D42965	tailin - chicken (f
757	11	47.8	17	2	A61019	17K basolateral pl	830	10	43.5	12	2	S26554	T-cell receptor be
758	11	47.8	17	2	PD0005	very-high-density	831	10	43.5	12	2	B46662	collagen alpha 2(V
759	11	47.8	18	2	B49215	urease (EC 3.5.1.5	832	10	43.5	12	2	S67528	napin - rape (frag

833	10	43.5	12	2	A09985	gamma-crystallin -	906	10	43.5	15	2	S26534	T-cell receptor al
834	10	43.5	12	2	A37933	Ig lambda chain J	907	10	43.5	15	2	S26517	T-cell receptor al
835	10	43.5	12	2	A20907	Ig kappa chain J1	908	10	43.5	15	2	S26529	T-cell receptor al
836	10	43.5	12	2	D20907	Ig kappa-1 chain J	909	10	43.5	15	2	S26528	T-cell receptor al
837	10	43.5	12	2	F20907	Ig kappa-2 chain J	910	10	43.5	15	2	I49407	placental calcium-
838	10	43.5	12	2	PH0785	T-cell receptor al	911	10	43.5	15	2	I29501	fibrinopeptide A -
839	10	43.5	12	2	PH0771	T-cell receptor be	912	10	43.5	15	2	F29501	fibrinopeptide A -
840	10	43.5	12	2	PH1454	T-cell receptor al	913	10	43.5	15	2	JP0101	fibrinogen alpha c
841	10	43.5	12	2	PH1469	T-cell receptor be	914	10	43.5	15	2	D48394	major fat-globule
842	10	43.5	12	2	PH1468	T-cell receptor be	915	10	43.5	15	2	PH0004	chlorophyll a/b-bi
843	10	43.5	13	2	S48210	collagen alpha 1(V	916	10	43.5	15	2	S21238	hydrogensulfate re
844	10	43.5	13	2	PC3492	dissimilatory sulf	917	10	43.5	15	2	PA0027	protein QA10006 -
845	10	43.5	13	2	PC2371	probable endopepti	918	10	43.5	15	2	PA0026	protein QA300027 -
846	10	43.5	13	2	PS0250	ribulose-bisphosph	919	10	43.5	15	2	S13973	chlorophyll a/b-bi
847	10	43.5	13	2	PS0325	tetrahydroberberin	920	10	43.5	15	2	PQ0192	stylar glycoprotei
848	10	43.5	13	2	S23640	Ig kappa chain J s	921	10	43.5	15	2	PQ0193	stylar glycoprotei
849	10	43.5	13	2	B20907	Ig kappa-1 chain J	922	10	43.5	15	2	PQ0194	Sz-glycoprotein -
850	10	43.5	13	2	E53275	Ig kappa-1 chain J	923	10	43.5	15	2	PA0092	protein QF200011 -
851	10	43.5	13	2	S22761	Ig lambda-2 chain	924	10	43.5	15	2	PA0097	starch phosphoryla
852	10	43.5	13	2	PH0787	T-cell receptor al	925	10	43.5	15	2	B61457	alpha-glucosidase
853	10	43.5	13	2	C47630	Ig kappa chain J r	926	10	43.5	15	2	C36198	T-cell receptor be
854	10	43.5	13	2	B47630	Ig kappa chain J r	927	10	43.5	15	2	PH1807	T-cell receptor al
855	10	43.5	13	2	D47630	Ig kappa chain J r	928	10	43.5	15	2	C24687	T-cell receptor be
856	10	43.5	13	2	E47630	Ig kappa chain J r	929	10	43.5	15	2	F28587	T-cell receptor be
857	10	43.5	13	2	S03063	Ig lambda chain J	930	10	43.5	15	2	E56978	collagen alpha 2(X
858	10	43.5	13	2	AB0764	his operon leader	931	10	43.5	15	2	PQ0074	T-cell receptor be
859	10	43.5	13	2	B19434	probable sex-speci	932	10	43.5	15	2	S53112	TSH protein beta c
860	10	43.5	13	2	S23638	Ig kappa chain J s	933	10	43.5	15	2	PN0662	dyscrophin-associa
861	10	43.5	13	2	H33932	Ig kappa chain J r	934	10	43.5	15	2	I53284	T-cell receptor be
862	10	43.5	13	2	A33933	Ig kappa chain J r	935	10	43.5	15	2	PH1619	Ig H chain V-D-J r
863	10	43.5	14	2	JH0460	corticostatic pept	936	10	43.5	15	2	PH0784	T-cell receptor al
864	10	43.5	14	2	A01250	angiotensin precur	937	10	43.5	15	2	PH0764	T-cell receptor be
865	10	43.5	14	2	S19803	ubiquitin - potato	938	10	43.5	15	2	C44101	calmodulin, vasoac
866	10	43.5	14	2	S50900	chlorophyll a/b-bi	939	10	43.5	15	2	PH1435	T-cell receptor al
867	10	43.5	14	2	S13864	methyl coenzyme M	940	10	43.5	15	2	PH1452	T-cell receptor al
868	10	43.5	14	2	S17766	beta-glucosidase (941	10	43.5	15	2	PH1449	T-cell receptor al
869	10	43.5	14	2	PS0278	ribulose-bisphosph	942	10	43.5	15	2	PH1436	T-cell receptor al
870	10	43.5	14	2	S23376	collagen alpha cha	943	10	43.5	15	2	PH1443	T-cell receptor al
871	10	43.5	14	2	S38307	DEB-A protein - fr	944	10	43.5	15	2	PH1441	T-cell receptor al
872	10	43.5	14	2	I64815	carbonic anhydrase	945	10	43.5	15	2	A35389	T-cell receptor al
873	10	43.5	14	2	PH1347	Ig heavy chain DJ	946	10	43.5	15	2	A35389	urease (EC 3.5.1.5
874	10	43.5	14	2	S23639	Ig kappa chain J s	947	10	43.5	15	2	PA0110	translation elonga
875	10	43.5	14	2	B28018	very late antigen-	948	10	43.5	15	2	E56819	PS I complex subun
876	10	43.5	14	2	C48394	major fat-globule	949	10	43.5	15	2	PA0063	hypothetical prote
877	10	43.5	14	2	A17150	glucose 1-dehydrog	950	10	43.5	15	2	PA0005	hemoglobin (N-term
878	10	43.5	14	2	PH1450	T-cell receptor al	951	10	43.5	15	2	S54712	ubiquitin - fungus
879	10	43.5	14	2	PH1450	T-cell receptor al	952	10	43.5	15	2	PA0093	ennitatin synthetas
880	10	43.5	14	2	S29632	xylan 1,4-beta-xy	953	10	43.5	16	1	LFEC	leucin Al - Psopho
881	10	43.5	14	2	I39753	nitrogenase (EC 1.	954	10	43.5	16	2	A45133	zein Zp22/6 protei
882	10	43.5	14	2	S07768	soluble hydrogenas	955	10	43.5	15	2	G24417	interphotoreceptor
883	10	43.5	14	2	S58862	botulinum neurotox	956	10	43.5	15	2	A28497	neurotensin-relate
884	10	43.5	14	2	S58866	botulinum neurotox	957	10	43.5	15	2	JT0610	leukocyte chemoatt
885	10	43.5	14	2	PQ0058	glycerol kinase (E	958	10	43.5	16	1	C45133	his operon leader
886	10	43.5	14	2	PQ0152	l8K iron-sulfur pr	959	10	43.5	16	2	S10807	casein kinase II (
887	10	43.5	14	2	PA0007	lectin B1 - Psopho	960	10	43.5	16	2	A44413	protein kinase C i
888	10	43.5	14	2	PS0249	porin - rice (etra	961	10	43.5	16	2	A59045	alpha-conotoxin Au
889	10	43.5	14	2	A56632	neoseulfakinin-II -	962	10	43.5	16	2	A59045	alpha-conotoxin Au
890	10	43.5	14	2	I56493	endothelial growth	963	10	43.5	16	2	A44101	calmodulin, vasoac
891	10	43.5	14	2	PC4376	telomeric and tetr	964	10	43.5	16	2	A29501	fibrinopeptide A -
892	10	43.5	14	2	S27140	hypothetical prote	965	10	43.5	16	2	B24180	fibrinogen alpha c
893	10	43.5	14	2	A32654	fibrinopeptide A -	966	10	43.5	16	2	A24180	fibrinogen alpha c
894	10	43.5	15	2	A60834	angiotensin I prec	967	10	43.5	16	2	B28854	fibrinopeptide A -
895	10	43.5	15	2	B59045	alpha-conotoxin Au	968	10	43.5	16	2	C28854	fibrinopeptide A -
896	10	43.5	15	2	S26524	T-cell receptor al	969	10	43.5	16	2	A28587	T-cell receptor al
897	10	43.5	15	2	S26527	T-cell receptor al	970	10	43.5	16	2	H29501	T-cell receptor be
898	10	43.5	15	2	S26532	T-cell receptor al	971	10	43.5	16	2	H29501	T-cell receptor be
899	10	43.5	15	2	S26535	T-cell receptor al	972	10	43.5	16	2	S01669	rRNA N-glycosidase
900	10	43.5	15	2	S26515	T-cell receptor al	973	10	43.5	16	2	F41299	T-cell receptor al
901	10	43.5	15	2	S26523	T-cell receptor al	974	10	43.5	16	2	H41299	T-cell receptor be
902	10	43.5	15	2	S26525	T-cell receptor al	975	10	43.5	16	2	C49048	T-cell receptor be
903	10	43.5	15	2	S26531	T-cell receptor al	976	10	43.5	16	2	G24687	T-cell receptor be
904	10	43.5	15	2	S26518	T-cell receptor al	977	10	43.5	16	2	A28587	T-cell receptor be
905	10	43.5	15	2	S26516	T-cell receptor al	978	10	43.5	16	2		

979 10 43.5 16 2 B28587 T-cell receptor be
 980 10 43.5 16 2 C28587 T-cell receptor be
 981 10 43.5 16 2 FS3284 T-cell receptor be
 982 10 43.5 16 2 G53284 T-cell receptor be
 983 10 43.5 16 2 B60566 cytochrome P450m51
 984 10 43.5 16 2 PH1580 Ig H chain V-D-J r
 985 10 43.5 16 2 A61530 triose-phosphate i
 986 10 43.5 16 2 PH1453 T-cell receptor al
 987 10 43.5 16 2 C90981 his operon leader
 988 10 43.5 16 2 S16376 L-serine dehydrata
 989 10 43.5 16 2 S42237 hypothetical prote
 990 10 43.5 16 2 B44896 heat shock protein
 991 10 43.5 16 2 S03732 photosystem I prot
 992 10 43.5 16 2 AS9155 multicystatin - co
 993 10 43.5 16 2 F54226 light-harvesting p
 994 10 43.5 16 2 A85827 his operon leader
 995 10 43.5 16 2 A61268 cytochrome P450-ch
 996 10 43.5 16 2 A36889 leu operon leader
 997 10 43.5 17 2 B49404 T-cell receptor be
 998 10 43.5 17 2 E23501 fibrinopeptide A -
 999 10 43.5 17 2 S05917 chorion class A pr
 1000 10 43.5 17 2 S05923 chorion class A pr

ALIGNMENTS

RESULT 1
 I46023
 C:Species: Bos primigenius taurus (catle)
 C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I46023
 R:Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
 M1. Cell. Endocrinol. 72, 187-200, 1990
 A:Title: Cloning and in vivo expression of bovine growth hormone receptor mRNA.
 A:Reference number: I46023; MUID:91146804; PMID:2289631
 A:Accession: I46023
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <HAU>
 A:Cross-references: UNIPROT:Q28121; EMBL:U24113; NID:g775221; PIDN:AAA91014.1; PID:g775221
 C:Genetics:
 A:Gene: GHR

Query Match 100.0%; Score 23; DB 2; Length 9;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
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 DB 1 FQFPWFVI 8

RESULT 2
 C39191
 C:Species: Bacteroides fragilis - Bacteroides fragilis
 C>Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
 C:Accession: C39191
 R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.
 J. Bacteriol. 173, 176-183, 1991
 A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
 A:Reference number: A39191; MUID:91100280; PMID:1846135
 A:Accession: C39191
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-10 <SPE>
 A:Cross-references: GB:M37699

Query Match 100.0%; Score 23; DB 2; Length 10;
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 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
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 DB 3 FSRPWTSI 10

RESULT 3
 T17063
 C:Species: cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragment)
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T17063
 R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
 J. Mol. Evol. 44, 660-674, 1997
 A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen
 A:Reference number: Z18674; MUID:97315309; PMID:9169559
 A:Accession: T17063
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <MAC>
 A:Cross-references: UNIPROT:Q79897; EMBL:U82683; NID:g3603124; PID:g3603127; PIDN:AAC622
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: COI
 C:Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 1e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
 |::|::|
 DB 2 FISRWLFS 9

RESULT 4
 T12325
 C:Species: cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fragme
 C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T12325
 R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
 Mol. Phylogenet. Evol. 10, 367-376, 1998
 A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi
 A:Reference number: Z17488; MUID:99162288; PMID:10051389
 A:Accession: T12325
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 <SCH>
 A:Cross-references: UNIPROT:Q9ZYT2; EMBL:AF049864; NID:g4105754; PID:g4105757; PIDN:AA0
 C:Genetics:
 A:Genome: mitochondrion
 A>Note: COI
 C:Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 1e+03;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
 |::|::|
 DB 2 FITRWLFS 9

RESULT 5
 T17066
 C:Species: cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T17066
 R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
 J. Mol. Evol. 44, 660-674, 1997
 A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen

A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: T17066
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: UNIPROT:O79903; EMBL:U82685; NID:g3603136; PID:g3603139; PIDN:AAC622
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 2 FFINRWFFS 9

RESULT 6

T17069
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglassii mitochondrion (fragment)
C;Species: mitochondrion Phrynosoma douglassii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17069
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: T17069
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>

A;Cross-references: UNIPROT:O79906; EMBL:U82686; NID:g3603144; PID:g3603147; PIDN:AAC622
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 2 FFINRWFFS 9

RESULT 7

T12329
cytochrome-c oxidase (EC 1.9.3.1) chain I - Stenocercus crassicaudatus mitochondrion (fragment)
C;Species: mitochondrion Stenocercus crassicaudatus
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12329
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998

A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example using
A;Reference number: Z17488; MUID:99162288; PMID:10051389

A;Accession: T12329
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>

A;Cross-references: UNIPROT:Q9ZYS6; EMBL:AF049866; NID:g4105762; PID:g4105765; PIDN:AAD0
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 25.0%; Pred. No. 1e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 2 FFINRWLFS 9

RESULT 8

PC4391
cysteine proteinase (EC 3.4.22.-) B - Freesia refracta ssp. 'Golden leader' (fragment)
C;Species: Freesia refracta ssp. 'Golden leader'
C;Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 09-Jul-2004
C;Accession: PC4391
R;Kameda, M.; Yonezawa, H.; Uchikoba, T.
Biosci. Biotechnol. Biochem. 61, 1554-1559, 1997

A;Title: Purification and characterization of a cysteine protease from corms of freesia
A;Reference number: PC4391; MUID:97480942; PMID:9339558
A;Accession: PC4391
A;Molecule type: protein
A;Residues: 1-13 <KAN>

A;Cross-references: UNIPROT:Q7M1F5
A;Experimental source: corms
C;Comment: This enzyme plays many proteolytic functions in intracellular and extracellular
C;Keywords: cysteine proteinase; hydrolase

Query Match 100.0%; Score 23; DB 2; Length 13;
Best Local Similarity 25.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 4 FFDDWRSG 11

RESULT 9

A34704
protein-tyrosine kinase (EC 2.7.1.12) 1, neuron-specific - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34704
R;Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990

A;Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
A;Reference number: A34704; MUID:90220588; PMID:1691439
A;Accession: A34704
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-17 <PYP>

A;Cross-references: UNIPROT:Q14925
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 100.0%; Score 23; DB 2; Length 17;
Best Local Similarity 25.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 10 FFERWLQR 17

RESULT 10

S32675
nitrogen fixation protein nifB - Anabaena variabilis (fragment)
C;Species: Anabaena variabilis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32675
R;Monnerjahn, U.; Boehme, H.

submitted to the EMBL Data Library, December 1992
A;Description: Cloning and expression in E. coli of the Anabaena.
A;Reference number: S32675
A;Accession: S32675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-19 <MON>

A;Cross-references: UNIPROT:Q44506; EMBL:X69898; NID:g296503; PIDN:CAA49521.1; PID:g296

```

C;Genetics:
A;Gene: nifB
C;Superfamily: Rhizobium nifB protein

Query Match      100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 25.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXXWXXX 8
   |:::|:::
Db 12 FYEQWNGK 19

RESULT 11
S77981
cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: S77981
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77981
A;Molecule type: protein
A;Residues: 1-20 <ARN>
A;Cross-references: UNIPROT:P80972
A;Experimental source: heart; liver
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Superfamily: mammalian cytochrome-c oxidase chain Va
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match      100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXXWXXX 8
   |:::|:::
Db 11 FDAQWVTV 18

RESULT 12
PN0171
peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichioides)
N;Contains: cyclophilin
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000
C;Accession: PN0171
R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Taugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PN0160
A;Accession: PN0171
A;Molecule type: protein
A;Residues: 1-20 <FUK>
A;Experimental source: strain M-1-1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match      100.0%; Score 23; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 1.8e+03;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXXWXXX 8
   |:::|:::
Db 6 FDIWEGXK 13

RESULT 13
PC1240
calcium-binding protein, 53K - spinach (fragment)

```

A;Cross-references: UNIPROT:P14596
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status predicted
F;1/Modified site: pyrrolidone carboxylic acid (Thr) #status predicted
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 95.7%; Score 22; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXX 7
|:::|:::
DB 4 FSPGWT 10

RESULT 16
S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C;Species: Gromphadorina portentosa
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S08997
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:P10939
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Thr) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXX 7
|:::|:::
DB 4 FSPGWT 10

RESULT 17
A60421
hypertrehalosemic hormone - German cockroach
N;Alternate names: Bld-HrTH
C;Species: Blattella germanica (German cockroach)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60421; S09137
R;Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica
A;Reference number: A60421; MUID:91179584; PMID:2080017
A;Accession: A60421
A;Molecule type: protein
A;Residues: 1-10 <VEE>
A;Cross-references: UNIPROT:P10939
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09137
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Thr) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;

Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXX 7
|:::|:::
DB 4 FSPGWT 10

RESULT 18
S08998
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S08998
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:P10939
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Thr) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXX 7
|:::|:::
DB 4 FSPGWT 10

RESULT 19
A26381
hypertrehalosemic hormone - gray cockroach
C;Species: Nauphoeta cinerea (gray cockroach)
C;Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: A26381
R;Gaede, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A;Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardiaca of Nauphoeta cinerea
A;Reference number: A26381; MUID:87100208; PMID:3801028
A;Accession: A26381
A;Molecule type: protein
A;Residues: 1-10 <GAD>
A;Cross-references: UNIPROT:P10939
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have used the sequence of the mature peptide
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Thr) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXX 7
|:::|:::
DB 4 FSPGWT 10

RESULT 20
JC1416
hypertrehalosemic hormone I - stick insect (Carausius morosus)
N;Alternate names: neuropeptide Cam-HrTH-I
N;Contains: hypertrehalosemic factor II
C;Species: Carausius morosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JCI416; S07157
 R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
 Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
 A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect
 A:Reference number: JCI416; MUID:93129188; PMID:1482345
 A:Accession: JCI416
 A:Molecule type: protein
 A:Residues: 1-10 <GAE1>
 A:Cross-references: UNIPROT:P11385
 R:Gaede, G.; Rinehart Jr., K.L.
 Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
 A:Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacaum
 A:Reference number: S07157; MUID:87157103; PMID:3828078
 A:Accession: S07157
 A:Molecule type: protein
 A:Residues: 'Z', 2-10 <GAE2>
 C:Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
 C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplaneta
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Binding site: carbohydrate (Trp) (covalent) #status experimental
 F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXX 7
 |::|::|
 Db 4 FTFNWGT 10

RESULT 21
 S09138
 hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
 N:Alternate names: Cam-HrTH-II
 C:Species: Extatosoma tiaratum
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C:Accession: S09138
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A:Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S09138
 A:Molecule type: protein
 A:Residues: 1-10 <GAE>
 A:Cross-references: UNIPROT:P11385
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXX 7
 |::|::|
 Db 4 FTFNWGT 10

RESULT 22
 A31571
 hypertrehalosemic/adipokinetic hormone - bollworm
 N:Alternate names: Hez-HrTH
 C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C:Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: A31571
 R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
 Biochem. Biophys. Res. Commun. 155, 344-350, 1988

A:Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea w
 A:Reference number: A31571; MUID:88326324; PMID:3415690
 A:Accession: A31571
 A:Molecule type: protein
 A:Residues: 1-10 <JAF>
 A:Cross-references: UNIPROT:P16353
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 95.7%; Score 22; DB 2; Length 10;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXX 7
 |::|::|
 Db 4 FSSGWGN 10

RESULT 23
 S53789
 neuropeptide Pec-HrTH - Platypleura capensis
 C:Species: Platypleura capensis
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S53789
 R:Gaede, G.; Janssens, M.P.E.
 Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
 A:Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalo
 A:Reference number: S53789; MUID:95225985; PMID:7710694
 A:Accession: S53789
 A:Molecule type: protein
 A:Residues: 1-10 <GAE>
 A:Cross-references: UNIPROT:Q7M465
 C:Keywords: blocked amino end; blocked carboxyl end

Query Match 95.7%; Score 22; DB 2; Length 10;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXX 7
 |::|::|
 Db 4 FSPSGWN 10

RESULT 24
 A24244
 adipokinetic hormone - bollworm
 N:Alternate names: Hez-AKH
 C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C:Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: A24244
 R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio
 A:Reference number: A24244; MUID:86186794; PMID:3964263
 A:Accession: A24244
 A:Molecule type: protein
 A:Residues: 1-9 <JAF>
 A:Cross-references: UNIPROT:P08901
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 91.3%; Score 21; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWX 6
 |::|::|
 Db 4 FTSSWG 9

RESULT 25
PH1613
IG H chain V-D-J region (clone B-less 17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1613
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 91.3%; Score 21; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWX 6
|:::|
Db 10 FTWLWT 15

RESULT 26
A33995
adipokinetic hormone - black horse fly
C;Species: Tabanus stratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: A33995
A;Molecule type: protein
A;Residues: 1-8 <JAF>
A;Cross-references: UNIPROT:P14595
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|:::|
Db 4 FTPGW 8

RESULT 27
A44960
neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: A44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04548
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|:::|
Db 4 FSPNW 8

RESULT 28
B44960
neuropeptide Led-CC-II - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: B44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04549
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|:::|
Db 4 FTPNW 8

RESULT 29
A58620
adipokinetic hormone - damselfly (Ischnura senegalensis)
C;Species: Ischnura senegalensis
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C;Accession: A58620
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudegria inconspic A;Reference number: S5310; MUID:94379987; PMID:8093008
A;Accession: A58620
A;Molecule type: protein
A;Residues: 1-8 <JAN>
A;Cross-references: UNIPROT:Q7M4H6
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|:::|
Db 4 FTPGW 8

RESULT 30
S11545
adipokinetic hormone - nestling-sucking blowfly
C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S11545
R;Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990

A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrating protein (RCP) family from the shrimp, *Pandalus borealis*.
A;Reference number: S11545; MUID:90351345; PMID:2386478
A;Accession: S11545
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P61856
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|::|
Db 4 FSPDW 8

RESULT 31
S55310
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N;Alternate names: Psi-AKH
C;Species: Pseudagrion inconspicuum
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C;Accession: S55310
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: S55310
A;Molecule type: protein
A;Residues: 1-8 <JAN>
A;Cross-references: UNIPROT:Q7M4H7
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|::|
Db 4 FSPGW 8

RESULT 32
A61348
red pigment-concentrating hormone - northern shrimp
N;Alternate names: blanching hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: A61348; S07139
R;Førnlund, P.; Jøsefsson, L.
Science 177, 173-175, 1972
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A;Reference number: A61348; MUID:7228738; PMID:50411363
A;Accession: A61348
A;Molecule type: protein
A;Residues: 1-8 <FER1>
A;Cross-references: UNIPROT:P08939
R;Førnlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, *Pandalus borealis*.
A;Reference number: S07139; MUID:75054965; PMID:4433569
A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E',2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pigment-concentrating cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|::|
Db 4 FSPGW 8

RESULT 33
S10596
adipokinetic hormone - pond skimmer
C;Species: Libellula auripennis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S10596
R;Gaede, G.
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone
A;Reference number: S10596; MUID:90359055; PMID:2390213
A;Accession: S10596
A;Molecule type: protein
A;Residues: 1-8 <BIO>
A;Cross-references: UNIPROT:P25418
C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|::|
Db 4 FSPGW 8

RESULT 34
S08995
hypertrehalosemic hormone I - oriental cockroach
N;Alternate names: Pea-CAH-I
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S08995
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment mass spectrometry.
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08995
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04548
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5
|::|

Db 4 FSPNW 8

RESULT 35

S08996
hypertrihaloemic hormone II - oriental cockroach
N;Alternate names: Pea-CAH-II
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S08996

R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrihaloemic neuropeptides isolated from the corpora cardiaca and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry of a peptide
A;Reference number: S08995; PMID:90253659; PMID:2340112

A;Accession: S08996
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04549
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FSPNW 8

RESULT 36

A49823
adipokinetic hormone I - American cockroach
N;Alternate names: periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A49823

R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activity
A;Reference number: A49823; PMID:84298179; PMID:6591205

A;Accession: A49823
A;Molecule type: protein
A;Residues: 1-8 <SCA>
A;Cross-references: UNIPROT:P04548
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FSPNW 8

RESULT 37

B49823
adipokinetic hormone II - American cockroach
N;Alternate names: neuropeptide M-II; periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: B49823; A05170

R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activity

A;Reference number: A49823; PMID:84298179; PMID:6591205

A;Accession: B49823
A;Molecule type: protein
A;Residues: 1-8 <SCA>
A;Cross-references: UNIPROT:P04549
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry of a peptide
A;Reference number: A90118; PMID:85046530; PMID:6548628

A;Accession: A05170
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FSPNW 8

RESULT 38

A28004
adipokinetic hormone G - two-spotted cricket
N;Alternate names: AKH-G
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: A28004

R;Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
A;Reference number: A28004; PMID:88106553; PMID:3426616
A;Accession: A28004

A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P14086
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FSPNW 8

RESULT 39

A43976
hypertrihaloemic hormone - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A43976

R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrihaloemic neuropeptide from tenebrio molitor
A;Reference number: A43976; PMID:90341081; PMID:2381871
A;Accession: A43976

A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P25419
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 87.0%; Score 20; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5

|::|

Db 4 FSPNW 8

RESULT 40

B43976

hypertrehalosemic hormone - beetle (Zophobas rugipes)

C:Species: Zophobas rugipes

C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004

C:Accession: B43976

R:Gaede, G.; Rosinski, G.

Peptides 11, 455-459, 1990

A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be

A:Reference number: A43976; MUID:90341081; PMID:2381871

A:Accession: B43976

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Cross-references: UNIPROT:P25419

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end, corpora cardiaca; hormone; neuropeptide; pyroglutamic

F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 40.0%; Score 20; DB 2; Length 8;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXW 5

|::|

Db 4 FSPNW 8

Search completed: October 19, 2005, 15:41:33

Job time : 26.1176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:37:00 ; Search time 102.118 Seconds
(without alignments)
32.655 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416930855 residues

Total number of hits satisfying chosen parameters: 377382

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	8	US-08-424-5508-252	Sequence 252, App
2	23	100.0	8	US-08-344-824-105	Sequence 105, App
3	23	100.0	8	US-09-214-371-10	Sequence 10, Appl
4	23	100.0	8	US-09-214-371-16	Sequence 13, Appl
5	23	100.0	8	US-09-780-070-13	Sequence 83, Appl
6	23	100.0	8	US-09-908-322-83	Sequence 4, Appl
7	23	100.0	8	US-09-794-517-4	Sequence 83, Appl
8	23	100.0	8	US-09-783-931-83	Sequence 4, Appl
9	23	100.0	8	US-09-794-529-4	Sequence 4, Appl
10	23	100.0	8	US-09-794-832-4	Sequence 4, Appl
11	23	100.0	8	US-10-052-578-144	Sequence 144, App

12	23	100.0	8	US-10-053-520-144	Sequence 144, App
13	23	100.0	8	US-10-170-713A-4	Sequence 4, Appl
14	23	100.0	8	US-10-171-734-4	Sequence 4, Appl
15	23	100.0	8	US-10-053-498B-144	Sequence 144, App
16	23	100.0	8	US-10-413-160-13	Sequence 13, Appl
17	23	100.0	8	US-10-442-909-69	Sequence 69, Appl
18	23	100.0	8	US-10-149-138-4613	Sequence 4613, App
19	23	100.0	8	US-10-149-138-4614	Sequence 4614, App
20	23	100.0	8	US-10-258-147-8	Sequence 8, Appl
21	23	100.0	8	US-10-387-957-39	Sequence 39, Appl
22	23	100.0	8	US-10-258-146A-2	Sequence 2, Appl
23	23	100.0	8	US-10-328-953-11	Sequence 11, Appl
24	23	100.0	8	US-10-367-580-4	Sequence 4, Appl
25	23	100.0	8	US-10-367-580-185	Sequence 185, App
26	23	100.0	8	US-10-367-593-4	Sequence 4, Appl
27	23	100.0	8	US-10-367-593-185	Sequence 185, App
28	23	100.0	8	US-10-367-594-4	Sequence 4, Appl
29	23	100.0	8	US-10-367-594-185	Sequence 185, App
30	23	100.0	8	US-10-367-654-4	Sequence 4, Appl
31	23	100.0	8	US-10-367-654-185	Sequence 185, App
32	23	100.0	8	US-10-367-658-4	Sequence 4, Appl
33	23	100.0	8	US-10-367-658-185	Sequence 185, App
34	23	100.0	8	US-10-367-668-4	Sequence 4, Appl
35	23	100.0	8	US-10-367-668-185	Sequence 185, App
36	23	100.0	8	US-10-387-934-39	Sequence 39, Appl
37	23	100.0	8	US-10-258-144-37	Sequence 37, Appl
38	23	100.0	8	US-10-440-190-52	Sequence 52, Appl
39	23	100.0	8	US-10-440-190-89	Sequence 89, Appl
40	23	100.0	8	US-10-149-138-4613	Sequence 4613, App
41	23	100.0	8	US-10-149-138-4614	Sequence 4614, App
42	23	100.0	8	US-10-367-674-4	Sequence 4, Appl
43	23	100.0	8	US-10-367-674-185	Sequence 185, App
44	23	100.0	8	US-10-340-179-3	Sequence 3, Appl
45	23	100.0	8	US-10-387-955-39	Sequence 39, Appl
46	23	100.0	8	US-10-488-219-39	Sequence 39, Appl
47	23	100.0	8	US-10-654-601-700	Sequence 700, App
48	23	100.0	8	US-10-927-262A-10	Sequence 10, Appl
49	23	100.0	8	US-10-927-262A-16	Sequence 16, Appl
50	23	100.0	8	US-10-927-262A-54	Sequence 54, Appl
51	23	100.0	8	US-10-927-262A-57	Sequence 57, Appl
52	23	100.0	8	US-10-927-262A-58	Sequence 58, Appl
53	23	100.0	8	US-10-927-262A-60	Sequence 60, Appl
54	23	100.0	8	US-10-927-262A-61	Sequence 61, Appl
55	23	100.0	8	US-10-927-262A-62	Sequence 62, Appl
56	23	100.0	8	US-10-994-106-192	Sequence 192, App
57	23	100.0	8	US-10-776-521B-222	Sequence 222, App
58	23	100.0	8	US-10-776-521B-224	Sequence 224, App
59	23	100.0	8	US-10-776-521B-226	Sequence 226, App
60	23	100.0	8	US-10-776-521B-230	Sequence 230, App
61	23	100.0	8	US-10-776-521B-233	Sequence 233, App
62	23	100.0	8	US-10-820-067A-164	Sequence 164, App
63	23	100.0	8	US-10-820-067A-268	Sequence 268, App
64	23	100.0	8	US-10-820-067A-732	Sequence 732, App
65	23	100.0	8	US-10-820-067A-734	Sequence 734, App
66	23	100.0	8	US-10-820-067A-736	Sequence 736, App
67	23	100.0	8	US-10-820-067A-740	Sequence 740, App
68	23	100.0	8	US-10-820-067A-743	Sequence 743, App
69	23	100.0	8	US-11-051-411-475	Sequence 475, App
70	23	100.0	9	US-09-214-371-11	Sequence 11, Appl
71	23	100.0	9	US-09-214-371-15	Sequence 15, Appl
72	23	100.0	9	US-09-214-371-55	Sequence 55, Appl
73	23	100.0	9	US-09-214-371-56	Sequence 56, Appl
74	23	100.0	9	US-09-214-371-59	Sequence 59, Appl
75	23	100.0	9	US-09-862-260A-9	Sequence 9, Appl
76	23	100.0	9	US-09-862-260A-13	Sequence 13, Appl
77	23	100.0	9	US-09-771-415-16	Sequence 16, Appl
78	23	100.0	9	US-09-884-456-5	Sequence 5, Appl
79	23	100.0	9	US-09-884-456-8	Sequence 8, Appl
80	23	100.0	9	US-09-884-456-11	Sequence 11, Appl
81	23	100.0	9	US-09-884-456-14	Sequence 14, Appl
82	23	100.0	9	US-09-884-456-427	Sequence 427, App
83	23	100.0	9	US-09-884-455-5	Sequence 5, Appl
84	23	100.0	9	US-09-884-455-8	Sequence 8, Appl

85	23	100.0	9	10	US-09-884-455-11	Sequence 11, Appl	158	23	100.0	9	20	US-11-051-411-346	Sequence 346, App
86	23	100.0	9	10	US-09-884-455-14	Sequence 14, Appl	159	23	100.0	9	20	US-11-051-411-1053	Sequence 1053, Ap
87	23	100.0	9	10	US-09-793-451-336	Sequence 336, App	160	23	100.0	10	9	US-09-214-371-3	Sequence 3, Appl
88	23	100.0	9	10	US-09-793-451-652	Sequence 652, App	161	23	100.0	10	9	US-09-214-371-4	Sequence 4, Appl
89	23	100.0	9	10	US-09-870-089B-3	Sequence 3, Appl	162	23	100.0	10	9	US-09-214-371-5	Sequence 5, Appl
90	23	100.0	9	10	US-09-870-089B-7	Sequence 7, Appl	163	23	100.0	10	9	US-09-253-794-25	Sequence 25, Appl
91	23	100.0	9	10	US-09-870-089B-9	Sequence 9, Appl	164	23	100.0	10	9	US-09-881-276-11	Sequence 11, Appl
92	23	100.0	9	11	US-09-920-480B-3	Sequence 3, Appl	165	23	100.0	10	9	US-09-881-276-12	Sequence 12, Appl
93	23	100.0	9	13	US-10-114-091-11	Sequence 11, Appl	166	23	100.0	10	9	US-09-826-290-390	Sequence 390, App
94	23	100.0	9	14	US-10-062-109A-372	Sequence 372, App	167	23	100.0	10	9	US-09-826-290-453	Sequence 453, App
95	23	100.0	9	14	US-10-283-618-5	Sequence 5, Appl	168	23	100.0	10	10	US-09-809-638-187	Sequence 187, App
96	23	100.0	9	14	US-10-005-480A-372	Sequence 372, App	169	23	100.0	10	10	US-09-809-638-388	Sequence 388, App
97	23	100.0	9	14	US-10-283-722-336	Sequence 336, App	170	23	100.0	10	10	US-09-809-638-483	Sequence 483, App
98	23	100.0	9	14	US-10-283-722-552	Sequence 652, App	171	23	100.0	10	10	US-09-572-404B-788	Sequence 788, App
99	23	100.0	9	15	US-10-334-726-212	Sequence 212, App	172	23	100.0	10	10	US-09-572-404B-790	Sequence 790, App
100	23	100.0	9	15	US-10-222-463-9	Sequence 9, Appl	173	23	100.0	10	10	US-09-572-404B-1039	Sequence 1039, Ap
101	23	100.0	9	15	US-10-024-652-1316	Sequence 1316, Ap	174	23	100.0	10	10	US-09-793-451-106	Sequence 106, App
102	23	100.0	9	15	US-10-024-652-1347	Sequence 1347, Ap	175	23	100.0	10	10	US-09-793-451-106	Sequence 410, App
103	23	100.0	9	15	US-10-024-652-1468	Sequence 1468, Ap	176	23	100.0	10	13	US-10-005-646-13	Sequence 13, Appl
104	23	100.0	9	15	US-10-283-903-336	Sequence 336, App	177	23	100.0	10	13	US-10-100-952-150	Sequence 150, App
105	23	100.0	9	15	US-10-283-903-652	Sequence 652, App	178	23	100.0	10	13	US-10-100-952-151	Sequence 151, App
106	23	100.0	9	15	US-10-245-871-693	Sequence 693, App	179	23	100.0	10	13	US-10-100-952-152	Sequence 152, App
107	23	100.0	9	15	US-10-245-871-702	Sequence 702, App	180	23	100.0	10	13	US-10-100-952-153	Sequence 153, App
108	23	100.0	9	15	US-10-442-909-25	Sequence 25, Appl	181	23	100.0	10	13	US-10-100-952-154	Sequence 154, App
109	23	100.0	9	15	US-10-424-955A-40	Sequence 40, Appl	182	23	100.0	10	13	US-10-100-952-155	Sequence 155, App
110	23	100.0	9	15	US-10-424-955A-47	Sequence 47, Appl	183	23	100.0	10	13	US-10-100-952-156	Sequence 156, App
111	23	100.0	9	15	US-10-424-955A-51	Sequence 51, Appl	184	23	100.0	10	13	US-10-100-952-157	Sequence 157, App
112	23	100.0	9	15	US-10-424-955A-55	Sequence 55, Appl	185	23	100.0	10	13	US-10-100-952-158	Sequence 158, App
113	23	100.0	9	15	US-10-363-208-237	Sequence 237, App	186	23	100.0	10	13	US-10-100-952-159	Sequence 159, App
114	23	100.0	9	15	US-10-258-146A-177	Sequence 177, App	187	23	100.0	10	13	US-10-100-952-160	Sequence 160, App
115	23	100.0	9	15	US-10-258-146A-178	Sequence 178, App	188	23	100.0	10	13	US-10-100-952-161	Sequence 161, App
116	23	100.0	9	15	US-10-253-286-633	Sequence 693, App	189	23	100.0	10	13	US-10-100-952-162	Sequence 162, App
117	23	100.0	9	15	US-10-253-286-702	Sequence 702, App	190	23	100.0	10	13	US-10-100-952-163	Sequence 163, App
118	23	100.0	9	15	US-10-182-252A-217	Sequence 217, App	191	23	100.0	10	13	US-10-100-952-164	Sequence 164, App
119	23	100.0	9	15	US-10-182-252A-508	Sequence 508, App	192	23	100.0	10	13	US-10-100-952-165	Sequence 165, App
120	23	100.0	9	15	US-10-182-252A-509	Sequence 509, App	193	23	100.0	10	14	US-10-177-725-129	Sequence 129, Appl
121	23	100.0	9	15	US-10-182-252A-530	Sequence 530, App	194	23	100.0	10	14	US-10-076-047A-47	Sequence 47, Appl
122	23	100.0	9	15	US-10-182-252A-531	Sequence 531, App	195	23	100.0	10	14	US-10-200-708-234	Sequence 234, App
123	23	100.0	9	15	US-10-182-252A-532	Sequence 532, App	196	23	100.0	10	14	US-10-200-708-350	Sequence 350, App
124	23	100.0	9	15	US-10-182-252A-564	Sequence 564, App	197	23	100.0	10	14	US-10-320-231A-55	Sequence 55, Appl
125	23	100.0	9	15	US-10-182-252A-565	Sequence 565, App	198	23	100.0	10	14	US-10-283-722-106	Sequence 106, App
126	23	100.0	9	15	US-10-182-252A-566	Sequence 566, App	199	23	100.0	10	14	US-10-283-722-410	Sequence 410, App
127	23	100.0	9	15	US-10-182-252A-567	Sequence 567, App	200	23	100.0	10	15	US-10-223-507-2	Sequence 2, Appl
128	23	100.0	9	15	US-10-182-252A-583	Sequence 583, App	201	23	100.0	10	15	US-10-024-852-196	Sequence 196, App
129	23	100.0	9	15	US-10-182-252A-1183	Sequence 1183, Ap	202	23	100.0	10	15	US-10-024-852-390	Sequence 390, App
130	23	100.0	9	16	US-10-440-390-96	Sequence 51, Appl	203	23	100.0	10	15	US-10-024-652-1543	Sequence 1543, Ap
131	23	100.0	9	16	US-10-440-390-96	Sequence 96, Appl	204	23	100.0	10	15	US-10-024-652-1617	Sequence 1617, Ap
132	23	100.0	9	16	US-10-657-363-16	Sequence 16, Appl	205	23	100.0	10	15	US-10-151-469-28	Sequence 28, Appl
133	23	100.0	9	16	US-10-340-179-1	Sequence 1, Appl	206	23	100.0	10	15	US-10-283-903-106	Sequence 106, App
134	23	100.0	9	16	US-10-363-204-198	Sequence 198, App	207	23	100.0	10	15	US-10-283-903-410	Sequence 410, App
135	23	100.0	9	16	US-10-685-838-12	Sequence 12, App	208	23	100.0	10	15	US-10-117-937-233	Sequence 233, App
136	23	100.0	9	17	US-10-813-859-3	Sequence 3, Appl	209	23	100.0	10	15	US-10-393-449-129	Sequence 129, App
137	23	100.0	9	17	US-10-813-859-7	Sequence 7, Appl	210	23	100.0	10	15	US-10-442-909-66	Sequence 66, Appl
138	23	100.0	9	17	US-10-813-859-9	Sequence 9, Appl	211	23	100.0	10	15	US-10-442-909-67	Sequence 67, Appl
139	23	100.0	9	17	US-10-833-951-133	Sequence 133, App	212	23	100.0	10	15	US-10-264-309-128	Sequence 128, App
140	23	100.0	9	17	US-10-654-601-774	Sequence 774, App	213	23	100.0	10	15	US-10-284-309-407	Sequence 407, App
141	23	100.0	9	17	US-10-654-601-2028	Sequence 2028, Ap	214	23	100.0	10	15	US-10-462-452-681	Sequence 681, App
142	23	100.0	9	17	US-10-916-064-91	Sequence 91, Appl	215	23	100.0	10	15	US-10-609-217-142	Sequence 142, App
143	23	100.0	9	17	US-10-363-205-230	Sequence 230, App	216	23	100.0	10	15	US-10-632-388-142	Sequence 142, App
144	23	100.0	9	17	US-10-950-378-1	Sequence 3, Appl	217	23	100.0	10	15	US-10-651-723-142	Sequence 142, App
145	23	100.0	9	17	US-10-950-378-3	Sequence 3, Appl	218	23	100.0	10	15	US-10-645-761-142	Sequence 142, App
146	23	100.0	9	18	US-10-927-262A-11	Sequence 11, Appl	219	23	100.0	10	15	US-10-666-696-142	Sequence 142, App
147	23	100.0	9	18	US-10-927-262A-15	Sequence 15, Appl	220	23	100.0	10	15	US-10-601-953-798	Sequence 798, App
148	23	100.0	9	18	US-10-927-262A-55	Sequence 55, Appl	221	23	100.0	10	15	US-10-653-048-142	Sequence 142, App
149	23	100.0	9	18	US-10-927-262A-56	Sequence 56, Appl	222	23	100.0	10	16	US-10-363-662A-23	Sequence 23, Appl
150	23	100.0	9	18	US-10-927-262A-59	Sequence 59, Appl	223	23	100.0	10	16	US-10-322-266-682	Sequence 682, App
151	23	100.0	9	18	US-10-982-514-41	Sequence 41, Appl	224	23	100.0	10	16	US-10-468-250A-109	Sequence 109, App
152	23	100.0	9	18	US-10-982-514-48	Sequence 48, Appl	225	23	100.0	10	16	US-10-381-275-42	Sequence 42, Appl
153	23	100.0	9	18	US-10-982-514-52	Sequence 52, Appl	226	23	100.0	10	16	US-10-680-734-45	Sequence 25, Appl
154	23	100.0	9	18	US-10-982-514-56	Sequence 56, Appl	227	23	100.0	10	16	US-10-473-127-228	Sequence 228, App
155	23	100.0	9	18	US-10-149-137A-467	Sequence 467, App	228	23	100.0	10	16	US-10-771-232-15	Sequence 15, Appl
156	23	100.0	9	18	US-10-491-008A-49	Sequence 49, Appl	229	23	100.0	10	17	US-10-718-071-13	Sequence 13, Appl
157	23	100.0	9	18	US-10-924-377-25	Sequence 25, Appl	230	23	100.0	10	17	US-10-901-923-18	Sequence 18, Appl

231	23	100.0	10	17	US-10-659-207-46	Sequence 46, Appl	304	23	100.0	11	17	US-10-659-207-444	Sequence 444, Appl
232	23	100.0	10	17	US-10-654-601-396	Sequence 396, App	305	23	100.0	11	17	US-10-654-601-1108	Sequence 1108, App
233	23	100.0	10	17	US-10-654-601-907	Sequence 907, App	306	23	100.0	11	17	US-10-654-601-1626	Sequence 1626, App
234	23	100.0	10	17	US-10-654-601-1654	Sequence 1654, App	307	23	100.0	11	17	US-10-656-250-43	Sequence 43, Appl
235	23	100.0	10	17	US-10-509-307-61	Sequence 61, Appl	308	23	100.0	11	17	US-10-656-250-44	Sequence 44, Appl
236	23	100.0	10	17	US-10-873-848B-5	Sequence 5, Appl	309	23	100.0	11	17	US-10-656-250-45	Sequence 45, Appl
237	23	100.0	10	17	US-10-755-382-25	Sequence 25, Appl	310	23	100.0	11	17	US-10-656-250-46	Sequence 46, Appl
238	23	100.0	10	17	US-10-876-343A-16	Sequence 16, Appl	311	23	100.0	11	17	US-10-656-250-47	Sequence 47, Appl
239	23	100.0	10	17	US-10-867-506-55	Sequence 55, Appl	312	23	100.0	11	17	US-10-656-250-171	Sequence 171, App
240	23	100.0	10	18	US-10-645-784-142	Sequence 142, App	313	23	100.0	11	17	US-10-656-250-171	Sequence 171, App
241	23	100.0	10	18	US-10-981-738-28	Sequence 28, Appl	314	23	100.0	11	17	US-10-876-343A-14	Sequence 14, Appl
242	23	100.0	10	18	US-10-927-262A-3	Sequence 3, Appl	315	23	100.0	11	18	US-10-645-784-325	Sequence 325, App
243	23	100.0	10	18	US-10-927-262A-4	Sequence 4, Appl	316	23	100.0	11	18	US-10-800-834-504	Sequence 504, App
244	23	100.0	10	18	US-10-927-262A-5	Sequence 5, Appl	317	23	100.0	11	20	US-11-066-697-1559	Sequence 1559, App
245	23	100.0	10	18	US-10-838-135A-15	Sequence 15, Appl	318	23	100.0	12	9	US-09-214-371-6	Sequence 6, Appl
246	23	100.0	10	18	US-10-975-157-114	Sequence 114, App	319	23	100.0	12	9	US-09-214-371-7	Sequence 7, Appl
247	23	100.0	10	18	US-10-264-309-128	Sequence 128, App	320	23	100.0	12	9	US-09-214-371-17	Sequence 17, Appl
248	23	100.0	10	18	US-10-264-309-407	Sequence 407, App	321	23	100.0	12	9	US-09-214-371-18	Sequence 18, Appl
249	23	100.0	10	20	US-11-067-064-233	Sequence 233, App	322	23	100.0	12	9	US-09-214-371-19	Sequence 19, Appl
250	23	100.0	10	20	US-11-066-697-145	Sequence 145, App	323	23	100.0	12	9	US-09-214-371-20	Sequence 20, Appl
251	23	100.0	10	20	US-11-051-411-74	Sequence 74, Appl	324	23	100.0	12	9	US-09-214-371-24	Sequence 24, Appl
252	23	100.0	10	20	US-11-051-411-282	Sequence 282, App	325	23	100.0	12	9	US-09-214-371-25	Sequence 25, Appl
253	23	100.0	10	20	US-11-051-411-474	Sequence 474, App	326	23	100.0	12	9	US-09-214-371-26	Sequence 26, Appl
254	23	100.0	10	20	US-11-067-159-233	Sequence 233, App	327	23	100.0	12	9	US-09-214-371-27	Sequence 27, Appl
255	23	100.0	11	9	US-09-756-594-5	Sequence 5, Appl	328	23	100.0	12	9	US-09-214-371-31	Sequence 31, Appl
256	23	100.0	11	9	US-09-881-276-4	Sequence 4, Appl	329	23	100.0	12	9	US-09-214-371-32	Sequence 32, Appl
257	23	100.0	11	9	US-09-881-276-5	Sequence 5, Appl	330	23	100.0	12	9	US-09-214-371-63	Sequence 63, Appl
258	23	100.0	11	9	US-09-881-276-6	Sequence 6, Appl	331	23	100.0	12	9	US-09-214-371-64	Sequence 64, Appl
259	23	100.0	11	9	US-09-881-276-7	Sequence 7, Appl	332	23	100.0	12	9	US-09-881-276-2	Sequence 2, Appl
260	23	100.0	11	9	US-09-881-276-8	Sequence 8, Appl	333	23	100.0	12	9	US-09-881-276-13	Sequence 13, Appl
261	23	100.0	11	9	US-09-881-276-9	Sequence 9, Appl	334	23	100.0	12	9	US-09-881-276-14	Sequence 14, Appl
262	23	100.0	11	9	US-09-881-276-10	Sequence 10, Appl	335	23	100.0	12	9	US-09-881-276-15	Sequence 15, Appl
263	23	100.0	11	9	US-09-881-276-17	Sequence 17, Appl	336	23	100.0	12	9	US-09-881-276-16	Sequence 16, Appl
264	23	100.0	11	9	US-09-881-276-18	Sequence 18, Appl	337	23	100.0	12	9	US-09-832-723-27	Sequence 27, Appl
265	23	100.0	11	9	US-09-881-276-19	Sequence 19, Appl	338	23	100.0	12	9	US-09-832-723-27	Sequence 27, Appl
266	23	100.0	11	9	US-09-881-276-20	Sequence 20, Appl	339	23	100.0	12	9	US-09-966-871-35	Sequence 35, Appl
267	23	100.0	11	9	US-09-977-827-10	Sequence 10, Appl	340	23	100.0	12	9	US-09-971-980-72	Sequence 72, Appl
268	23	100.0	11	9	US-09-748-739A-12	Sequence 12, Appl	341	23	100.0	12	9	US-09-971-980-73	Sequence 73, Appl
269	23	100.0	11	9	US-09-966-871-24	Sequence 24, Appl	342	23	100.0	12	10	US-09-892-877-458	Sequence 458, App
270	23	100.0	11	10	US-09-840-085-31	Sequence 31, Appl	343	23	100.0	12	10	US-09-820-053A-98	Sequence 98, Appl
271	23	100.0	11	13	US-10-039-645-24	Sequence 24, Appl	344	23	100.0	12	10	US-09-948-783-465	Sequence 465, App
272	23	100.0	11	13	US-10-155-059-21	Sequence 21, Appl	345	23	100.0	12	10	US-09-954-385-391	Sequence 391, App
273	23	100.0	11	14	US-10-136-666-1	Sequence 1, Appl	346	23	100.0	12	13	US-10-039-645-35	Sequence 35, Appl
274	23	100.0	11	14	US-10-012-542-504	Sequence 504, App	347	23	100.0	12	14	US-10-092-908-22	Sequence 22, Appl
275	23	100.0	11	14	US-10-097-175-70	Sequence 70, Appl	348	23	100.0	12	14	US-10-092-908-42	Sequence 42, Appl
276	23	100.0	11	14	US-10-097-175-90	Sequence 90, Appl	349	23	100.0	12	14	US-10-139-084-35	Sequence 35, Appl
277	23	100.0	11	14	US-10-193-651-11	Sequence 11, Appl	350	23	100.0	12	14	US-10-032-918-31	Sequence 31, Appl
278	23	100.0	11	14	US-10-014-340-216	Sequence 216, App	351	23	100.0	12	14	US-10-012-363A-4	Sequence 4, Appl
279	23	100.0	11	14	US-10-115-123-504	Sequence 504, App	352	23	100.0	12	14	US-10-322-142-1	Sequence 1, Appl
280	23	100.0	11	14	US-10-139-084-24	Sequence 24, Appl	353	23	100.0	12	14	US-10-322-142-2	Sequence 2, Appl
281	23	100.0	11	14	US-10-158-847-104	Sequence 104, App	354	23	100.0	12	14	US-10-225-567A-2041	Sequence 2041, App
282	23	100.0	11	14	US-10-150-475A-3	Sequence 3, Appl	355	23	100.0	12	14	US-10-303-331-27	Sequence 27, Appl
283	23	100.0	11	14	US-10-158-825-104	Sequence 104, App	356	23	100.0	12	14	US-10-303-331-78	Sequence 78, Appl
284	23	100.0	11	14	US-10-072-419-37	Sequence 37, Appl	357	23	100.0	12	14	US-10-167-831-65	Sequence 65, Appl
285	23	100.0	11	14	US-10-272-497-5	Sequence 5, Appl	358	23	100.0	12	15	US-10-180-648-18	Sequence 18, Appl
286	23	100.0	11	14	US-10-272-497-57	Sequence 57, Appl	359	23	100.0	12	15	US-10-609-217-131	Sequence 131, App
287	23	100.0	11	15	US-10-186-229-1	Sequence 1, Appl	360	23	100.0	12	15	US-10-609-217-137	Sequence 137, App
288	23	100.0	11	15	US-10-609-217-325	Sequence 325, App	361	23	100.0	12	15	US-10-609-217-132	Sequence 132, App
289	23	100.0	11	15	US-10-398-104-238	Sequence 238, App	362	23	100.0	12	15	US-10-609-217-133	Sequence 133, App
290	23	100.0	11	15	US-10-458-860-24	Sequence 24, Appl	363	23	100.0	12	15	US-10-609-217-134	Sequence 134, App
291	23	100.0	11	15	US-10-632-388-325	Sequence 325, App	364	23	100.0	12	15	US-10-609-217-135	Sequence 135, App
292	23	100.0	11	15	US-10-651-723-325	Sequence 325, App	365	23	100.0	12	15	US-10-609-217-136	Sequence 136, App
293	23	100.0	11	15	US-10-645-761-325	Sequence 325, App	366	23	100.0	12	15	US-10-609-217-137	Sequence 137, App
294	23	100.0	11	15	US-10-666-696-325	Sequence 325, App	367	23	100.0	12	15	US-10-609-217-143	Sequence 143, App
295	23	100.0	11	15	US-10-653-048-325	Sequence 325, App	368	23	100.0	12	15	US-10-609-217-144	Sequence 144, App
296	23	100.0	11	16	US-10-704-522-3	Sequence 3, Appl	369	23	100.0	12	15	US-10-609-217-145	Sequence 145, App
297	23	100.0	11	16	US-10-158-825-104	Sequence 104, App	370	23	100.0	12	15	US-10-609-217-146	Sequence 146, App
298	23	100.0	11	16	US-10-645-215-3	Sequence 3, Appl	371	23	100.0	12	15	US-10-458-860-35	Sequence 35, Appl
299	23	100.0	11	16	US-10-742-379-14	Sequence 14, Appl	372	23	100.0	12	15	US-10-258-146A-172	Sequence 172, App
300	23	100.0	11	16	US-10-869-768-37	Sequence 37, Appl	373	23	100.0	12	15	US-10-258-146A-173	Sequence 173, App
301	23	100.0	11	16	US-10-149-835C-113	Sequence 113, App	374	23	100.0	12	15	US-10-258-146A-174	Sequence 174, App
302	23	100.0	11	17	US-10-879-994-83	Sequence 83, Appl	375	23	100.0	12	15	US-10-632-388-131	Sequence 131, App
303	23	100.0	11	17	US-10-879-994-99	Sequence 99, Appl	376	23	100.0	12	15	US-10-632-388-132	Sequence 132, App

377	23	100.0	12	15	US-10-632-388-133	Sequence 133, App	450	23	100.0	12	17	US-10-912-812-391	Sequence 391, App
378	23	100.0	12	15	US-10-632-388-134	Sequence 134, App	451	23	100.0	12	17	US-10-235-043-391	Sequence 391, App
379	23	100.0	12	15	US-10-632-388-135	Sequence 135, App	452	23	100.0	12	17	US-10-873-848B-1	Sequence 1, Appli
380	23	100.0	12	15	US-10-632-388-136	Sequence 136, App	453	23	100.0	12	17	US-10-873-848B-2	Sequence 2, Appli
381	23	100.0	12	15	US-10-632-388-137	Sequence 137, App	454	23	100.0	12	17	US-10-968-732-27	Sequence 27, Appl
382	23	100.0	12	15	US-10-632-388-143	Sequence 143, App	455	23	100.0	12	17	US-10-968-732-78	Sequence 78, Appl
383	23	100.0	12	15	US-10-632-388-144	Sequence 144, App	456	23	100.0	12	17	US-10-968-732-131	Sequence 131, App
384	23	100.0	12	15	US-10-632-388-145	Sequence 145, App	457	23	100.0	12	18	US-10-645-784-131	Sequence 131, App
385	23	100.0	12	15	US-10-632-388-146	Sequence 146, App	458	23	100.0	12	18	US-10-645-784-132	Sequence 132, App
386	23	100.0	12	15	US-10-632-388-816	Sequence 816, App	459	23	100.0	12	18	US-10-645-784-133	Sequence 133, App
387	23	100.0	12	15	US-10-651-723-131	Sequence 131, App	460	23	100.0	12	18	US-10-645-784-134	Sequence 134, App
388	23	100.0	12	15	US-10-651-723-132	Sequence 132, App	461	23	100.0	12	18	US-10-645-784-135	Sequence 135, App
389	23	100.0	12	15	US-10-651-723-133	Sequence 133, App	462	23	100.0	12	18	US-10-645-784-136	Sequence 136, App
390	23	100.0	12	15	US-10-651-723-134	Sequence 134, App	463	23	100.0	12	18	US-10-645-784-137	Sequence 137, App
391	23	100.0	12	15	US-10-651-723-135	Sequence 135, App	464	23	100.0	12	18	US-10-645-784-143	Sequence 143, App
392	23	100.0	12	15	US-10-651-723-136	Sequence 136, App	465	23	100.0	12	18	US-10-645-784-144	Sequence 144, App
393	23	100.0	12	15	US-10-651-723-137	Sequence 137, App	466	23	100.0	12	18	US-10-645-784-145	Sequence 145, App
394	23	100.0	12	15	US-10-651-723-143	Sequence 143, App	467	23	100.0	12	18	US-10-645-784-146	Sequence 146, App
395	23	100.0	12	15	US-10-651-723-144	Sequence 144, App	468	23	100.0	12	18	US-10-645-784-816	Sequence 816, App
396	23	100.0	12	15	US-10-651-723-145	Sequence 145, App	469	23	100.0	12	18	US-10-927-262A-6	Sequence 6, Appli
397	23	100.0	12	15	US-10-651-723-146	Sequence 146, App	470	23	100.0	12	18	US-10-927-262A-7	Sequence 7, Appli
398	23	100.0	12	15	US-10-651-723-816	Sequence 816, App	471	23	100.0	12	18	US-10-927-262A-17	Sequence 17, Appl
399	23	100.0	12	15	US-10-645-761-131	Sequence 131, App	472	23	100.0	12	18	US-10-927-262A-18	Sequence 18, Appl
400	23	100.0	12	15	US-10-645-761-132	Sequence 132, App	473	23	100.0	12	18	US-10-927-262A-19	Sequence 19, Appl
401	23	100.0	12	15	US-10-645-761-133	Sequence 133, App	474	23	100.0	12	18	US-10-927-262A-20	Sequence 20, Appl
402	23	100.0	12	15	US-10-645-761-134	Sequence 134, App	475	23	100.0	12	18	US-10-927-262A-24	Sequence 24, Appl
403	23	100.0	12	15	US-10-645-761-135	Sequence 135, App	476	23	100.0	12	18	US-10-927-262A-25	Sequence 25, Appl
404	23	100.0	12	15	US-10-645-761-136	Sequence 136, App	477	23	100.0	12	18	US-10-927-262A-26	Sequence 26, Appl
405	23	100.0	12	15	US-10-645-761-137	Sequence 137, App	478	23	100.0	12	18	US-10-927-262A-27	Sequence 27, Appl
406	23	100.0	12	15	US-10-645-761-143	Sequence 143, App	479	23	100.0	12	18	US-10-927-262A-31	Sequence 31, Appl
407	23	100.0	12	15	US-10-645-761-144	Sequence 144, App	480	23	100.0	12	18	US-10-927-262A-32	Sequence 32, Appl
408	23	100.0	12	15	US-10-645-761-145	Sequence 145, App	481	23	100.0	12	18	US-10-927-262A-63	Sequence 63, Appl
409	23	100.0	12	15	US-10-645-761-146	Sequence 146, App	482	23	100.0	12	18	US-10-927-262A-64	Sequence 64, Appl
410	23	100.0	12	15	US-10-645-761-816	Sequence 816, App	483	23	100.0	12	18	US-10-312-637-1	Sequence 1, Appli
411	23	100.0	12	15	US-10-666-696-131	Sequence 131, App	484	23	100.0	12	20	US-11-093-906-12	Sequence 12, Appl
412	23	100.0	12	15	US-10-666-696-132	Sequence 132, App	485	23	100.0	12	20	US-11-003-951-32	Sequence 32, Appl
413	23	100.0	12	15	US-10-666-696-133	Sequence 133, App	486	23	100.0	12	20	US-11-003-951-33	Sequence 33, Appl
414	23	100.0	12	15	US-10-666-696-134	Sequence 134, App	487	23	100.0	12	20	US-11-136-186-98	Sequence 98, Appl
415	23	100.0	12	15	US-10-666-696-135	Sequence 135, App	488	23	100.0	13	9	US-09-935-682-61	Sequence 61, Appl
416	23	100.0	12	15	US-10-666-696-136	Sequence 136, App	489	23	100.0	13	9	US-09-894-018-69	Sequence 69, Appl
417	23	100.0	12	15	US-10-666-696-137	Sequence 137, App	490	23	100.0	13	9	US-09-949-375A-18	Sequence 18, Appl
418	23	100.0	12	15	US-10-666-696-143	Sequence 143, App	491	23	100.0	13	10	US-09-785-215-19	Sequence 19, Appl
419	23	100.0	12	15	US-10-666-696-144	Sequence 144, App	492	23	100.0	13	13	US-09-852-455-68	Sequence 68, Appl
420	23	100.0	12	15	US-10-666-696-145	Sequence 145, App	493	23	100.0	13	13	US-10-155-059-9	Sequence 9, Appli
421	23	100.0	12	15	US-10-666-696-816	Sequence 816, App	494	23	100.0	13	14	US-10-092-135-24	Sequence 24, Appl
422	23	100.0	12	15	US-10-666-696-816	Sequence 816, App	495	23	100.0	13	14	US-10-094-401-227	Sequence 227, App
423	23	100.0	12	15	US-10-653-048-131	Sequence 131, App	496	23	100.0	13	14	US-10-170-645-2	Sequence 2, Appli
424	23	100.0	12	15	US-10-653-048-132	Sequence 132, App	497	23	100.0	13	14	US-10-158-847-103	Sequence 103, App
425	23	100.0	12	15	US-10-653-048-133	Sequence 133, App	498	23	100.0	13	14	US-10-158-847-105	Sequence 105, App
426	23	100.0	12	15	US-10-653-048-134	Sequence 134, App	499	23	100.0	13	14	US-10-158-847-108	Sequence 108, App
427	23	100.0	12	15	US-10-653-048-135	Sequence 135, App	500	23	100.0	13	14	US-10-158-847-109	Sequence 109, App
428	23	100.0	12	15	US-10-653-048-136	Sequence 136, App	501	23	100.0	13	14	US-10-158-847-110	Sequence 110, App
429	23	100.0	12	15	US-10-653-048-137	Sequence 137, App	502	23	100.0	13	14	US-10-133-797-17	Sequence 17, Appl
430	23	100.0	12	15	US-10-653-048-143	Sequence 143, App	503	23	100.0	13	14	US-10-133-797-28	Sequence 28, Appl
431	23	100.0	12	15	US-10-653-048-144	Sequence 144, App	504	23	100.0	13	14	US-10-253-532-28	Sequence 28, Appl
432	23	100.0	12	15	US-10-653-048-145	Sequence 145, App	505	23	100.0	13	14	US-10-253-532-29	Sequence 29, Appl
433	23	100.0	12	15	US-10-653-048-146	Sequence 146, App	506	23	100.0	13	14	US-10-253-532-30	Sequence 30, Appl
434	23	100.0	12	15	US-10-653-048-816	Sequence 816, App	507	23	100.0	13	14	US-10-158-825-103	Sequence 103, App
435	23	100.0	12	16	US-10-467-758-26	Sequence 26, Appl	508	23	100.0	13	14	US-10-158-825-105	Sequence 105, App
436	23	100.0	12	16	US-10-467-758-27	Sequence 27, Appl	509	23	100.0	13	14	US-10-158-825-108	Sequence 108, App
437	23	100.0	12	16	US-10-467-758-28	Sequence 28, Appl	510	23	100.0	13	14	US-10-158-825-109	Sequence 109, App
438	23	100.0	12	16	US-10-467-758-29	Sequence 29, Appl	511	23	100.0	13	14	US-10-158-825-110	Sequence 110, App
439	23	100.0	12	16	US-10-467-758-31	Sequence 31, Appl	512	23	100.0	13	14	US-10-116-118-36	Sequence 36, Appl
440	23	100.0	12	16	US-10-467-758-32	Sequence 32, Appl	513	23	100.0	13	14	US-10-223-809A-17	Sequence 17, Appl
441	23	100.0	12	16	US-10-467-758-33	Sequence 33, Appl	514	23	100.0	13	14	US-10-160-506-101	Sequence 101, App
442	23	100.0	12	16	US-10-467-758-35	Sequence 35, Appl	515	23	100.0	13	14	US-10-058-053A-275	Sequence 275, App
443	23	100.0	12	16	US-10-467-758-36	Sequence 36, Appl	516	23	100.0	13	14	US-10-295-074-7	Sequence 7, Appli
444	23	100.0	12	16	US-10-363-204-228	Sequence 228, App	517	23	100.0	13	14	US-10-295-074-20	Sequence 20, Appl
445	23	100.0	12	16	US-10-652-407-29	Sequence 29, App	518	23	100.0	13	14	US-10-300-694A-2	Sequence 2, Appli
446	23	100.0	12	16	US-10-685-838-11	Sequence 11, Appl	519	23	100.0	13	14	US-10-300-694A-4	Sequence 4, Appli
447	23	100.0	12	16	US-10-433-492-37	Sequence 37, Appl	520	23	100.0	13	14	US-10-300-694A-5	Sequence 5, Appli
448	23	100.0	12	16	US-10-839-525-98	Sequence 98, Appl	521	23	100.0	13	14	US-10-300-694A-18	Sequence 18, Appl
449	23	100.0	12	16	US-10-771-232-18	Sequence 18, Appl	522	23	100.0	13	15	US-10-300-694A-66	Sequence 66, Appl
												US-10-371-069-52	Sequence 52, Appl

523	23	100.0	13	15	US-10-371-645-52	Sequence 52, Appl	596	23	100.0	14	13	US-10-100-952-190	Sequence 190, App
524	23	100.0	13	15	US-10-371-260-52	Sequence 52, Appl	597	23	100.0	14	13	US-10-100-952-191	Sequence 191, App
525	23	100.0	13	15	US-10-405-877-126	Sequence 126, Appl	598	23	100.0	14	13	US-10-100-952-192	Sequence 192, App
526	23	100.0	13	15	US-10-405-877-128	Sequence 128, Appl	599	23	100.0	14	13	US-10-100-952-193	Sequence 193, App
527	23	100.0	13	15	US-10-405-877-130	Sequence 130, Appl	600	23	100.0	14	13	US-10-100-952-194	Sequence 194, App
528	23	100.0	13	15	US-10-405-877-131	Sequence 131, Appl	601	23	100.0	14	13	US-10-100-952-195	Sequence 195, App
529	23	100.0	13	15	US-10-462-262-135	Sequence 135, Appl	602	23	100.0	14	13	US-10-100-952-196	Sequence 196, App
530	23	100.0	13	15	US-10-403-104-35	Sequence 35, Appl	603	23	100.0	14	13	US-10-012-542-508	Sequence 508, App
531	23	100.0	13	15	US-10-383-592A-5	Sequence 5, Appl	604	23	100.0	14	14	US-10-115-123-508	Sequence 508, App
532	23	100.0	13	16	US-10-449-379-101	Sequence 101, Appl	605	23	100.0	14	14	US-10-094-401-230	Sequence 230, App
533	23	100.0	13	16	US-10-158-825-103	Sequence 103, Appl	606	23	100.0	14	14	US-10-158-847-115	Sequence 115, App
534	23	100.0	13	16	US-10-158-825-105	Sequence 105, Appl	607	23	100.0	14	14	US-10-158-847-116	Sequence 116, App
535	23	100.0	13	16	US-10-158-825-108	Sequence 108, Appl	608	23	100.0	14	14	US-10-158-847-119	Sequence 119, App
536	23	100.0	13	16	US-10-158-825-109	Sequence 109, Appl	609	23	100.0	14	14	US-10-098-093-45	Sequence 45, Appl
537	23	100.0	13	16	US-10-158-825-110	Sequence 110, Appl	610	23	100.0	14	14	US-10-186-867-7	Sequence 7, Appl
538	23	100.0	13	16	US-10-688-015-101	Sequence 101, Appl	611	23	100.0	14	14	US-10-150-475A-2	Sequence 2, Appl
539	23	100.0	13	16	US-10-441-779C-33	Sequence 33, Appl	612	23	100.0	14	14	US-10-225-567A-2196	Sequence 2196, App
540	23	100.0	13	16	US-10-470-957-7	Sequence 7, Appl	613	23	100.0	14	14	US-10-158-825-115	Sequence 115, App
541	23	100.0	13	16	US-10-363-954A-18	Sequence 18, Appl	614	23	100.0	14	14	US-10-158-825-116	Sequence 116, App
542	23	100.0	13	16	US-10-838-226-275	Sequence 275, Appl	615	23	100.0	14	14	US-10-158-825-119	Sequence 119, App
543	23	100.0	13	16	US-10-468-496-693	Sequence 693, Appl	616	23	100.0	14	14	US-10-303-331-28	Sequence 28, Appl
544	23	100.0	13	16	US-10-468-496-694	Sequence 694, Appl	617	23	100.0	14	14	US-10-083-768-33	Sequence 33, Appl
545	23	100.0	13	16	US-10-468-496-695	Sequence 695, Appl	618	23	100.0	14	14	US-10-083-768-213	Sequence 213, App
546	23	100.0	13	16	US-10-468-496-1718	Sequence 1718, Ap	619	23	100.0	14	14	US-10-083-259-14	Sequence 14, Appl
547	23	100.0	13	16	US-10-468-496-1719	Sequence 1719, Ap	620	23	100.0	14	14	US-10-145-206-29	Sequence 29, Appl
548	23	100.0	13	16	US-10-468-496-1720	Sequence 1720, Ap	621	23	100.0	14	14	US-10-109-274A-14	Sequence 14, Appl
549	23	100.0	13	16	US-10-468-496-1721	Sequence 1721, Ap	622	23	100.0	14	15	US-10-308-905A-23	Sequence 23, Appl
550	23	100.0	13	16	US-10-643-103-3	Sequence 3, Appl	623	23	100.0	14	15	US-10-462-262-198	Sequence 198, App
551	23	100.0	13	16	US-10-160-505-101	Sequence 101, Appl	624	23	100.0	14	15	US-10-436-715-430	Sequence 430, Appl
552	23	100.0	13	16	US-10-474-960A-69	Sequence 69, Appl	625	23	100.0	14	15	US-10-222-595-16	Sequence 16, Appl
553	23	100.0	13	16	US-10-846-911-7	Sequence 7, Appl	626	23	100.0	14	15	US-10-609-217-68	Sequence 68, Appl
554	23	100.0	13	16	US-10-846-911-20	Sequence 20, Appl	627	23	100.0	14	15	US-10-632-388-68	Sequence 68, Appl
555	23	100.0	13	16	US-10-495-146-186	Sequence 186, Appl	628	23	100.0	14	15	US-10-651-723-68	Sequence 68, Appl
556	23	100.0	13	16	US-10-495-146-187	Sequence 187, Appl	629	23	100.0	14	15	US-10-328-953-320	Sequence 320, App
557	23	100.0	13	16	US-10-495-146-188	Sequence 188, Appl	630	23	100.0	14	15	US-10-328-953-321	Sequence 321, App
558	23	100.0	13	17	US-10-884-355A-50	Sequence 50, Appl	631	23	100.0	14	15	US-10-328-953-322	Sequence 322, App
559	23	100.0	13	17	US-10-893-018-15	Sequence 15, Appl	632	23	100.0	14	15	US-10-645-761-68	Sequence 68, Appl
560	23	100.0	13	18	US-10-942-711-40	Sequence 40, Appl	633	23	100.0	14	15	US-10-240-641-22	Sequence 22, Appl
561	23	100.0	13	18	US-10-732-862A-233	Sequence 233, Appl	634	23	100.0	14	15	US-10-666-696-68	Sequence 68, Appl
562	23	100.0	13	18	US-10-783-317A-17	Sequence 17, Appl	635	23	100.0	14	15	US-10-653-048-68	Sequence 68, Appl
563	23	100.0	13	18	US-10-939-107-7	Sequence 7, Appl	636	23	100.0	14	16	US-10-704-522-2	Sequence 2, Appl
564	23	100.0	13	18	US-10-939-107-20	Sequence 20, Appl	637	23	100.0	14	16	US-10-158-825-115	Sequence 115, App
565	23	100.0	13	20	US-11-093-103-7	Sequence 7, Appl	638	23	100.0	14	16	US-10-158-825-116	Sequence 116, App
566	23	100.0	14	9	US-09-214-371-33	Sequence 33, Appl	639	23	100.0	14	16	US-10-158-825-119	Sequence 119, App
567	23	100.0	14	9	US-09-214-371-34	Sequence 34, Appl	640	23	100.0	14	16	US-10-158-825-119	Sequence 119, App
568	23	100.0	14	9	US-09-214-371-65	Sequence 65, Appl	641	23	100.0	14	16	US-10-645-715-2	Sequence 2, Appl
569	23	100.0	14	9	US-09-832-723-28	Sequence 28, Appl	642	23	100.0	14	16	US-10-661-471-23	Sequence 23, Appl
570	23	100.0	14	13	US-10-003-858-20	Sequence 20, Appl	643	23	100.0	14	16	US-10-742-179-7	Sequence 7, Appl
571	23	100.0	14	13	US-10-100-952-118	Sequence 118, Appl	644	23	100.0	14	16	US-10-742-179-8	Sequence 8, Appl
572	23	100.0	14	13	US-10-100-952-119	Sequence 119, Appl	645	23	100.0	14	16	US-10-742-179-10	Sequence 10, Appl
573	23	100.0	14	13	US-10-100-952-120	Sequence 120, Appl	646	23	100.0	14	16	US-10-742-179-26	Sequence 26, Appl
574	23	100.0	14	13	US-10-100-952-121	Sequence 121, Appl	647	23	100.0	14	16	US-10-742-179-36	Sequence 36, Appl
575	23	100.0	14	13	US-10-100-952-122	Sequence 122, Appl	648	23	100.0	14	16	US-10-387-955-49	Sequence 49, Appl
576	23	100.0	14	13	US-10-100-952-123	Sequence 123, Appl	649	23	100.0	14	16	US-10-387-955-61	Sequence 61, Appl
577	23	100.0	14	13	US-10-100-952-124	Sequence 124, Appl	650	23	100.0	14	16	US-10-712-447-158	Sequence 158, App
578	23	100.0	14	13	US-10-100-952-125	Sequence 125, Appl	651	23	100.0	14	16	US-10-712-447-159	Sequence 159, App
579	23	100.0	14	13	US-10-100-952-126	Sequence 126, Appl	652	23	100.0	14	16	US-10-712-447-160	Sequence 160, App
580	23	100.0	14	13	US-10-100-952-127	Sequence 127, Appl	653	23	100.0	14	16	US-10-712-447-194	Sequence 194, App
581	23	100.0	14	13	US-10-100-952-128	Sequence 128, Appl	654	23	100.0	14	16	US-10-712-447-195	Sequence 195, App
582	23	100.0	14	13	US-10-100-952-129	Sequence 129, Appl	655	23	100.0	14	16	US-10-712-447-196	Sequence 196, App
583	23	100.0	14	13	US-10-100-952-130	Sequence 130, Appl	656	23	100.0	14	16	US-10-712-447-204	Sequence 204, App
584	23	100.0	14	13	US-10-100-952-131	Sequence 131, Appl	657	23	100.0	14	16	US-10-865-478-745	Sequence 745, App
585	23	100.0	14	13	US-10-100-952-132	Sequence 132, Appl	658	23	100.0	14	16	US-10-865-478-746	Sequence 746, App
586	23	100.0	14	13	US-10-100-952-133	Sequence 133, Appl	659	23	100.0	14	17	US-10-808-187-1052	Sequence 1052, Ap
587	23	100.0	14	13	US-10-100-952-134	Sequence 134, Appl	660	23	100.0	14	17	US-10-659-207-87	Sequence 87, Appl
588	23	100.0	14	13	US-10-100-952-135	Sequence 135, Appl	661	23	100.0	14	17	US-10-930-313-16	Sequence 16, Appl
589	23	100.0	14	13	US-10-100-952-136	Sequence 136, Appl	662	23	100.0	14	17	US-10-968-732-28	Sequence 28, Appl
590	23	100.0	14	13	US-10-100-952-137	Sequence 137, Appl	663	23	100.0	14	18	US-10-645-784-68	Sequence 68, Appl
591	23	100.0	14	13	US-10-100-952-138	Sequence 138, Appl	664	23	100.0	14	18	US-10-927-262A-33	Sequence 33, Appl
592	23	100.0	14	13	US-10-100-952-139	Sequence 139, Appl	665	23	100.0	14	18	US-10-927-262A-34	Sequence 34, Appl
593	23	100.0	14	13	US-10-100-952-140	Sequence 140, Appl	666	23	100.0	14	18	US-10-800-834-508	Sequence 508, App
594	23	100.0	14	13	US-10-100-952-141	Sequence 141, Appl	667	23	100.0	14	18	US-10-807-807-1052	Sequence 1052, Ap
595	23	100.0	14	13	US-10-100-952-142	Sequence 142, Appl	668	23	100.0	14	18	US-10-946-647-1237	Sequence 1237, Ap
												US-10-496-905-583	Sequence 583, App

669	23	100.0	14	20	US-11-066-697-179	Sequence 179, App	742	23	100.0	15	15	US-10-403-104-21	Sequence 21, Appl
670	23	100.0	14	20	US-11-093-103-45	Sequence 45, Appl	743	23	100.0	15	15	US-10-446-628-51	Sequence 51, Appl
671	23	100.0	15	9	US-09-214-371-8	Sequence 8, Appl	744	23	100.0	15	15	US-10-609-217-138	Sequence 138, App
672	23	100.0	15	9	US-09-214-371-28	Sequence 28, Appl	745	23	100.0	15	15	US-10-609-217-139	Sequence 139, App
673	23	100.0	15	9	US-09-214-371-29	Sequence 29, App	746	23	100.0	15	15	US-10-609-217-140	Sequence 140, App
674	23	100.0	15	9	US-09-214-371-30	Sequence 30, App	747	23	100.0	15	15	US-10-609-217-141	Sequence 141, App
675	23	100.0	15	9	US-09-214-371-66	Sequence 66, Appl	748	23	100.0	15	15	US-10-425-970-4	Sequence 4, Appl
676	23	100.0	15	9	US-09-765-527-9	Sequence 9, Appl	749	23	100.0	15	15	US-10-632-388-138	Sequence 138, App
677	23	100.0	15	9	US-09-829-549A-23	Sequence 23, Appl	750	23	100.0	15	15	US-10-632-388-139	Sequence 139, App
678	23	100.0	15	9	US-09-953-510-51	Sequence 51, Appl	751	23	100.0	15	15	US-10-632-388-140	Sequence 140, App
679	23	100.0	15	9	US-09-953-510-52	Sequence 52, Appl	752	23	100.0	15	15	US-10-632-388-141	Sequence 141, App
680	23	100.0	15	9	US-09-732-384-6	Sequence 6, Appl	753	23	100.0	15	15	US-10-651-723-138	Sequence 138, App
681	23	100.0	15	10	US-09-894-594-27	Sequence 27, Appl	754	23	100.0	15	15	US-10-651-723-139	Sequence 139, App
682	23	100.0	15	10	US-09-894-594-28	Sequence 28, Appl	755	23	100.0	15	15	US-10-651-723-140	Sequence 140, App
683	23	100.0	15	10	US-09-894-594-31	Sequence 31, Appl	756	23	100.0	15	15	US-10-651-723-141	Sequence 141, App
684	23	100.0	15	10	US-09-894-594-43	Sequence 43, Appl	757	23	100.0	15	15	US-10-645-761-138	Sequence 138, App
685	23	100.0	15	10	US-09-798-869-6	Sequence 6, Appl	758	23	100.0	15	15	US-10-645-761-139	Sequence 139, App
686	23	100.0	15	10	US-09-798-869-29	Sequence 29, App	759	23	100.0	15	15	US-10-645-761-140	Sequence 140, App
687	23	100.0	15	10	US-09-798-869-30	Sequence 30, Appl	760	23	100.0	15	15	US-10-645-761-141	Sequence 141, App
688	23	100.0	15	10	US-09-316-393-10	Sequence 10, Appl	761	23	100.0	15	15	US-10-645-761-141	Sequence 141, App
689	23	100.0	15	10	US-09-798-026B-6	Sequence 6, Appl	762	23	100.0	15	15	US-10-666-696-138	Sequence 138, App
690	23	100.0	15	10	US-09-798-026B-30	Sequence 30, Appl	763	23	100.0	15	15	US-10-666-696-139	Sequence 139, App
691	23	100.0	15	10	US-09-798-026B-31	Sequence 31, Appl	764	23	100.0	15	15	US-10-666-696-140	Sequence 140, App
692	23	100.0	15	10	US-09-840-085-33	Sequence 33, Appl	765	23	100.0	15	15	US-10-666-696-141	Sequence 141, App
693	23	100.0	15	10	US-09-840-085-34	Sequence 34, Appl	766	23	100.0	15	15	US-10-653-048-138	Sequence 138, App
694	23	100.0	15	10	US-09-840-085-35	Sequence 35, Appl	766	23	100.0	15	15	US-10-653-048-139	Sequence 139, App
695	23	100.0	15	10	US-09-840-085-36	Sequence 36, Appl	767	23	100.0	15	15	US-10-653-048-140	Sequence 140, App
696	23	100.0	15	10	US-09-840-085-37	Sequence 37, Appl	768	23	100.0	15	15	US-10-653-048-141	Sequence 141, App
697	23	100.0	15	11	US-09-953-413-51	Sequence 51, Appl	770	23	100.0	15	15	US-10-432-236-16	Sequence 16, Appl
698	23	100.0	15	11	US-09-953-413-52	Sequence 52, Appl	771	23	100.0	15	15	US-10-240-403-15	Sequence 15, Appl
699	23	100.0	15	13	US-10-155-059-24	Sequence 24, Appl	772	23	100.0	15	16	US-10-695-155-51	Sequence 51, Appl
700	23	100.0	15	13	US-10-103-395-247	Sequence 247, App	773	23	100.0	15	16	US-10-695-155-52	Sequence 52, Appl
701	23	100.0	15	14	US-10-005-530-28	Sequence 28, App	774	23	100.0	15	16	US-10-695-155-110	Sequence 110, App
702	23	100.0	15	14	US-10-012-542-295	Sequence 295, App	775	23	100.0	15	16	US-10-695-155-111	Sequence 111, App
703	23	100.0	15	14	US-10-115-123-295	Sequence 295, App	776	23	100.0	15	16	US-10-495-146-24	Sequence 24, Appl
704	23	100.0	15	14	US-10-093-093-120	Sequence 120, App	777	23	100.0	15	16	US-10-495-146-25	Sequence 25, Appl
705	23	100.0	15	14	US-10-269-171A-7	Sequence 7, Appl	778	23	100.0	15	16	US-10-495-146-26	Sequence 26, Appl
706	23	100.0	15	14	US-10-120-604-219	Sequence 219, App	779	23	100.0	15	17	US-10-654-601-2142	Sequence 2142, Ap
707	23	100.0	15	14	US-10-161-097-54	Sequence 54, Appl	780	23	100.0	15	17	US-10-661-156-198	Sequence 198, App
708	23	100.0	15	14	US-10-067-649-89	Sequence 89, Appl	781	23	100.0	15	17	US-10-182-613A-6	Sequence 6, Appl
709	23	100.0	15	14	US-10-067-649-90	Sequence 90, Appl	782	23	100.0	15	17	US-10-182-613A-7	Sequence 7, Appl
710	23	100.0	15	14	US-10-186-867-28	Sequence 28, Appl	783	23	100.0	15	18	US-10-645-784-138	Sequence 138, App
711	23	100.0	15	14	US-10-186-867-29	Sequence 29, Appl	784	23	100.0	15	18	US-10-645-784-139	Sequence 139, App
712	23	100.0	15	14	US-10-133-210-251	Sequence 251, App	785	23	100.0	15	18	US-10-645-784-140	Sequence 140, App
713	23	100.0	15	14	US-10-211-088-141	Sequence 141, App	786	23	100.0	15	18	US-10-645-784-141	Sequence 141, App
714	23	100.0	15	14	US-10-091-724-48	Sequence 48, Appl	787	23	100.0	15	18	US-10-927-262A-8	Sequence 8, Appl
715	23	100.0	15	14	US-10-216-122-22	Sequence 22, Appl	788	23	100.0	15	18	US-10-927-262A-28	Sequence 28, Appl
716	23	100.0	15	14	US-10-147-255-51	Sequence 51, Appl	789	23	100.0	15	18	US-10-927-262A-29	Sequence 29, Appl
717	23	100.0	15	14	US-10-147-255-52	Sequence 52, Appl	790	23	100.0	15	18	US-10-927-262A-30	Sequence 30, Appl
718	23	100.0	15	14	US-10-354-240-88	Sequence 88, Appl	791	23	100.0	15	18	US-10-927-262A-65	Sequence 65, Appl
719	23	100.0	15	14	US-10-080-608A-165	Sequence 165, App	792	23	100.0	15	18	US-10-927-262A-66	Sequence 66, Appl
720	23	100.0	15	14	US-10-293-693-89	Sequence 89, Appl	793	23	100.0	15	18	US-10-800-834-295	Sequence 295, App
721	23	100.0	15	14	US-10-293-693-90	Sequence 90, Appl	794	23	100.0	15	18	US-10-946-647-790	Sequence 790, App
722	23	100.0	15	15	US-10-350-405-218	Sequence 218, App	795	23	100.0	15	18	US-10-946-647-957	Sequence 957, App
723	23	100.0	15	15	US-10-350-405-222	Sequence 222, App	796	23	100.0	15	18	US-10-496-905-576	Sequence 576, App
724	23	100.0	15	15	US-10-370-685-74	Sequence 74, Appl	797	23	100.0	15	18	US-10-920-244A-286	Sequence 286, App
725	23	100.0	15	15	US-10-222-433-25	Sequence 25, Appl	798	23	100.0	15	18	US-10-705-165-9	Sequence 9, Appl
726	23	100.0	15	15	US-10-024-652-2104	Sequence 2104, Ap	799	23	100.0	15	18	US-10-754-473-30	Sequence 30, Appl
727	23	100.0	15	15	US-10-024-652-2211	Sequence 2211, Ap	800	23	100.0	15	20	US-11-070-456-219	Sequence 219, App
728	23	100.0	15	15	US-10-024-652-2251	Sequence 2251, Ap	801	23	100.0	15	20	US-11-011-422-76	Sequence 76, Appl
729	23	100.0	15	15	US-10-024-652-2294	Sequence 2294, Ap	802	23	100.0	15	20	US-11-051-411-1069	Sequence 1069, Ap
730	23	100.0	15	15	US-10-024-652-2340	Sequence 2340, Ap	803	23	100.0	16	9	US-09-214-371-39	Sequence 39, Appl
731	23	100.0	15	15	US-10-024-652-2383	Sequence 2383, Ap	804	23	100.0	16	9	US-09-214-371-40	Sequence 40, Appl
732	23	100.0	15	15	US-10-024-652-2422	Sequence 2422, Ap	805	23	100.0	16	9	US-09-214-371-41	Sequence 41, Appl
733	23	100.0	15	15	US-10-024-652-2472	Sequence 2472, Ap	806	23	100.0	16	9	US-09-962-805-13	Sequence 13, Appl
734	23	100.0	15	15	US-10-024-652-2543	Sequence 2543, Ap	807	23	100.0	16	9	US-09-920-552-109	Sequence 109, App
735	23	100.0	15	15	US-10-346-162-158	Sequence 158, App	808	23	100.0	16	9	US-09-736-973-587	Sequence 587, App
736	23	100.0	15	15	US-10-346-162-206	Sequence 206, App	809	23	100.0	16	9	US-09-894-018-159	Sequence 159, App
737	23	100.0	15	15	US-10-346-162-219	Sequence 219, App	810	23	100.0	16	9	US-09-854-133-587	Sequence 587, App
738	23	100.0	15	15	US-10-442-909-41	Sequence 41, Appl	811	23	100.0	16	10	US-09-825-517A-4	Sequence 4, Appl
739	23	100.0	15	15	US-10-431-048-48	Sequence 48, Appl	812	23	100.0	16	10	US-09-825-517A-20	Sequence 20, Appl
740	23	100.0	15	15	US-10-442-456-1	Sequence 1, Appl	813	23	100.0	16	10	US-09-825-517A-35	Sequence 35, Appl
741	23	100.0	15	15	US-10-436-715-393	Sequence 393, App	814	23	100.0	16	10	US-09-825-517A-37	Sequence 37, Appl

815	23	100.0	16	10	US-09-825-517A-38	Sequence 38, Appl	888	23	100.0	16	14	US-10-193-795-11	Sequence 11, Appl
816	23	100.0	16	10	US-09-825-517A-39	Sequence 39, Appl	889	23	100.0	16	14	US-10-219-834-102	Sequence 102, Appl
817	23	100.0	16	10	US-09-825-517A-40	Sequence 40, Appl	890	23	100.0	16	14	US-10-251-385-285	Sequence 285, Appl
818	23	100.0	16	10	US-09-825-517A-41	Sequence 41, Appl	891	23	100.0	16	14	US-10-062-831-88	Sequence 88, Appl
819	23	100.0	16	10	US-09-825-517A-42	Sequence 42, Appl	892	23	100.0	16	14	US-10-225-567A-942	Sequence 942, Appl
820	23	100.0	16	10	US-09-825-517A-43	Sequence 43, Appl	893	23	100.0	16	14	US-10-225-567A-1078	Sequence 1078, Appl
821	23	100.0	16	10	US-09-825-517A-44	Sequence 44, Appl	894	23	100.0	16	14	US-10-144-649A-587	Sequence 587, Appl
822	23	100.0	16	10	US-09-825-517A-45	Sequence 45, Appl	895	23	100.0	16	14	US-10-267-251-4	Sequence 4, Appl
823	23	100.0	16	10	US-09-825-517A-46	Sequence 46, Appl	896	23	100.0	16	14	US-10-224-356-36	Sequence 36, Appl
824	23	100.0	16	10	US-09-825-517A-47	Sequence 47, Appl	897	23	100.0	16	14	US-10-058-053A-309	Sequence 309, Appl
825	23	100.0	16	10	US-09-825-517A-48	Sequence 48, Appl	898	23	100.0	16	14	US-10-047-264A-16	Sequence 16, Appl
826	23	100.0	16	10	US-09-825-517A-49	Sequence 49, Appl	899	23	100.0	16	14	US-10-062-599-88	Sequence 88, Appl
827	23	100.0	16	10	US-09-825-517A-50	Sequence 50, Appl	900	23	100.0	16	14	US-10-125-869A-137	Sequence 137, Appl
828	23	100.0	16	10	US-09-825-517A-51	Sequence 51, Appl	901	23	100.0	16	15	US-10-371-525-308	Sequence 308, Appl
829	23	100.0	16	10	US-09-825-517A-52	Sequence 52, Appl	902	23	100.0	16	15	US-10-371-069-308	Sequence 308, Appl
830	23	100.0	16	10	US-09-825-517A-53	Sequence 53, Appl	903	23	100.0	16	15	US-10-371-645-308	Sequence 308, Appl
831	23	100.0	16	10	US-09-825-517A-54	Sequence 54, Appl	904	23	100.0	16	15	US-10-371-260-308	Sequence 308, Appl
832	23	100.0	16	10	US-09-825-517A-55	Sequence 55, Appl	905	23	100.0	16	15	US-10-369-214-6	Sequence 6, Appl
833	23	100.0	16	10	US-09-825-517A-56	Sequence 56, Appl	906	23	100.0	16	15	US-10-462-262-186	Sequence 186, Appl
834	23	100.0	16	10	US-09-825-517A-57	Sequence 57, Appl	907	23	100.0	16	15	US-10-462-262-188	Sequence 188, Appl
835	23	100.0	16	10	US-09-825-517A-58	Sequence 58, Appl	908	23	100.0	16	15	US-10-462-262-361	Sequence 361, Appl
836	23	100.0	16	10	US-09-825-517A-59	Sequence 59, Appl	909	23	100.0	16	15	US-10-373-238-68	Sequence 68, Appl
837	23	100.0	16	10	US-09-825-517A-60	Sequence 60, Appl	910	23	100.0	16	15	US-10-436-715-249	Sequence 249, Appl
838	23	100.0	16	10	US-09-825-517A-61	Sequence 61, Appl	911	23	100.0	16	15	US-10-436-715-288	Sequence 288, Appl
839	23	100.0	16	10	US-09-825-517A-62	Sequence 62, Appl	912	23	100.0	16	15	US-10-436-715-313	Sequence 313, Appl
840	23	100.0	16	10	US-09-825-517A-63	Sequence 63, Appl	913	23	100.0	16	15	US-10-319-786-51	Sequence 51, Appl
841	23	100.0	16	10	US-09-825-517A-64	Sequence 64, Appl	914	23	100.0	16	16	US-10-258-144-277	Sequence 277, Appl
842	23	100.0	16	10	US-09-825-517A-65	Sequence 65, Appl	915	23	100.0	16	16	US-10-467-758-14	Sequence 14, Appl
843	23	100.0	16	10	US-09-825-517A-66	Sequence 66, Appl	916	23	100.0	16	16	US-10-096-525-1	Sequence 1, Appl
844	23	100.0	16	10	US-09-825-517A-67	Sequence 67, Appl	917	23	100.0	16	16	US-10-096-525-1	Sequence 1, Appl
845	23	100.0	16	10	US-09-825-517A-68	Sequence 68, Appl	918	23	100.0	16	16	US-10-474-960A-199	Sequence 199, Appl
846	23	100.0	16	10	US-09-825-517A-69	Sequence 69, Appl	919	23	100.0	16	17	US-10-659-207-89	Sequence 89, Appl
847	23	100.0	16	10	US-09-825-517A-70	Sequence 70, Appl	920	23	100.0	16	17	US-10-659-207-445	Sequence 445, Appl
848	23	100.0	16	10	US-09-825-517A-71	Sequence 71, Appl	921	23	100.0	16	18	US-10-927-262A-39	Sequence 39, Appl
849	23	100.0	16	10	US-09-825-517A-72	Sequence 72, Appl	922	23	100.0	16	18	US-10-927-262A-40	Sequence 40, Appl
850	23	100.0	16	10	US-09-825-517A-73	Sequence 73, Appl	923	23	100.0	16	18	US-10-962-760-11	Sequence 11, Appl
851	23	100.0	16	10	US-09-825-517A-74	Sequence 74, Appl	924	23	100.0	16	18	US-10-962-760-11	Sequence 11, Appl
852	23	100.0	16	10	US-09-825-517A-75	Sequence 75, Appl	925	23	100.0	16	18	US-10-470-045-47	Sequence 47, Appl
853	23	100.0	16	10	US-09-825-517A-76	Sequence 76, Appl	926	23	100.0	16	18	US-10-946-647-368	Sequence 368, Appl
854	23	100.0	16	10	US-09-825-517A-77	Sequence 77, Appl	927	23	100.0	16	18	US-10-946-647-368	Sequence 368, Appl
855	23	100.0	16	10	US-09-825-517A-78	Sequence 78, Appl	928	23	100.0	16	18	US-10-946-647-368	Sequence 368, Appl
856	23	100.0	16	10	US-09-825-517A-79	Sequence 79, Appl	929	23	100.0	16	18	US-10-946-647-368	Sequence 368, Appl
857	23	100.0	16	10	US-09-825-517A-80	Sequence 80, Appl	930	23	100.0	16	18	US-10-792-582-7	Sequence 7, Appl
858	23	100.0	16	10	US-09-825-517A-81	Sequence 81, Appl	931	23	100.0	16	20	US-11-045-477-4	Sequence 4, Appl
859	23	100.0	16	10	US-09-825-517A-82	Sequence 82, Appl	932	23	100.0	16	20	US-11-045-477-20	Sequence 20, Appl
860	23	100.0	16	10	US-09-825-517A-83	Sequence 83, Appl	933	23	100.0	16	20	US-11-045-477-35	Sequence 35, Appl
861	23	100.0	16	10	US-09-825-517A-84	Sequence 84, Appl	934	23	100.0	16	20	US-11-045-477-37	Sequence 37, Appl
862	23	100.0	16	10	US-09-825-517A-85	Sequence 85, Appl	935	23	100.0	16	20	US-11-045-477-38	Sequence 38, Appl
863	23	100.0	16	10	US-09-825-517A-86	Sequence 86, Appl	936	23	100.0	16	20	US-11-045-477-39	Sequence 39, Appl
864	23	100.0	16	10	US-09-825-517A-87	Sequence 87, Appl	937	23	100.0	16	20	US-11-045-477-40	Sequence 40, Appl
865	23	100.0	16	10	US-09-825-517A-88	Sequence 88, Appl	938	23	100.0	16	20	US-11-045-477-41	Sequence 41, Appl
866	23	100.0	16	10	US-09-825-517A-89	Sequence 89, Appl	939	23	100.0	16	20	US-11-045-477-42	Sequence 42, Appl
867	23	100.0	16	10	US-09-825-517A-90	Sequence 90, Appl	940	23	100.0	16	20	US-11-045-477-43	Sequence 43, Appl
868	23	100.0	16	10	US-09-825-517A-91	Sequence 91, Appl	941	23	100.0	16	20	US-11-045-477-44	Sequence 44, Appl
869	23	100.0	16	10	US-09-825-517A-92	Sequence 92, Appl	942	23	100.0	16	20	US-11-045-477-45	Sequence 45, Appl
870	23	100.0	16	10	US-09-825-517A-93	Sequence 93, Appl	943	23	100.0	16	20	US-11-045-477-46	Sequence 46, Appl
871	23	100.0	16	10	US-09-825-517A-94	Sequence 94, Appl	944	23	100.0	16	20	US-11-045-477-47	Sequence 47, Appl
872	23	100.0	16	10	US-09-825-517A-95	Sequence 95, Appl	945	23	100.0	16	20	US-11-045-477-48	Sequence 48, Appl
873	23	100.0	16	10	US-09-825-517A-96	Sequence 96, Appl	946	23	100.0	16	20	US-11-045-477-50	Sequence 50, Appl
874	23	100.0	16	10	US-09-825-517A-97	Sequence 97, Appl	947	23	100.0	16	20	US-11-045-477-51	Sequence 51, Appl
875	23	100.0	16	10	US-09-825-517A-98	Sequence 98, Appl	948	23	100.0	16	20	US-11-045-477-52	Sequence 52, Appl
876	23	100.0	16	10	US-09-825-517A-99	Sequence 99, Appl	949	23	100.0	16	20	US-11-045-477-53	Sequence 53, Appl
877	23	100.0	16	10	US-09-825-517A-100	Sequence 100, Appl	950	23	100.0	16	20	US-11-045-477-55	Sequence 55, Appl
878	23	100.0	16	10	US-09-825-517A-101	Sequence 101, Appl	951	23	100.0	16	20	US-11-045-477-56	Sequence 56, Appl
879	23	100.0	16	10	US-09-825-517A-102	Sequence 102, Appl	952	23	100.0	16	20	US-11-045-477-57	Sequence 57, Appl
880	23	100.0	16	10	US-09-825-517A-103	Sequence 103, Appl	953	23	100.0	16	20	US-11-045-477-58	Sequence 58, Appl
881	23	100.0	16	10	US-09-825-517A-104	Sequence 104, Appl	954	23	100.0	16	20	US-11-045-477-59	Sequence 59, Appl
882	23	100.0	16	10	US-09-825-517A-105	Sequence 105, Appl	955	23	100.0	16	20	US-11-045-477-61	Sequence 61, Appl
883	23	100.0	16	10	US-09-825-517A-106	Sequence 106, Appl	956	23	100.0	16	20	US-11-045-477-62	Sequence 62, Appl
884	23	100.0	16	10	US-09-825-517A-107	Sequence 107, Appl	957	23	100.0	16	20	US-11-045-477-63	Sequence 63, Appl
885	23	100.0	16	10	US-09-825-517A-108	Sequence 108, Appl	958	23	100.0	16	20	US-11-045-477-64	Sequence 64, Appl
886	23	100.0	16	10	US-09-825-517A-109	Sequence 109, Appl	959	23	100.0	16	20	US-11-045-477-66	Sequence 66, Appl
887	23	100.0	16	10	US-09-825-517A-110	Sequence 110, Appl	960	23	100.0	16	20	US-11-045-477-68	Sequence 68, Appl

Sequence 69, Appl
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Sequence 83, Appl
Sequence 84, Appl
Sequence 85, Appl
Sequence 86, Appl
Sequence 89, Appl
Sequence 91, Appl
Sequence 92, Appl
Sequence 96, Appl
Sequence 98, Appl
Sequence 99, Appl
Sequence 100, App
Sequence 104, App
Sequence 105, App
Sequence 106, App
Sequence 108, App
Sequence 109, App
Sequence 115, App
Sequence 119, App
Sequence 120, App
Sequence 121, App
Sequence 124, App
Sequence 128, App
Sequence 129, App
Sequence 130, App
Sequence 131, App
Sequence 132, App
Sequence 134, App
Sequence 136, App
Sequence 137, App
Sequence 139, App
Sequence 145, App

23 100.0 16 20 US-11-045-477-69
23 100.0 16 20 US-11-045-477-71
23 100.0 16 20 US-11-045-477-73
23 100.0 16 20 US-11-045-477-74
23 100.0 16 20 US-11-045-477-75
23 100.0 16 20 US-11-045-477-76
23 100.0 16 20 US-11-045-477-77
23 100.0 16 20 US-11-045-477-79
23 100.0 16 20 US-11-045-477-81
23 100.0 16 20 US-11-045-477-83
23 100.0 16 20 US-11-045-477-84
23 100.0 16 20 US-11-045-477-85
23 100.0 16 20 US-11-045-477-86
23 100.0 16 20 US-11-045-477-89
23 100.0 16 20 US-11-045-477-91
23 100.0 16 20 US-11-045-477-92
23 100.0 16 20 US-11-045-477-96
23 100.0 16 20 US-11-045-477-98
23 100.0 16 20 US-11-045-477-99
23 100.0 16 20 US-11-045-477-100
23 100.0 16 20 US-11-045-477-104
23 100.0 16 20 US-11-045-477-105
23 100.0 16 20 US-11-045-477-106
23 100.0 16 20 US-11-045-477-108
23 100.0 16 20 US-11-045-477-109
23 100.0 16 20 US-11-045-477-115
23 100.0 16 20 US-11-045-477-119
23 100.0 16 20 US-11-045-477-120
23 100.0 16 20 US-11-045-477-121
23 100.0 16 20 US-11-045-477-124
23 100.0 16 20 US-11-045-477-128
23 100.0 16 20 US-11-045-477-129
23 100.0 16 20 US-11-045-477-130
23 100.0 16 20 US-11-045-477-131
23 100.0 16 20 US-11-045-477-132
23 100.0 16 20 US-11-045-477-134
23 100.0 16 20 US-11-045-477-136
23 100.0 16 20 US-11-045-477-137
23 100.0 16 20 US-11-045-477-139
23 100.0 16 20 US-11-045-477-145

ALIGNMENTS

RESULT 1
US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-252
Query Match 100.0%; Score 23; DB 8; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0;
Gaps 0;
QY 1 FXXKXXXX 8
|::|:::
DB 1 FSHLWTSG 8
RESULT 2
US-08-344-824-105
; Sequence 105, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-344-824-105

Query Match 100.0%; Score 23; DB 8; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FPRWLHL 8

RESULT 3

US-09-214-371-10
; Sequence 10, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: X = methionine, isoleucine, threonine, arginine,
; OTHER INFORMATION: alanine or serine, preferably methionine
; NAME/KEY: VARIANT
; LOCATION: (3)
; OTHER INFORMATION: X = arginine, histidine, glutamic acid, cysteine,
; OTHER INFORMATION: serine, or preferably aspartic acid.
; NAME/KEY: VARIANT
; LOCATION: (4)
; OTHER INFORMATION: X = histidine, phenylalanine, or preferably
; OTHER INFORMATION: tyrosine
; NAME/KEY: VARIANT
; LOCATION: (6)
; OTHER INFORMATION: X = glutamic acid, threonine, alanine,
; OTHER INFORMATION: phenylalanine or serine, preferably glutamic acid
; NAME/KEY: VARIANT
; LOCATION: (7)
; OTHER INFORMATION: X = glycine, glutamine, threonine, alanine or
; OTHER INFORMATION: aspartic acid, preferably glycine.
; NAME/KEY: VARIANT
; LOCATION: (8)
; OTHER INFORMATION: X = phenylalanine, glutamine or preferably
; OTHER INFORMATION: leucine.
US-09-214-371-10

Query Match 100.0%; Score 23; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FXXXWXXX 8

RESULT 4

US-09-214-371-16
; Sequence 16, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-16

Query Match 100.0%; Score 23; DB 9; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FMDYWEGL 8

RESULT 5

US-09-780-070-13
; Sequence 13, Application US/097800070
; Patent No. US20020009752A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmatter, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-780-070-13

Query Match 100.0%; Score 23; DB 9; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FIGPWWKW 8

RESULT 6
US-09-908-322-83
; Sequence 83, Application US/09908322

Patent No. US20020107194A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Miarock, S Lealie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-908-322-83
Query Match 100.0%; Score 23; DB 9; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
DB 1 FGFTWPGT 8
RESULT 7
US-09-794-517-4
Sequence 4, Application US/09794517
Publication No. US20030021794A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOE, Mee H.
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon

STREET: One Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,517
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/011,645
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: DeLucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: heat shock protein binding motif
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-517-4
Query Match 100.0%; Score 23; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
DB 1 FWGLWPWE 8
RESULT 8
US-09-783-931-83
Sequence 83, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-783-931-83

Query Match 100.0%; Score 23; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
DB 1 FGFTWPGT 8

RESULT 9
US-09-794-529-4
Sequence 4, Application US/09794529
Publication No. US20030082197A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOE, Mee H.
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,529
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645

FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 60/002,479
FILING DATE: August 18, 1995
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: heat shock protein binding motif
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-529-4

Query Match 100.0%; Score 23; DB 10; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
DB 1 FWGLWPWE 8

RESULT 10
US-09-794-832-4
Sequence 4, Application US/09794832
Publication No. US20030082198A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
ROTHMAN, James E.
HARTL, F. Ulrich
HOE, Mee H.
HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,832
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645

```
Query Match      100.0%; Score 23; DB 14; Length 8;
Best Local Similarity 25.0%; Pred. NO. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
US-10-170-713A-4
; Sequence 4, Application US/10170713A
; Publication No. US20030185942A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTLL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,713A
; FILING DATE: 13-Jun-2002

```

? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/002,479
? FILING DATE: August 18, 1995
? APPLICATION NUMBER: 60/002,490
? FILING DATE: August 18, 1995
? APPLICATION NUMBER: PCT/US96/13363
? FILING DATE: August 16, 1996
? APPLICATION NUMBER: 09/011,645
? FILING DATE: February 13, 1998
? APPLICATION NUMBER: 09/636,295
? FILING DATE: August 10, 2000
? ATTORNEY/AGENT INFORMATION:
? NAME: Cabson, Lawrence P.
? REGISTRATION NUMBER: 46,606
? REFERENCE/DOCKET NUMBER: 11746/461031
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 425-7200
? TELEFAX: (212) 425-5288
? TELEX: <Unknown>
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8
? TYPE: amino acid
? STRANDEDNESS: <Unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHETICAL: no
? FRAGMENT TYPE: internal
? ORIGINAL SOURCE:
? ORGANISM: <Unknown>
? FEATURE:
? OTHER INFORMATION: heat shock protein binding motif
? SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-171-734-4

Query Match 100.0%; Score 23; DB 14; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0;

Qy 1 FXXXWXXX 8
|::|:::
Db 1 FWGLWPWE 8

RESULT 15
US-10-053-498B-144
; Sequence 144, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 144
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-144

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Query Match      100.0%; Score 23; DB 14; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
|::|::|
Db      1 FVGLWPWE 8

RESULT 16
US-10-413-160-13
; Sequence 13, Application US/10413160
; Publication No. US20030229019A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James R.
; APPLICANT: Strittmatter, Warren J.
; APPLICANT: Naga, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; FILE REFERENCE: 5405.242DV
; CURRENT APPLICATION NUMBER: US/10/413,160
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: PCT/US01/08222
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-413-160-13

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
|::|::|
Db      1 FIGPWWKW 8

RESULT 17
US-10-442-909-69
; Sequence 69, Application US/10442909
; Publication No. US20040001845A1
; GENERAL INFORMATION:
; APPLICANT: Altfield, Marcus
; APPLICANT: Yu, Xu
; APPLICANT: Walker, Bruce
; APPLICANT: Addo, Marylyn
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
; FILE REFERENCE: 24028-010
; CURRENT APPLICATION NUMBER: US/10/442,909
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/382,120
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-69

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FXXXWXXX 8
|::|::|
Db      1 FPRILWLG 8

RESULT 18
US-10-149-138-4613
; Sequence 4613, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4613
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4613

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
|::|::|
Db      1 FPIKWMAI 8

RESULT 19
US-10-149-138-4614
; Sequence 4614, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4614
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4614

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FPIKWMAL 8

RESULT 20

US-10-258-147-8
; Sequence 8, Application US/10258147
; Publication No. US20040043419A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: JAVELINIZATION OF PROTEINS
; FILE REFERENCE: 11746/46276
; CURRENT APPLICATION NUMBER: US/10/258,147
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/197,462
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: insert in M13 coliphage
US-10-258-147-8

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FWGLWPWE 8

RESULT 21

US-10-387-957-39
; Sequence 39, Application US/10387957
; Publication No. US20040052809A1
; GENERAL INFORMATION:
; APPLICANT: GlaxoSmithKline Biologicals s.a.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45284
; CURRENT APPLICATION NUMBER: US/10/387,957
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Homo sapiens
US-10-387-957-39

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FSEFWLDL 8

RESULT 22

US-10-258-146A-2
; Sequence 2, Application US/10258146A
; Publication No. US20040052812A1
; GENERAL INFORMATION:
; APPLICANT: Mee Hoe
; APPLICANT: Frank Landberger
; TITLE OF INVENTION: HEAT SHOCK PROTEIN-BASED ANTIVIRAL
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: 11390/46301
; CURRENT APPLICATION NUMBER: US/10/258,146A
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/US01/12568
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/197,462
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: human
US-10-258-146A-2

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FWGLWPWE 8

RESULT 23

US-10-328-953-11
; Sequence 11, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-328-953-11

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FWGLWPWE 8

RESULT 24

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US-10-367-580-4
; Sequence 4, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
      |::|::|
Db      1 FWGLWPWE 8

RESULT 25
US-10-367-580-185
; Sequence 185, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 185
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-185

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
      |::|::|
Db      1 FWGLWPWE 8

RESULT 26
US-10-367-593-4
; Sequence 4, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
      |::|::|
Db      1 FWGLWPWE 8

RESULT 27
US-10-367-593-185
; Sequence 185, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
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US-10-367-580-185
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-185

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
      |::|::|
Db      1 FWFPWDRS 8

RESULT 26
US-10-367-593-4
; Sequence 4, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXWXXX 8
      |::|::|
Db      1 FWGLWPWE 8

RESULT 27
US-10-367-593-185
; Sequence 185, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
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;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 185
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-593-185

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FWFPWDRS 8

RESULT 28
US-10-367-594-4
;; Sequence 4, Application US/10367594
;; Publication No. US20040071722A1
;; GENERAL INFORMATION:
;; APPLICANT: Rothman, James E.
;; APPLICANT: Hartl, F. Ulrich
;; APPLICANT: Hoe, Mee H.
;; APPLICANT: Houghton, Alan
;; APPLICANT: Takechi, Yoshizumi
;; APPLICANT: Mayhew, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;; FILE REFERENCE: 11746/461041
;; CURRENT APPLICATION NUMBER: US/10/367,594
;; CURRENT FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 09/680,806
;; PRIOR FILING DATE: 2000-10-05
;; PRIOR APPLICATION NUMBER: US 09/011,645
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 4
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-594-4

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FWGLPWME 8

RESULT 29
US-10-367-594-185
;; Sequence 185, Application US/10367594
;; Publication No. US20040071722A1

;; GENERAL INFORMATION:
;; APPLICANT: Rothman, James E.
;; APPLICANT: Hartl, F. Ulrich
;; APPLICANT: Hoe, Mee H.
;; APPLICANT: Houghton, Alan
;; APPLICANT: Takechi, Yoshizumi
;; APPLICANT: Mayhew, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;; FILE REFERENCE: 11746/461041
;; CURRENT APPLICATION NUMBER: US/10/367,594
;; CURRENT FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 09/680,806
;; PRIOR FILING DATE: 2000-10-05
;; PRIOR APPLICATION NUMBER: US 09/011,645
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 185
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-594-185

Query Match 100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|:::|:::
Db 1 FWFPWDRS 8

RESULT 30
US-10-367-654-4
;; Sequence 4, Application US/10367654
;; Publication No. US20040071723A1
;; GENERAL INFORMATION:
;; APPLICANT: Rothman, James E.
;; APPLICANT: Hartl, F. Ulrich
;; APPLICANT: Hoe, Mee H.
;; APPLICANT: Houghton, Alan
;; APPLICANT: Takechi, Yoshizumi
;; APPLICANT: Mayhew, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;; FILE REFERENCE: 11746/461032
;; CURRENT APPLICATION NUMBER: US/10/367,654
;; CURRENT FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 10/171,734
;; PRIOR FILING DATE: 2002-06-13
;; PRIOR APPLICATION NUMBER: US 09/636,295
;; PRIOR FILING DATE: 2000-08-10
;; PRIOR APPLICATION NUMBER: US 09/011,645
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 4
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-654-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXWXXX 8
Db      1 FWGLWPWE 8

RESULT 31
US-10-367-654-185
; Sequence 185, Application US/10367654
; Publication No. US20040071723A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461032
; CURRENT APPLICATION NUMBER: US/10/367,654
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/171,734
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/636,295
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 185
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-654-185

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXWXXX 8
Db      1 FWFPWDRS 8

RESULT 32
US-10-367-658-4
; Sequence 4, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
```

```
;
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXWXXX 8
Db      1 FWGLWPWE 8

RESULT 33
US-10-367-658-185
; Sequence 185, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 185
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-185

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXWXXX 8
Db      1 FWFPWDRS 8
```

```
RESULT 34
US-10-367-668-4
; Sequence 4, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXXWXXX 8
Db      1 FWGLWPWE 8

RESULT 35
US-10-367-668-185
; Sequence 185, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 185
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-4

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXXWXXX 8
Db      1 FWGLWPWE 8

RESULT 36
US-10-387-934-39
; Sequence 39, Application US/10387934
; Publication No. US20040091496A1
; GENERAL INFORMATION:
; APPLICANT: Mettens, Pascal
; APPLICANT: Meykins, Rene
; APPLICANT: Monteyne, Philippe
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: VB60137
; CURRENT APPLICATION NUMBER: US/10/387,934
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: PCT/EP02/09650
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-387-934-39

Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 FXXXXWXXX 8
Db      1 FSEFWDL D 8

RESULT 37
US-10-258-144-37
; Sequence 37, Application US/10258144
; Publication No. US20040101532A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Alan
; APPLICANT: Livingston, Phil
; APPLICANT: Al-Awqati, Qais
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT SHOCK
; FILE REFERENCE: 11746/46401
; CURRENT APPLICATION NUMBER: US/10/258,144
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/197,642
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 502
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: ml3 coliphage insert
US-10-258-144-37

Query Match      100.0%; Score 23; DB 16; Length 8;
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```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-185
```

```
Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FXXXXWXXX 8
Db      1 FWFWD R S 8
```

```
RESULT 36
US-10-387-934-39
; Sequence 39, Application US/10387934
; Publication No. US20040091496A1
; GENERAL INFORMATION:
; APPLICANT: Mettens, Pascal
; APPLICANT: Meykins, Rene
; APPLICANT: Monteyne, Philippe
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: VB60137
; CURRENT APPLICATION NUMBER: US/10/387,934
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: PCT/EP02/09650
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-387-934-39
```

```
Query Match      100.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FXXXXWXXX 8
Db      1 FSEFWDL D 8
```

```
RESULT 37
US-10-258-144-37
; Sequence 37, Application US/10258144
; Publication No. US20040101532A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Alan
; APPLICANT: Livingston, Phil
; APPLICANT: Al-Awqati, Qais
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT SHOCK
; FILE REFERENCE: 11746/46401
; CURRENT APPLICATION NUMBER: US/10/258,144
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/197,642
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 502
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: ml3 coliphage insert
US-10-258-144-37
```

```
Query Match      100.0%; Score 23; DB 16; Length 8;
```

Best Local Similarity 25.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 2; Conservative 6; Mismatches 0;

QY 1 FXXWXXX 8
|::|::|
Db 1 FGLMPWE 8

RESULT 38

US-10-440-390-52
; Sequence 52, Application US/10440390
; Publication No. US20040105868A1
; GENERAL INFORMATION:
; APPLICANT: Lauer et al.
; TITLE OF INVENTION: Epitopes of Hepatitis C Virus
; FILE REFERENCE: 24028-011
; CURRENT APPLICATION NUMBER: US/10/440,390
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/381,273
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-440-390-52

Query Match 100.0%; Score 23; DB 16; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
Db 1 FYGMPPL 8

RESULT 39

US-10-440-390-89
; Sequence 89, Application US/10440390
; Publication No. US20040105868A1
; GENERAL INFORMATION:
; APPLICANT: Lauer et al.
; TITLE OF INVENTION: Epitopes of Hepatitis C Virus
; FILE REFERENCE: 24028-011
; CURRENT APPLICATION NUMBER: US/10/440,390
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/381,273
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-440-390-89

Query Match 100.0%; Score 23; DB 16; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
Db 1 FYGMPPL 8

RESULT 40

US-10-149-138-4613
; Sequence 4613, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4613
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4613

Query Match 100.0%; Score 23; DB 16; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
Db 1 FFIKMAI 8

Search completed: October 19, 2005, 15:50:59
Job time : 103.118 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:26:26 ; Search time 109.647 Seconds
(without alignments)
28.219 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	8	2	AAR11090 LHRH pseu
2	23	100.0	8	2	AAR35839 Hepatitis
3	23	100.0	8	2	AAR19954 Heat choc
4	23	100.0	8	2	AAR37211 Human onc
5	23	100.0	8	2	AAR37218 Human onc
6	23	100.0	8	2	AAR37174 Human onc
7	23	100.0	8	2	AAR37217 Human onc
8	23	100.0	8	2	AAR37215 Human onc
9	23	100.0	8	2	AAR37214 Human onc
10	23	100.0	8	2	AAR37180 Human onc
11	23	100.0	8	2	AAR37219 Human onc
12	23	100.0	8	2	AAR40286 Amino aci
13	23	100.0	8	2	AAR25556 Human MHC
14	23	100.0	8	2	AAR53417 HIV-1 Gpl
15	23	100.0	8	2	AAR26758 HIV-deriv
16	23	100.0	8	2	AAR16874 Peptide S
17	23	100.0	8	3	AAR09130 Hepatitis
18	23	100.0	8	4	AAG88890 HER2/neu
19	23	100.0	8	4	AAG88891 HER2/neu
20	23	100.0	8	4	AAB59632 Neuromedi
21	23	100.0	8	4	AAR72016 Melanoma
22	23	100.0	8	4	AAB76081 Tumour as
23	23	100.0	8	4	AAB76082 Tumour as
24	23	100.0	8	4	AAR02206 Trichoder
25	23	100.0	8	4	ABP20955 HIV A03 m

26	23	100.0	8	4	ABP23018 HIV All m
27	23	100.0	8	4	ABP15754 HIV A24 s
28	23	100.0	8	4	AAE12180 Polygluta
29	23	100.0	8	4	AAAI10739 HLA-B8 oc
30	23	100.0	8	5	AAU80566 Heat choc
31	23	100.0	8	5	ABJ08627 Hepatitis
32	23	100.0	8	5	ABJ06552 Hepatitis
33	23	100.0	8	5	AAE13438 Javelin s
34	23	100.0	8	6	ABG72769 Human FNF
35	23	100.0	8	6	ABP98084 Amino aci
36	23	100.0	8	6	ABP68156 Bacillus
37	23	100.0	8	6	ABP68179 Bacillus
38	23	100.0	8	6	ABP68175 Bacillus
39	23	100.0	8	6	ABP68180 Bacillus
40	23	100.0	8	6	ABP68151 Bacillus
41	23	100.0	8	6	ABP68152 Bacillus
42	23	100.0	8	6	ABP68177 Bacillus
43	23	100.0	8	6	ABP68159 Bacillus
44	23	100.0	8	6	ABP68162 Bacillus
45	23	100.0	8	6	ABP68173 Bacillus
46	23	100.0	8	6	ABP68170 Bacillus
47	23	100.0	8	6	ABP68172 Bacillus
48	23	100.0	8	6	ABP68161 Bacillus
49	23	100.0	8	6	ABP68163 Bacillus
50	23	100.0	8	6	ABP68167 Bacillus
51	23	100.0	8	6	ABP68181 Bacillus
52	23	100.0	8	6	ABP68169 Bacillus
53	23	100.0	8	6	ABP68153 Bacillus
54	23	100.0	8	6	ABP68158 Bacillus
55	23	100.0	8	6	ABP68150 Bacillus
56	23	100.0	8	6	ABP68164 Bacillus
57	23	100.0	8	6	ABP68168 Bacillus
58	23	100.0	8	6	ABP68154 Bacillus
59	23	100.0	8	6	ABP68171 Bacillus
60	23	100.0	8	6	ABP68174 Bacillus
61	23	100.0	8	6	ABP68166 Bacillus
62	23	100.0	8	6	ABP68160 Bacillus
63	23	100.0	8	7	ABP68178 Bacillus
64	23	100.0	8	7	ADD57481 HLA bindi
65	23	100.0	8	7	ADD57831 HLA bindi
66	23	100.0	8	7	ADD57832 HLA bindi
67	23	100.0	8	7	ADD56967 HLA bindi
68	23	100.0	8	7	ADD56968 HLA bindi
69	23	100.0	8	7	ADD57482 HLA bindi
70	23	100.0	8	7	ADD56966 HLA bindi
71	23	100.0	8	7	ADG72530 Heat choc
72	23	100.0	8	8	ADI24652 HIV-1 HLA
73	23	100.0	8	8	ADI34265 8mer pept
74	23	100.0	8	8	ADK37832 Hepatitis
75	23	100.0	8	8	ADK10578 Human pap
76	23	100.0	8	8	ADO08669 Hepatitis
77	23	100.0	8	8	ADO08706 HCV epito
78	23	100.0	8	8	ADQ28800 Human cel
79	23	100.0	8	8	ADR69606 Novel hyb
80	23	100.0	8	8	ADR69598 Novel hyb
81	23	100.0	8	8	ADR69600 Novel hyb
82	23	100.0	8	8	ADR69609 Novel hyb
83	23	100.0	8	8	ADR69602 Novel hyb
84	23	100.0	8	8	ADS00535 Human Apo
85	23	100.0	8	8	ADR99995 Human apo
86	23	100.0	8	8	ADS54216 Human apo
87	23	100.0	9	2	AAR14230 Somatosta
88	23	100.0	9	2	AAR14233 Somatosta
89	23	100.0	9	2	AAR14232 Somatosta
90	23	100.0	9	2	AAR14231 Somatosta
91	23	100.0	9	2	AAR70548 HIV(B35)A
92	23	100.0	9	2	AAW39594 Human mel
93	23	100.0	9	2	AAW46351 Amino aci
94	23	100.0	9	2	AAW46349 Amino aci
95	23	100.0	9	2	AAW46348 Amino aci
96	23	100.0	9	2	AAW46350 Amino aci
97	23	100.0	9	2	AAW37216 Human onc
98	23	100.0	9	2	AAW37175 Human onc

99	23	100.0	9	2	AAW37212	Aaw37212 Human onc	172	23	100.0	9	5	ABG60517	ABG60517 Selective
100	23	100.0	9	2	AAW37179	Aaw37179 Human onc	173	23	100.0	9	5	ABP53424	ABP53424 Backbone
101	23	100.0	9	2	AAW37213	Aaw37213 Human onc	174	23	100.0	9	5	ABP53363	ABP53363 Backbone
102	23	100.0	9	2	AAW47628	Aay47628 Immunogen	175	23	100.0	9	5	ABP53420	ABP53420 Backbone
103	23	100.0	9	2	AAW47059	Aay47059 Immunogen	176	23	100.0	9	5	AAE31317	AAE31317 Human p53
104	23	100.0	9	2	AAW47928	Aay47928 Immunogen	177	23	100.0	9	5	AAE31347	AAE31347 Human tyr
105	23	100.0	9	2	AAW46459	Aay46459 Immunogen	178	23	100.0	9	5	AAE31160	AAE31160 Human spl
106	23	100.0	9	2	AAW25555	Aay25555 Human MHC	179	23	100.0	9	5	AAE31346	AAE31346 Human tyr
107	23	100.0	9	2	AAW55520	Aay55520 HLA bindi	180	23	100.0	9	5	AAU09701	AAU09701 Anti-mela
108	23	100.0	9	3	AAW84757	Aay84757 Antigenic	181	23	100.0	9	5	AAU09699	AAU09699 Anti-mela
109	23	100.0	9	3	AAW84765	Aay84765 Antigenic	182	23	100.0	9	5	ABJ16944	ABJ16944 Zinc tran
110	23	100.0	9	3	AAW84756	Aay84756 Antigenic	183	23	100.0	9	5	ABJ16792	ABJ16792 Zinc tran
111	23	100.0	9	3	AAW84760	Aay84760 Antigenic	184	23	100.0	9	5	ABJ16823	ABJ16823 Zinc tran
112	23	100.0	9	3	AAW84762	Aay84762 Consensus	185	23	100.0	9	6	ABR56915	ABR56915 Pancreati
113	23	100.0	9	3	AAW84758	Aay84758 Antigenic	186	23	100.0	9	6	AAO30510	AAO30510 HIV vpr m
114	23	100.0	9	3	AAW84759	Aay84759 Antigenic	187	23	100.0	9	6	ABR44093	ABR44093 HIV-1 der
115	23	100.0	9	3	AAW76798	Aay76798 Somatosta	188	23	100.0	9	6	ABP96410	ABP96410 HIV-1 Vpr
116	23	100.0	9	3	AAW76773	Aay76773 Somatosta	189	23	100.0	9	6	ABR24615	ABR24615 Human can
117	23	100.0	9	4	AAW22332	Aam22332 HIV pepi	190	23	100.0	9	6	ABR13450	ABR13450 Human can
118	23	100.0	9	4	AAW22682	Aam22682 HIV pepi	191	23	100.0	9	6	ABR13770	ABR13770 Human can
119	23	100.0	9	4	AAW22679	Aam22679 HIV pepi	192	23	100.0	9	6	ABR14212	ABR14212 Human can
120	23	100.0	9	4	AAW22680	Aam22680 HIV pepi	193	23	100.0	9	6	ABR25041	ABR25041 Human can
121	23	100.0	9	4	AAW22645	Aam22645 HIV pepi	194	23	100.0	9	6	ABR13428	ABR13428 Human can
122	23	100.0	9	4	AAW22624	Aam22624 HIV pepi	195	23	100.0	9	6	ABR14464	ABR14464 Human can
123	23	100.0	9	4	AAW22647	Aam22647 HIV pepi	196	23	100.0	9	6	ABR24408	ABR24408 Human can
124	23	100.0	9	4	AAW23398	Aam23398 HIV pepi	197	23	100.0	9	6	ABR13820	ABR13820 Human can
125	23	100.0	9	4	AAW22623	Aam22623 HIV pepi	198	23	100.0	9	6	ABR14018	ABR14018 Human can
126	23	100.0	9	4	AAW22646	Aam22646 HIV pepi	199	23	100.0	9	6	ABR14224	ABR14224 Human can
127	23	100.0	9	4	AAW22698	Aam22698 HIV pepi	200	23	100.0	9	6	ABR14030	ABR14030 Human can
128	23	100.0	9	4	AAW22681	Aam22681 HIV pepi	201	23	100.0	9	6	ABR13445	ABR13445 Human can
129	23	100.0	9	4	AAW59614	Aab59614 Neuromedi	202	23	100.0	9	6	ABR13575	ABR13575 Human can
130	23	100.0	9	4	AAW63357	Aag63357 Complemen	203	23	100.0	9	6	ABR03544	ABR03544 Human can
131	23	100.0	9	4	AAW24137	Aau24137 Human MHC	204	23	100.0	9	6	ABR13182	ABR13182 Human can
132	23	100.0	9	4	AAW24453	Aau24453 Human MHC	205	23	100.0	9	6	ABR13966	ABR13966 Human can
133	23	100.0	9	4	ABP76106	Aab76106 Tumour as	206	23	100.0	9	6	ABR04164	ABR04164 Human can
134	23	100.0	9	4	ABP15780	Abp15780 HIV A24 s	207	23	100.0	9	6	ABR13839	ABR13839 Human can
135	23	100.0	9	4	ABP20958	Abp20958 HIV A03 m	208	23	100.0	9	6	ABR14454	ABR14454 Human can
136	23	100.0	9	4	ABP22220	Abp22220 HIV A03 m	209	23	100.0	9	6	ABG71762	ABG71762 Antigenic
137	23	100.0	9	4	ABP23020	Abp23020 HIV A11 m	210	23	100.0	9	6	ADA10602	ADA10602 Human T c
138	23	100.0	9	4	ABP23978	Abp23978 HIV A11 m	211	23	100.0	9	6	ABJ58972	ABJ58972 184P1E2-r
139	23	100.0	9	4	AAU02306	Aau02306 HLA bindi	212	23	100.0	9	6	ABJ59510	ABJ59510 184P1E2-r
140	23	100.0	9	4	AAU02261	Aau02261 HLA bindi	213	23	100.0	9	6	ABJ63999	ABJ63999 184P1E2-r
141	23	100.0	9	4	AAU02330	Aau02330 HLA bindi	214	23	100.0	9	6	ABJ64840	ABJ64840 184P1E2-r
142	23	100.0	9	4	AAW11964	Aam11964 HLA-B *15	215	23	100.0	9	6	ABJ62084	ABJ62084 184P1E2-r
143	23	100.0	9	4	AAW112502	Aam112502 HLA-B8 no	216	23	100.0	9	6	ABJ62495	ABJ62495 184P1E2-r
144	23	100.0	9	4	AAW08958	Aam08958 HLA-A *02	217	23	100.0	9	6	ABJ58585	ABJ58585 184P1E2-r
145	23	100.0	9	4	AAW08038	Aam08038 HLA-A *07	218	23	100.0	9	6	ABJ60738	ABJ60738 184P1E2-r
146	23	100.0	9	4	AAW08636	Aam08636 HLA-B *07	219	23	100.0	9	6	ABJ65172	ABJ65172 184P1E2-r
147	23	100.0	9	4	AAW11046	Aam11046 HLA-A26 n	220	23	100.0	9	6	ABJ59945	ABJ59945 184P1E2-r
148	23	100.0	9	4	AAW07514	Aam07514 HLA-B *27	221	23	100.0	9	6	ABJ60623	ABJ60623 184P1E2-r
149	23	100.0	9	4	AAW08879	Aam08879 HLA-B *07	222	23	100.0	9	6	ABJ61114	ABJ61114 184P1E2-r
150	23	100.0	9	4	AAW07847	Aam07847 HLA-A1 no	223	23	100.0	9	6	ABJ63481	ABJ63481 184P1E2-r
151	23	100.0	9	4	AAW08894	Aam08894 HLA-B *27	224	23	100.0	9	6	ABJ61514	ABJ61514 184P1E2-r
152	23	100.0	9	4	AAW112269	Aam112269 HLA-B8 no	225	23	100.0	9	6	ABJ62639	ABJ62639 184P1E2-r
153	23	100.0	9	4	AAW11670	Aam11670 HLA-A26 n	226	23	100.0	9	6	ABJ63337	ABJ63337 184P1E2-r
154	23	100.0	9	4	AAW112223	Aam112223 HLA-B *15	227	23	100.0	9	6	ABJ61556	ABJ61556 184P1E2-r
155	23	100.0	9	4	AAW08572	Aam08572 HLA-A1 no	228	23	100.0	9	6	ABJ60622	ABJ60622 184P1E2-r
156	23	100.0	9	4	AAJ02986	Aaj02986 Hepatitis	229	23	100.0	9	6	ABJ63965	ABJ63965 184P1E2-r
157	23	100.0	9	4	AAJ03291	Aaj03291 Hepatitis	230	23	100.0	9	6	ABJ57333	ABJ57333 184P1E2-r
158	23	100.0	9	5	AAU74683	Aau74683 Human can	231	23	100.0	9	6	ABJ65025	ABJ65025 184P1E2-r
159	23	100.0	9	5	AAU74684	Aau74684 Human can	232	23	100.0	9	6	ABJ63111	ABJ63111 184P1E2-r
160	23	100.0	9	5	AAU74681	Aau74681 Human can	233	23	100.0	9	6	ABO27023	ABO27023 Yellow fe
161	23	100.0	9	5	AAU80742	Aau80742 Javelin p	234	23	100.0	9	6	ABO27024	ABO27024 West Nile
162	23	100.0	9	5	AAU80741	Aau80741 Javelin p	235	23	100.0	9	6	ABO27025	ABO27025 Murray va
163	23	100.0	9	5	ABG35129	Abg35129 Pancreati	236	23	100.0	9	6	ABO27026	ABO27026 Kunjin vi
164	23	100.0	9	5	ABJ04579	Abj04579 Bone marr	237	23	100.0	9	7	ADA07879	Ada07879 Viral pro
165	23	100.0	9	5	ABJ12495	Abj12495 Human 125	238	23	100.0	9	7	ADA07878	Ada07878 Viral pro
166	23	100.0	9	5	ABJ12352	Abj12352 Human 125	239	23	100.0	9	7	ADA07881	Ada07881 Viral pro
167	23	100.0	9	5	ABJ11913	Abj11913 Human 125	240	23	100.0	9	7	ADA07880	Ada07880 Viral pro
168	23	100.0	9	5	ABJ09158	Abj09158 Hepatitis	241	23	100.0	9	7	ABR82209	ABR82209 Human can
169	23	100.0	9	5	ABJ06626	Abj06626 Hepatitis	242	23	100.0	9	7	ABR82208	ABR82208 Human can
170	23	100.0	9	5	ABJ08866	Abj08866 Hepatitis	243	23	100.0	9	7	ABR82206	ABR82206 Human can
171	23	100.0	9	5	ABJ08649	Abj08649 Hepatitis	244	23	100.0	9	7	ADD26353	ADD26353 Staphyloc

245	23	100.0	9	7	ADP56984	Add56984 HLA bindi	318	23	100.0	10	1	AAP40332	Aap40332 Sequence
246	23	100.0	9	7	ADP57480	Add57480 HLA bindi	319	23	100.0	10	1	AAP50790	Aap50790 Sequence
247	23	100.0	9	7	ADP57830	Add57830 HLA bindi	320	23	100.0	10	1	AAP50792	Aap50792 Sequence
248	23	100.0	9	7	ADP56982	Add56982 HLA bindi	321	23	100.0	10	1	AAP50477	Aap50477 Luliberin
249	23	100.0	9	7	ADP568466	Ades68466 Human 161	322	23	100.0	10	1	AAP70926	Aap70926 Luteinisi
250	23	100.0	9	7	ADP568739	Ades68739 Human 161	323	23	100.0	10	1	AAP71235	Aap71235 Luteinisi
251	23	100.0	9	7	ADP568096	Ades68096 Human 161	324	23	100.0	10	1	AAP82754	Aap82754 Example o
252	23	100.0	9	7	ADP566983	Ades66983 Human 161	325	23	100.0	10	1	AAR14235	Aar14235 Somatosta
253	23	100.0	9	7	ADP568884	Ades68884 Human 161	326	23	100.0	10	2	AAR45329	Aar45329 Conserved
254	23	100.0	9	7	ADP580812	Ades80812 Caspase-5	327	23	100.0	10	2	AAR77426	Aar77426 Gonadotro
255	23	100.0	9	7	ADP39751	Ades39751 Peptide p	328	23	100.0	10	2	AAR97318	Aar97318 Humanised
256	23	100.0	9	7	ADP65171	Adk65171 Human VEG	329	23	100.0	10	2	AAW16738	AAw16738 p185 bind
257	23	100.0	9	7	ADP65120	Adk65120 Human VEG	330	23	100.0	10	2	AAW16748	AAw16748 p185 bind
258	23	100.0	9	8	ADP86052	Adf86052 Human FGF	331	23	100.0	10	2	AAW16746	AAw16746 p185 bind
259	23	100.0	9	8	ADP86045	Adf86045 Human FGF	332	23	100.0	10	2	AAW16739	AAw16739 p185 bind
260	23	100.0	9	8	ADP86056	Adf86056 Human FGF	333	23	100.0	10	2	AAW16741	AAw16741 p185 bind
261	23	100.0	9	8	ADP86060	Adf86060 Human FGF	334	23	100.0	10	2	AAW16742	AAw16742 p185 bind
262	23	100.0	9	8	ADP09989	Adh09989 Backbone	335	23	100.0	10	2	AAW16744	AAw16744 p185 bind
263	23	100.0	9	8	ADP09987	Adh09987 Backbone	336	23	100.0	10	2	AAW16749	AAw16749 p185 bind
264	23	100.0	9	8	ADP124608	Adi24608 HIV-1 HLA	337	23	100.0	10	2	AAW16750	AAw16750 p185 bind
265	23	100.0	9	8	ADP100690	Adi00690 Human rin	338	23	100.0	10	2	AAW16753	AAw16753 p185 bind
266	23	100.0	9	8	ADK39160	Adk39160 Hepatitis	339	23	100.0	10	2	AAW16747	AAw16747 p185 bind
267	23	100.0	9	8	ADK37906	Adk37906 Hepatitis	340	23	100.0	10	2	AAW16740	AAw16740 p185 bind
268	23	100.0	9	8	ADK03285	Adk03285 Hepatitis	341	23	100.0	10	2	AAW16751	AAw16751 p185 bind
269	23	100.0	9	8	ADK09130	Adk09130 Human pap	342	23	100.0	10	2	AAW16745	AAw16745 p185 bind
270	23	100.0	9	8	ADK10587	Adk10587 Human pap	343	23	100.0	10	2	AAW16752	AAw16752 p185 bind
271	23	100.0	9	8	ADK09595	Adk09595 Human pap	344	23	100.0	10	2	AAW16743	AAw16743 p185 bind
272	23	100.0	9	8	ADW12725	Adm12725 MHC class	345	23	100.0	10	2	AAW03315	AAw03315 Tyrosinas
273	23	100.0	9	8	ADW12716	Adm12716 MHC class	346	23	100.0	10	2	AAW32725	AAw32725 Human pla
274	23	100.0	9	8	ADL19157	Adl19157 125P5C8 p	347	23	100.0	10	2	AAW25684	AAw25684 Antimicro
275	23	100.0	9	8	ADL19603	Adl19603 125P5C8 p	348	23	100.0	10	2	AAW37226	AAw37226 MDM2 bind
276	23	100.0	9	8	ADL19746	Adl19746 125P5C8 p	349	23	100.0	10	2	AAW37169	AAw37169 Human onc
277	23	100.0	9	8	ADN67919	Adn67919 Human 273	350	23	100.0	10	2	AAW96797	AAw96797 Lamprey I
278	23	100.0	9	8	ADN65877	Adn65877 HLA bindi	351	23	100.0	10	2	AAW96796	AAw96796 Lamprey I
279	23	100.0	9	8	ADN64416	Adn64416 HLA bindi	352	23	100.0	10	2	AAW96798	AAw96798 Lamprey I
280	23	100.0	9	8	ADQ38962	Ado38962 Anthrax p	353	23	100.0	10	2	AAW72987	AAw72987 Bovine be
281	23	100.0	9	8	ADQ38953	Ado38953 Anthrax p	354	23	100.0	10	2	AAW47097	AAw47097 Immunogen
282	23	100.0	9	8	ADQ43380	Ado43380 Antigenic	355	23	100.0	10	2	AAW46796	AAw46796 Immunogen
283	23	100.0	9	8	ADQ08713	Ado08713 HCV epito	356	23	100.0	10	2	AAW25554	AAw25554 Human MHC
284	23	100.0	9	8	ADQ08668	Ado08668 Hepatitis	357	23	100.0	10	2	AAW40648	AAw40648 S2 deriva
285	23	100.0	9	8	ADQ71598	Adq71598 Cancer re	358	23	100.0	10	3	AAW85376	AAw85376 IL-2 deri
286	23	100.0	9	8	ADQ72073	Adq72073 Cancer re	359	23	100.0	10	3	AAW93384	AAw93384 Binding m
287	23	100.0	9	8	ADQ68606	Adq68606 Cancer re	360	23	100.0	10	3	AAW93385	AAw93385 Binding m
288	23	100.0	9	8	ADQ72380	Adq72380 Cancer re	361	23	100.0	10	3	AAW17086	AAw17086 Mdm/hdm a
289	23	100.0	9	8	ADQ69652	Adq69652 Cancer re	362	23	100.0	10	3	AAW02722	AAw02722 Human thr
290	23	100.0	9	8	ADQ72453	Adq72453 Cancer re	363	23	100.0	10	3	AAW26393	AAw26393 Human CAS
291	23	100.0	9	8	ADQ69664	Adq69664 Cancer re	364	23	100.0	10	3	AAW27141	AAw27141 Human CAS
292	23	100.0	9	8	ADQ71463	Adq71463 Cancer re	365	23	100.0	10	3	AAW29987	AAw29987 Scaffold
293	23	100.0	9	8	ADQ69952	Adq69952 Cancer re	366	23	100.0	10	4	ABW55959	ABw55959 Vascular
294	23	100.0	9	8	ADQ70871	Adq70871 Cancer re	367	23	100.0	10	4	ABW68078	ABw68078 Antitumou
295	23	100.0	9	8	ADQ72479	Adq72479 Cancer re	368	23	100.0	10	4	ABW90971	ABw90971 Luteinisi
296	23	100.0	9	8	ADQ70322	Adq70322 Cancer re	369	23	100.0	10	4	ABW87239	ABw87239 Breast-ca
297	23	100.0	9	8	ADP25993	Adp25993 Plasmodiu	370	23	100.0	10	4	AAW94594	AAw94594 Human com
298	23	100.0	9	8	ADP25921	Adp25921 Plasmodiu	371	23	100.0	10	4	AAW94596	AAw94596 Human com
299	23	100.0	9	8	ADP26047	Adp26047 Plasmodiu	372	23	100.0	10	4	AAW94845	AAw94845 Human com
300	23	100.0	9	8	ADQ12824	Adq12824 Hepatitis	373	23	100.0	10	4	AAU23907	AAu23907 Human MHC
301	23	100.0	9	8	ADQ12754	Adq12754 Hepatitis	374	23	100.0	10	4	AAU24211	AAu24211 Human MHC
302	23	100.0	9	8	ADQ12823	Adq12823 Hepatitis	375	23	100.0	10	4	ABP16563	ABp16563 HIV A24 s
303	23	100.0	9	8	ADQ28798	Adq28798 Human cel	376	23	100.0	10	4	ABP16968	ABp16968 HIV B07 s
304	23	100.0	9	8	ADP80098	Adp80098 Human HLA	377	23	100.0	10	4	ABP23023	ABp23023 HIV A11 m
305	23	100.0	10	1	AAW10179	AAw10179 Sequence	378	23	100.0	10	4	ABP24000	ABp24000 HIV A11 m
306	23	100.0	10	1	AAW10176	AAw10176 Sequence	379	23	100.0	10	4	ABP16969	ABp16969 HIV B07 s
307	23	100.0	10	1	AAW10175	AAw10175 Sequence	380	23	100.0	10	4	ABP20961	ABp20961 HIV A03 m
308	23	100.0	10	1	AAW10533	AAw10533 1.6 subat	381	23	100.0	10	4	ABP16564	ABp16564 HIV A24 s
309	23	100.0	10	1	AAW10532	AAw10532 1.6 subat	382	23	100.0	10	4	AAW10630	AAw10630 HLA-A *02
310	23	100.0	10	1	AAW10261	AAw10261 Peptide a	383	23	100.0	10	4	AAW13190	AAw13190 HLA-A26 d
311	23	100.0	10	1	AAW10168	AAw10168 Sequence	384	23	100.0	10	4	AAW12977	AAw12977 HLA-A26 d
312	23	100.0	10	1	AAW10166	AAw10166 Sequence	385	23	100.0	10	4	AAW10909	AAw10909 HLA-B *07
313	23	100.0	10	1	AAW10169	AAw10169 Sequence	386	23	100.0	10	4	AAW09968	AAw09968 HLA-A1 de
314	23	100.0	10	1	AAW30545	AAw30545 Sequence	387	23	100.0	10	4	AAW12812	AAw12812 HLA-A26 d
315	23	100.0	10	1	AAW30525	AAw30525 Sequence	388	23	100.0	10	4	AAW10289	AAw10289 HLA-A *02
316	23	100.0	10	1	AAW40331	AAw40331 Sequence	389	23	100.0	10	4	AAW10317	AAw10317 HLA-A1 de
317	23	100.0	10	1	AAW40333	AAw40333 Sequence	390	23	100.0	10	4	AAW10910	AAw10910 HLA-B *07

391	23	100.0	10	4	AAW09747	Aam09747 HLA-A *02	464	23	100.0	10	6	ABJ66221	Abj66221 184P1E2-r
392	23	100.0	10	4	AAW09967	Aam09967 HLA-A1 de	465	23	100.0	10	6	ABJ67498	Abj67498 184P1E2-r
393	23	100.0	10	4	AAW10703	Aam10703 HLA-B *07	466	23	100.0	10	6	ABJ69492	Abj69492 184P1E2-r
394	23	100.0	10	4	ABB52377	Abb52377 Human API	467	23	100.0	10	6	ABJ66633	Abj66633 184P1E2-r
395	23	100.0	10	4	ABB52440	Abb52440 Human API	468	23	100.0	10	6	ABJ66805	Abj66805 184P1E2-r
396	23	100.0	10	5	ABR06172	Abbr06172 Gonadotro	469	23	100.0	10	6	ABJ69386	Abj69386 184P1E2-r
397	23	100.0	10	5	ABR73181	Abbr73181 Mdm/hdm a	470	23	100.0	10	6	ABJ68555	Abj68555 184P1E2-r
398	23	100.0	10	5	ABJ15205	Abj15205 Immunogen	471	23	100.0	10	6	ABJ58245	Abj58245 184P1E2-r
399	23	100.0	10	5	ABG93457	Abg93457 Alcr amin	472	23	100.0	10	6	ABJ68357	Abj68357 184P1E2-r
400	23	100.0	10	5	ABJ13899	Abj13899 Human 125	473	23	100.0	10	6	ABJ58624	Abj58624 184P1E2-r
401	23	100.0	10	5	ABJ11874	Abj11874 Human 125	474	23	100.0	10	6	ABJ57961	Abj57961 184P1E2-r
402	23	100.0	10	5	ABJ13671	Abj13671 Human 125	475	23	100.0	10	6	ABJ57757	Abj57757 184P1E2-r
403	23	100.0	10	5	ABJ14074	Abj14074 Human 125	476	23	100.0	10	6	ABJ67679	Abj67679 184P1E2-r
404	23	100.0	10	5	ABJ13684	Abj13684 Human 125	477	23	100.0	10	6	ABJ68832	Abj68832 184P1E2-r
405	23	100.0	10	5	ABJ11673	Abj11673 Human 125	478	23	100.0	10	6	ABJ69385	Abj69385 184P1E2-r
406	23	100.0	10	5	ABJ11969	Abj11969 Human 125	479	23	100.0	10	6	ABJ67907	Abj67907 184P1E2-r
407	23	100.0	10	5	ABJ13459	Abj13459 Human 125	480	23	100.0	10	6	ABJ66586	Abj66586 184P1E2-r
408	23	100.0	10	5	ABJ13896	Abj13896 Human 125	481	23	100.0	10	6	ABJ67609	Abj67609 184P1E2-r
409	23	100.0	10	5	ABJ06759	Abj06759 Hepatitis	482	23	100.0	10	6	ABJ65863	Abj65863 184P1E2-r
410	23	100.0	10	5	ABJ06227	Abj06227 Hepatitis	483	23	100.0	10	6	ABJ58400	Abj58400 184P1E2-r
411	23	100.0	10	5	ABJ07697	Abj07697 Hepatitis	484	23	100.0	10	6	ABJ68082	Abj68082 184P1E2-r
412	23	100.0	10	5	AAU93233	Aau93233 Granulocy	485	23	100.0	10	6	ABJ68164	Abj68164 184P1E2-r
413	23	100.0	10	5	AAE15696	Aae15696 Lamprey 1	486	23	100.0	10	6	AAQ31089	Aao31089 Human DS-
414	23	100.0	10	5	AAE15695	Aae15695 Lamprey 1	487	23	100.0	10	7	ADB79048	Adb79048 Human ant
415	23	100.0	10	5	ABG78903	Abg78903 Multiple	488	23	100.0	10	7	ADC09208	Adc09208 Epitope w
416	23	100.0	10	5	ABJ17093	Abj17093 Zinc tran	489	23	100.0	10	7	ADC39986	Adc39986 Human pro
417	23	100.0	10	5	ABJ15736	Abj15736 Zinc tran	490	23	100.0	10	7	ADD57477	Add57477 HLA bindi
418	23	100.0	10	5	ABJ17019	Abj17019 Zinc tran	491	23	100.0	10	7	ADD57022	Add57022 HLA bindi
419	23	100.0	10	5	ABJ15542	Abj15542 Zinc tran	492	23	100.0	10	7	ADD57478	Add57478 HLA bindi
420	23	100.0	10	6	ABR13871	Abri13871 Human can	493	23	100.0	10	7	ADD57828	Add57828 HLA bindi
421	23	100.0	10	6	ABR13940	Abri13940 Human can	494	23	100.0	10	7	ADD57021	Add57021 HLA bindi
422	23	100.0	10	6	ABR14555	Abri14555 Human can	495	23	100.0	10	7	ADD57020	Add57020 HLA bindi
423	23	100.0	10	6	ABR25335	Abri25335 Human can	496	23	100.0	10	7	ADD57827	Add57827 HLA bindi
424	23	100.0	10	6	ABR13738	Abri13738 Human can	497	23	100.0	10	7	ADD24677	Add24677 Lamprey 1
425	23	100.0	10	6	ABR14071	Abri14071 Human can	498	23	100.0	10	7	ADD24676	Add24676 Lamprey 1
426	23	100.0	10	6	ABR14077	Abri14077 Human can	499	23	100.0	10	7	ADD96565	Add96565 HIV-1 cro
427	23	100.0	10	6	ABR04038	Abri04038 Human can	500	23	100.0	10	7	ADD96449	Add96449 HIV-1 cro
428	23	100.0	10	6	ABR13298	Abri13298 Human can	501	23	100.0	10	7	ADB10722	Adb10722 Structura
429	23	100.0	10	6	ABR13704	Abri13704 Human can	502	23	100.0	10	7	ADB69879	Adb69879 Human 161
430	23	100.0	10	6	ABR14279	Abri14279 Human can	503	23	100.0	10	7	ADB69670	Adb69670 Human 161
431	23	100.0	10	6	ABR13318	Abri13318 Human can	504	23	100.0	10	7	ADJ94632	Adj94632 Human SIM
432	23	100.0	10	6	ABR14140	Abri14140 Human can	505	23	100.0	10	7	ADJ73335	Adj73335 Mdm/hdm a
433	23	100.0	10	6	ABR03638	Abri03638 Human can	506	23	100.0	10	8	ADP09831	Adp09831 Partial o
434	23	100.0	10	6	ABR13308	Abri13308 Human can	507	23	100.0	10	8	ADG98133	Adg98133 Apoptosis
435	23	100.0	10	6	ABR14326	Abri14326 Human can	508	23	100.0	10	8	ADG78885	Adg78885 Human p53
436	23	100.0	10	6	ABR13141	Abri13141 Human can	509	23	100.0	10	8	ADH09996	Adh09996 Backbone
437	23	100.0	10	6	ABR13670	Abri13670 Human can	510	23	100.0	10	8	ADH09997	Adh09997 Backbone
438	23	100.0	10	6	ABR14541	Abri14541 Human can	511	23	100.0	10	8	ADH09999	Adh09999 Backbone
439	23	100.0	10	6	ABR04206	Abri04206 Human can	512	23	100.0	10	8	ADH09995	Adh09995 Backbone
440	23	100.0	10	6	ABR13155	Abri13155 Human can	513	23	100.0	10	8	ADG94702	Adg94702 Human JAM
441	23	100.0	10	6	ABR13890	Abri13890 Human can	514	23	100.0	10	8	ADI24649	Adi24649 HIV-1 HLA
442	23	100.0	10	6	ABR14472	Abri14472 Human can	515	23	100.0	10	8	ADI24650	Adi24650 HIV-1 HLA
443	23	100.0	10	6	ABR03828	Abri03828 Human can	516	23	100.0	10	8	ADI82158	Adi82158 Plasma re
444	23	100.0	10	6	ABR14336	Abri14336 Human can	517	23	100.0	10	8	ADJ52969	Adj52969 CHI delet
445	23	100.0	10	6	ABR04044	Abri04044 Human can	518	23	100.0	10	8	ADJ51930	Adj51930 CHI delet
446	23	100.0	10	6	ABR13285	Abri13285 Human can	519	23	100.0	10	8	ADK15741	Adk15741 Fusion pr
447	23	100.0	10	6	ABR13555	Abri13555 Human can	520	23	100.0	10	8	ADI47088	Adi47088 Permeabil
448	23	100.0	10	6	ABR13690	Abri13690 Human can	521	23	100.0	10	8	ADK38039	Adk38039 Hepatitis
449	23	100.0	10	6	ABR13877	Abri13877 Human can	522	23	100.0	10	8	ADK38786	Adk38786 Hepatitis
450	23	100.0	10	6	ABR14090	Abri14090 Human can	523	23	100.0	10	8	ADK09188	Adk09188 Human pap
451	23	100.0	10	6	ABR24520	Abri24520 Human can	524	23	100.0	10	8	ADK05480	Adk05480 Hepatitis
452	23	100.0	10	6	ABR13505	Abri13505 Human can	525	23	100.0	10	8	ADK03263	Adk03263 Hepatitis
453	23	100.0	10	6	ABR13072	Abri13072 Human can	526	23	100.0	10	8	ADK03268	Adk03268 Hepatitis
454	23	100.0	10	6	ABR13469	Abri13469 Human can	527	23	100.0	10	8	ADK10596	Adk10596 Human pap
455	23	100.0	10	6	ABR59148	Abri59148 Alzheimer	528	23	100.0	10	8	ADK09671	Adk09671 Human pap
456	23	100.0	10	6	ABR58766	Abri58766 Alzheimer	529	23	100.0	10	8	ADK05480	Adk05480 Hepatitis
457	23	100.0	10	6	ABP74349	Abp74349 Human tyr	530	23	100.0	10	8	ADL21133	Adl21133 125P5C8 p
458	23	100.0	10	6	ABR47241	Abri47241 Staphyloc	531	23	100.0	10	8	ADL20921	Adl20921 125P5C8 p
459	23	100.0	10	6	ABR47280	Abri47280 Human imm	532	23	100.0	10	8	ADL19213	Adl19213 125P5C8 p
460	23	100.0	10	6	ABU70032	Abu70032 Human imm	533	23	100.0	10	8	ADL19118	Adl19118 125P5C8 p
461	23	100.0	10	6	ABU69916	Abu69916 Human imm	534	23	100.0	10	8	ADL21311	Adl21311 125P5C8 p
462	23	100.0	10	6	ABU03448	Abu03448 Human exp	535	23	100.0	10	8	ADL21136	Adl21136 125P5C8 p
463	23	100.0	10	6	ABJ57466	Abj57466 184P1E2-r	536	23	100.0	10	8	ADL20709	Adl20709 125P5C8 p

537	23	100.0	10	8	ADL18917	Adl18917 125P5C8 p	610	23	100.0	11	6	AAE34309	Aae34309 Human dop
538	23	100.0	10	8	ADL20908	Adl20908 125P5C8 p	611	23	100.0	11	6	ADA03306	Ada03306 Angiotens
539	23	100.0	10	8	ADN32081	Adn32081 Human Alz	612	23	100.0	11	6	ABR56676	Abr56676 Angiotens
540	23	100.0	10	8	ADN31802	Adn31802 Human Alz	613	23	100.0	11	6	ABR53325	Abr53325 Human CD4
541	23	100.0	10	8	ADO17375	Ado17375 Different	614	23	100.0	11	6	AAE31825	Aae31825 Androgen
542	23	100.0	10	8	ADO17682	Ado17682 Different	615	23	100.0	11	6	AAE31805	Aae31805 Androgen
543	23	100.0	10	8	ADN66262	Adn66262 Human 273	616	23	100.0	11	6	ABR59507	Abr59507 S. aureus
544	23	100.0	10	8	ADN66446	Adn66446 Human 273	617	23	100.0	11	6	ABO53728	Abo53728 Novel hum
545	23	100.0	10	8	ADN69764	Adn69764 Human 273	618	23	100.0	11	6	ADA23607	Ada23607 Alzheimer
546	23	100.0	10	8	ADN70291	Adn70291 Human 273	619	23	100.0	11	7	ADC07163	Adc07163 Painted l
547	23	100.0	10	8	ADN69699	Adn69699 Human 273	620	23	100.0	11	7	ADJ73501	Adj73501 Exemplary
548	23	100.0	10	8	ADN69624	Adn69624 Human 273	621	23	100.0	11	8	ADGI5910	Adgi5910 Synthetic
549	23	100.0	10	8	ADN48959	Adn48959 Peptide #	622	23	100.0	11	8	ADGI5914	Adgi5914 Synthetic
550	23	100.0	10	8	ADO49156	Ado49156 Human car	623	23	100.0	11	8	ADGI5913	Adgi5913 Synthetic
551	23	100.0	10	8	ADM95107	Adm95107 Murine MN	624	23	100.0	11	8	ADGI5912	Adgi5912 Synthetic
552	23	100.0	10	8	ADM98316	Adm98316 Humanised	625	23	100.0	11	8	ADGI5911	Adgi5911 Synthetic
553	23	100.0	10	8	ADP18399	Adp18399 Neurogene	626	23	100.0	11	8	ADH50032	Adh50032 Active G
554	23	100.0	10	8	ADO77933	Ado77933 Gonadotro	627	23	100.0	11	8	ADJ53135	Adj53135 CHI delet
555	23	100.0	10	8	ADQ72837	Adq72837 Cancer re	628	23	100.0	11	8	ADJ52096	Adj52096 CHI delet
556	23	100.0	10	8	ADQ73638	Adq73638 Cancer re	629	23	100.0	11	8	ADK38758	Adk38758 Hepatitis
557	23	100.0	10	8	ADQ69764	Adq69764 Cancer re	630	23	100.0	11	8	ADK38240	Adk38240 Hepatitis
558	23	100.0	10	8	ADQ673285	Adq673285 Cancer re	631	23	100.0	11	8	ADL15440	Adl15440 Human cel
559	23	100.0	10	8	ADQ73425	Adq73425 Cancer re	632	23	100.0	11	8	ADJ25786	Adj25786 MDM2 bind
560	23	100.0	10	8	ADQ68777	Adq68777 Cancer re	633	23	100.0	11	8	ADJ25784	Adj25784 MDM2 bind
561	23	100.0	10	8	ADP87277	Adp87277 Human cla	634	23	100.0	11	8	ADJ25912	Adj25912 MDM2 bind
562	23	100.0	10	8	ADP26044	Adp26044 Plasmodiu	635	23	100.0	11	8	ADJ25783	Adj25783 MDM2 bind
563	23	100.0	10	8	ADQ90923	Adq90923 Pancreatit	636	23	100.0	11	8	ADJ25787	Adj25787 MDM2 bind
564	23	100.0	10	8	ADR19445	Adr19445 TRPI deri	637	23	100.0	11	8	ADJ25785	Adj25785 MDM2 bind
565	23	100.0	10	8	ADR20482	Adr20482 Aromatic-	638	23	100.0	11	8	ADN64806	Adn64806 HLA bind1
566	23	100.0	10	8	ADR70840	Adr70840 Synthetic	639	23	100.0	11	8	ADO00848	Ado00848 Human CD4
567	23	100.0	11	1	AAP71510	Aap71510 Growth ho	640	23	100.0	11	8	ADQ11533	Adq11533 Myostatin
568	23	100.0	11	1	AAP71234	Aap71234 Luteinisi	641	23	100.0	11	8	ADR20392	Adr20392 Tyroptic d
569	23	100.0	11	1	AAAP82068	Aaap82068 Polyptepi	642	23	100.0	11	8	ADP80368	Adp80368 Human HLA
570	23	100.0	11	1	AAAR41331	Aaar41331 HIV gp120	643	23	100.0	11	8	ADM42685	Adm42685 Factor VI
571	23	100.0	11	2	AAAR74938	Aaar74938 H-CDR-3 o	644	23	100.0	11	8	ADM42645	Adm42645 Factor VI
572	23	100.0	11	2	AAAR8686	Aaar8686 Allergen	645	23	100.0	12	1	AAP93573	Aap93573 Extracell
573	23	100.0	11	2	AAW24022	Aaw24022 Variable	646	23	100.0	12	2	AAR83388	Aar83388 Kbm1-bind
574	23	100.0	11	2	AAW62112	Aaw62112 Human MDM	647	23	100.0	12	2	AAR83372	Aar83372 Kbm1-bind
575	23	100.0	11	2	AAW62115	Aaw62115 Human MDM	648	23	100.0	12	2	AAR83375	Aar83375 Kbm1-bind
576	23	100.0	11	2	AAW62111	Aaw62111 Human MDM	649	23	100.0	12	2	AAR83323	Aar83323 Kb-bindin
577	23	100.0	11	2	AAW62113	Aaw62113 Human MDM	650	23	100.0	12	2	AAR83344	Aar83344 Kb-bindin
578	23	100.0	11	2	AAW62114	Aaw62114 Human MDM	651	23	100.0	12	2	AAW32655	Aaw32655 Human pla
579	23	100.0	11	2	AAAY25553	Aay25553 Human MHC	652	23	100.0	12	2	AAW32654	Aaw32654 Human pla
580	23	100.0	11	3	AAAY85394	Aay85394 IL-2 deri	653	23	100.0	12	2	AAW16160	Aaw16160 Peptide c
581	23	100.0	11	3	AAAY93383	Aay93383 Binding m	654	23	100.0	12	2	AAW18715	Aaw18715 C-src exo
582	23	100.0	11	3	AAAY93379	Aay93379 Binding m	655	23	100.0	12	2	AAW81309	Aaw81309 Human iNO
583	23	100.0	11	3	AAAY93378	Aay93378 Binding m	656	23	100.0	12	2	AAW81249	Aaw81249 Human iNO
584	23	100.0	11	3	AAAY93377	Aay93377 Binding m	657	23	100.0	12	2	AAW68800	Aaw68800 Peptide b
585	23	100.0	11	3	AAAY93393	Aay93393 Binding m	658	23	100.0	12	2	AAW71785	Aaw71785 Mimotope
586	23	100.0	11	3	AAAY93390	Aay93390 Binding m	659	23	100.0	12	2	AAW71784	Aaw71784 Mimotope
587	23	100.0	11	3	AAAY93381	Aay93381 Binding m	660	23	100.0	12	2	AAW58287	Aaw58287 IL-18rti b
588	23	100.0	11	3	AAAY93391	Aay93391 Binding m	661	23	100.0	12	2	AAW37190	Aaw37190 Human onc
589	23	100.0	11	3	AAAY93392	Aay93392 Binding m	662	23	100.0	12	2	AAW37184	Aaw37184 Human onc
590	23	100.0	11	3	AAAY93382	Aay93382 Binding m	663	23	100.0	12	2	AAW37191	Aaw37191 Human onc
591	23	100.0	11	3	AAAY93380	Aay93380 Binding m	664	23	100.0	12	2	AAW37221	Aaw37221 MDM2 bind
592	23	100.0	11	3	AAAB17269	Aab17269 Anti-canc	665	23	100.0	12	2	AAW37195	Aaw37195 Human onc
593	23	100.0	11	3	AAAY86558	Aay86558 Human gen	666	23	100.0	12	2	AAW37171	Aaw37171 Human onc
594	23	100.0	11	3	AAAB52116	Aab52116 Human sec	667	23	100.0	12	2	AAW37182	Aaw37182 Human onc
595	23	100.0	11	3	AAAB15239	Aab15239 Specific	668	23	100.0	12	2	AAW37181	Aaw37181 Human p53
596	23	100.0	11	4	AAAB92383	Aab92383 Miscellan	669	23	100.0	12	2	AAW37188	Aaw37188 Human onc
597	23	100.0	11	4	AAAB18965	Aab18965 HIV B62 s	670	23	100.0	12	2	AAW37196	Aaw37196 Human onc
598	23	100.0	11	4	AAAJ02147	Aaj02147 Hepatitis	671	23	100.0	12	2	AAW37183	Aaw37183 Human onc
599	23	100.0	11	5	AAAB73347	Aab73347 Exemplary	672	23	100.0	12	2	AAW37220	Aaw37220 MDM2 bind
600	23	100.0	11	5	ABPA47662	Abp47662 N. mening	673	23	100.0	12	2	AAW37170	Aaw37170 Human onc
601	23	100.0	11	5	ABG97334	Abg97334 Human leu	674	23	100.0	12	2	AAW37189	Aaw37189 Human onc
602	23	100.0	11	5	ABJ07782	Abj07782 Hepatitis	675	23	100.0	12	2	AAW37222	Aaw37222 MDM2 bind
603	23	100.0	11	5	ABJ06960	Abj06960 Hepatitis	676	23	100.0	12	2	AAAY25552	Aay25552 Human MHC
604	23	100.0	11	5	AAU93631	Aau93631 Granulocy	677	23	100.0	12	2	AAAY09933	Aay09933 Interleuk
605	23	100.0	11	5	AAU96261	Aau96261 Class I G	678	23	100.0	12	3	AAAY44672	Aay44672 N-termina
606	23	100.0	11	5	AAU52269	Aau52269 Miniature	679	23	100.0	12	3	AAAY85378	Aay85378 IL-2 deri
607	23	100.0	11	5	ABG67493	Abg67493 Human ADP	680	23	100.0	12	3	AAAY66808	Aay66808 T cell an
608	23	100.0	11	5	AAO18916	Aao18916 Human but	681	23	100.0	12	3	AAAY85107	Aay85107 HBV surfa
609	23	100.0	11	6	AAE34237	Aae34237 Human dop	682	23	100.0	12	3	AAAY85105	Aay85105 HBV surfa

683	23	100.0	12	3	AAV85104	Aay85104	HBV surfa	756	23	100.0	12	7	ADE15576	Melanoma
684	23	100.0	12	3	AAV93376	Aay93376	Binding m	757	23	100.0	12	7	ADE15578	Melanoma
685	23	100.0	12	3	AAV93389	Aay93389	Binding m	758	23	100.0	12	7	ADE12093	Human sec
686	23	100.0	12	3	AAV93387	Aay93387	Binding m	759	23	100.0	12	7	ADE39750	Peptide p
687	23	100.0	12	3	AAV93388	Aay93388	Binding m	760	23	100.0	12	7	ADJ03010	Human mon
688	23	100.0	12	3	AAV93386	Aay93386	Binding m	761	23	100.0	12	7	ADJ73329	Mdm/hdm a
689	23	100.0	12	3	AAV17076	Aab17076	Mdm/hdm a	762	23	100.0	12	7	ADJ73326	Mdm/hdm a
690	23	100.0	12	3	AAV17087	Aab17087	Mdm/hdm a	763	23	100.0	12	7	ADJ72921	Interleuk
691	23	100.0	12	3	AAV17089	Aab17089	Mdm/hdm a	764	23	100.0	12	7	ADJ73330	Mdm/hdm a
692	23	100.0	12	3	AAV17081	Aab17081	Mdm/hdm a	765	23	100.0	12	7	ADJ72619	Interleuk
693	23	100.0	12	3	AAV17078	Aab17078	Mdm/hdm a	766	23	100.0	12	7	ADJ73339	Mdm/hdm a
694	23	100.0	12	3	AAV17090	Aab17090	Mdm/hdm a	767	23	100.0	12	7	ADJ72801	Interleuk
695	23	100.0	12	3	AAV17079	Aab17079	Mdm/hdm a	768	23	100.0	12	7	ADJ72622	Interleuk
696	23	100.0	12	3	AAV17088	Aab17088	Mdm/hdm a	769	23	100.0	12	7	ADJ73324	Mdm/hdm a
697	23	100.0	12	3	AAV17712	Aab17712	Il-1 anta	770	23	100.0	12	7	ADJ73336	Mdm/hdm a
698	23	100.0	12	3	AAV17075	Aab17075	Mdm/hdm a	771	23	100.0	12	7	ADJ73328	Mdm/hdm a
699	23	100.0	12	3	AAV17080	Aab17080	Mdm/hdm a	772	23	100.0	12	7	ADJ73327	Mdm/hdm a
700	23	100.0	12	3	AAV17077	Aab17077	Mdm/hdm a	773	23	100.0	12	7	ADJ73337	Mdm/hdm a
701	23	100.0	12	3	AAV76424	Aay76424	Fragment	774	23	100.0	12	7	ADJ72608	Interleuk
702	23	100.0	12	3	AAV02747	Aab02747	Human thr	775	23	100.0	12	7	ADJ72929	Interleuk
703	23	100.0	12	3	AAV93867	Aay93867	Reactive	776	23	100.0	12	7	ADJ73338	Mdm/hdm a
704	23	100.0	12	3	AAV93837	Aay93837	Reactive	777	23	100.0	12	7	ADJ73325	Mdm/hdm a
705	23	100.0	12	3	AAV32176	Aab32176	Peptide m	778	23	100.0	12	8	ADH50043	Active G
706	23	100.0	12	3	AAV94486	Aay94486	Human som	779	23	100.0	12	8	ADI34263	12 mer pe
707	23	100.0	12	3	AAV30372	Aab30372	T. brucei	780	23	100.0	12	8	ADI34264	Wild type
708	23	100.0	12	3	AAV23185	Aab23185	Hep47-bin	781	23	100.0	12	8	ADJ52964	CH1 delet
709	23	100.0	12	4	AAV07310	Aae07310	Human MMP	782	23	100.0	12	8	ADJ52964	CH1 delet
710	23	100.0	12	4	AAV86005	Aae86005	DCM-assoc	783	23	100.0	12	8	ADJ52964	CH1 delet
711	23	100.0	12	4	ABP24353	Abp24353	HIV A24 m	784	23	100.0	12	8	ADJ52959	CH1 delet
712	23	100.0	12	4	ABP24364	Abp24364	HIV A24 m	785	23	100.0	12	8	ADJ52243	CH1 delet
713	23	100.0	12	5	ABG06167	Abg06167	Gonadotro	786	23	100.0	12	8	ADJ52556	CH1 delet
714	23	100.0	12	5	ABG78401	Abg78401	Memapsin	787	23	100.0	12	8	ADJ52971	CH1 delet
715	23	100.0	12	5	AAU80738	Aau80738	Javelin p	788	23	100.0	12	8	ADJ52962	CH1 delet
716	23	100.0	12	5	AAU80737	Aau80737	Javelin p	789	23	100.0	12	8	ADJ52963	CH1 delet
717	23	100.0	12	5	AAU80736	Aau80736	Javelin p	790	23	100.0	12	8	ADJ52972	CH1 delet
718	23	100.0	12	5	ABB05292	Abb05292	Collar so	791	23	100.0	12	8	ADJ52970	CH1 delet
719	23	100.0	12	5	ABB05293	Abb05293	Collar so	792	23	100.0	12	8	ADJ52254	CH1 delet
720	23	100.0	12	5	ABV72608	Abb72608	Interleuk	793	23	100.0	12	8	ADJ52958	CH1 delet
721	23	100.0	12	5	ABV73170	Abb73170	Mdm/hdm a	794	23	100.0	12	8	ADJ52961	CH1 delet
722	23	100.0	12	5	ABV73175	Abb73175	Mdm/hdm a	795	23	100.0	12	8	ADJ52973	CH1 delet
723	23	100.0	12	5	ABV73172	Abb73172	Mdm/hdm a	796	23	100.0	12	8	ADJ52257	CH1 delet
724	23	100.0	12	5	ABV73185	Abb73185	Mdm/hdm a	797	23	100.0	12	8	ADJ52436	CH1 delet
725	23	100.0	12	5	ABV73184	Abb73184	Mdm/hdm a	798	23	100.0	12	8	ADJ51527	CH1 delet
726	23	100.0	12	5	ABV73174	Abb73174	Mdm/hdm a	799	23	100.0	12	8	ADJ51921	CH1 delet
727	23	100.0	12	5	ABV73176	Abb73176	Mdm/hdm a	800	23	100.0	12	8	ADJ51922	CH1 delet
728	23	100.0	12	5	ABV73183	Abb73183	Mdm/hdm a	801	23	100.0	12	8	ADJ51920	CH1 delet
729	23	100.0	12	5	ABV73173	Abb73173	Mdm/hdm a	802	23	100.0	12	8	ADJ51923	CH1 delet
730	23	100.0	12	5	ABV73171	Abb73171	Mdm/hdm a	803	23	100.0	12	8	ADJ51932	CH1 delet
731	23	100.0	12	5	ABV73182	Abb73182	Mdm/hdm a	804	23	100.0	12	8	ADJ51216	CH1 delet
732	23	100.0	12	5	AAE29104	Aae29104	Human DBH	805	23	100.0	12	8	ADJ51931	CH1 delet
733	23	100.0	12	5	AAE29118	Aae29118	Human DBH	806	23	100.0	12	8	ADJ51919	CH1 delet
734	23	100.0	12	5	ABJ05649	Abj05649	Peptide m	807	23	100.0	12	8	ADJ51924	CH1 delet
735	23	100.0	12	5	ABG60547	Abg60547	Selective	808	23	100.0	12	8	ADJ51934	CH1 delet
736	23	100.0	12	5	AAU96272	Aau96272	Class I G	809	23	100.0	12	8	ADJ51925	CH1 delet
737	23	100.0	12	5	ABG68991	Abg68991	Signature	810	23	100.0	12	8	ADJ51519	CH1 delet
738	23	100.0	12	5	ABB83231	Abb83231	Hepatitis	811	23	100.0	12	8	ADJ51219	CH1 delet
739	23	100.0	12	5	ABG30921	Abg30921	DR2*0101	812	23	100.0	12	8	ADJ51205	CH1 delet
740	23	100.0	12	6	AAE30893	Aae30893	MDM2-bind	813	23	100.0	12	8	ADJ51399	CH1 delet
741	23	100.0	12	6	AAE30886	Aae30886	MDM2-bind	814	23	100.0	12	8	ADJ51933	CH1 delet
742	23	100.0	12	6	AAE30888	Aae30888	MDM2-bind	815	23	100.0	12	8	ADJ57768	Surface g
743	23	100.0	12	6	AAE30890	Aae30890	MDM2-bind	816	23	100.0	12	8	ADJ57296	Provasopr
744	23	100.0	12	6	AAE30887	Aae30887	MDM2-bind	817	23	100.0	12	8	ADJ23636	RAD51C pr
745	23	100.0	12	6	AAE30883	Aae30883	p300-bind	818	23	100.0	12	8	ADJ23639	RAD51C pr
746	23	100.0	12	6	AAE30892	Aae30892	MDM2-bind	819	23	100.0	12	8	ADN96401	Immature
747	23	100.0	12	6	AAE34248	Aae34248	Human bra	820	23	100.0	12	8	ADN31958	Eph famil
748	23	100.0	12	6	ABP68069	Abp68069	Bacillus	821	23	100.0	12	8	ADN65746	HIA bindi
749	23	100.0	12	6	ABP83368	Abp83368	G. protein	822	23	100.0	12	8	ADR20485	Aromatic-
750	23	100.0	12	6	ABP71371	Abp71371	Anti-OPGL	823	23	100.0	13	2	AAR49316	Beta2m po
751	23	100.0	12	6	ABR00856	AbR00856	Bioactive	824	23	100.0	13	2	AAR57883	LCAR mini
752	23	100.0	12	7	ADC28198	Adc28198	Synthetic	825	23	100.0	13	2	AAR70250	Pan DR-bl
753	23	100.0	12	7	ABR63069	AbR63069	Pathogen	826	23	100.0	13	2	AAW25682	Antimicro
754	23	100.0	12	7	ADD25408	Add25408	Complemen	827	23	100.0	13	2	AAW12897	Antimicro
755	23	100.0	12	7	ADD25407	Add25407	Complemen	828	23	100.0	13	2	AAW26066	M30 deriv

829	23	100.0	13	2	AAW22121	Aaw22121 Padre (pa	902	23	100.0	13	7	ADE36944	Interfacci
830	23	100.0	13	2	AAW67036	Aaw67036 Polioviru	903	23	100.0	13	7	AD37005	Polycarbo
831	23	100.0	13	2	AAW21821	Aay21821 Mimetic p	904	23	100.0	13	7	AD10455	Serum alb
832	23	100.0	13	2	AAW25551	Aay25551 Human MHC	905	23	100.0	13	7	AD157984	Anti-TNF-
833	23	100.0	13	2	AAW85093	Aay85093 HBV surfa	906	23	100.0	13	7	AD157985	Anti-TNF-
834	23	100.0	13	3	AAW85092	Aay85092 HBV surfa	907	23	100.0	13	7	AD157986	Anti-TNF-
835	23	100.0	13	3	AAW85095	Aay85095 HBV surfa	908	23	100.0	13	7	ADW75100	Potential
836	23	100.0	13	3	AAW802721	Aab02721 Human thr	909	23	100.0	13	7	ADW75629	Potential
837	23	100.0	13	3	AAW52558	Aay52558 Universal	910	23	100.0	13	7	ADW74835	Potential
838	23	100.0	13	3	AAW57799	Aay57799 TPAM-inte	911	23	100.0	13	8	ADH94540	Lecithin
839	23	100.0	13	3	AAW00067	Aab00067 VRN2 pept	912	23	100.0	13	8	ADK39825	PNA molec
840	23	100.0	13	3	AAW20975	Aab20975 Phosphory	913	23	100.0	13	8	ADK39871	PNA molec
841	23	100.0	13	3	AAW36289	Aab36289 Promiscuo	914	23	100.0	13	8	ADJ50658	Human ser
842	23	100.0	13	3	AAW08611	Aab08611 Peptide i	915	23	100.0	13	8	ADJ93375	Human BGS
843	23	100.0	13	4	AAW20427	Aab20427 Anti-FIX/	916	23	100.0	13	8	ADJ73543	Cyclic hu
844	23	100.0	13	4	AAW20390	Aab20390 Anti-FIX/	917	23	100.0	13	8	ADM06893	Pan DR bi
845	23	100.0	13	4	AAW99710	Aab99710 Pan-DR-bi	918	23	100.0	13	8	ADO57845	Porcine f
846	23	100.0	13	4	AAW05735	Aae05735 Complemen	919	23	100.0	13	8	ADO57860	Human for
847	23	100.0	13	4	AAW73644	Aab73644 Pan-DR bi	920	23	100.0	13	8	ADO24819	Polioviru
848	23	100.0	13	4	AAW86009	Aab86009 DCM-assoc	921	23	100.0	13	8	ADQ27050	Human hol
849	23	100.0	13	4	AAW86007	Aab86007 DCM-assoc	922	23	100.0	13	8	ADQ27052	Human hol
850	23	100.0	13	4	AAW86006	Aab86006 DCM-assoc	923	23	100.0	13	8	ADP73620	PADRE T c
851	23	100.0	13	4	AAW20154	Aab20154 PADRE pep	924	23	100.0	13	8	ADP48563	Pan DR ep
852	23	100.0	13	4	ABP17586	Abp17586 HIV B27 s	925	23	100.0	13	8	ADQ90852	Mouse com
853	23	100.0	13	4	ABP17587	Abp17587 HIV B27 s	926	23	100.0	13	8	ADR05553	Novel ssd
854	23	100.0	13	5	AAW48084	Aam48084 Tie-1 bin	927	23	100.0	13	8	ADP79777	HLA epit
855	23	100.0	13	5	ABP68836	Abp68836 Marine an	928	23	100.0	14	1	ADP61005	Disco
856	23	100.0	13	5	AAW80293	Aau80293 Pan DR ep	929	23	100.0	14	1	ADP61006	Disco
857	23	100.0	13	5	ABW54330	Abp54330 Human HGP	930	23	100.0	14	2	AAW62082	Porcine p
858	23	100.0	13	5	ABG31776	Abg31776 Pan DR ep	931	23	100.0	14	2	AAW69553	Human CD4
859	23	100.0	13	5	AAW26369	Aae26369 PADRE pep	932	23	100.0	14	2	AAW91596	Synthetic
860	23	100.0	13	5	AAW52369	Abp52369 Human C-S	933	23	100.0	14	2	AAW16718	p185 bind
861	23	100.0	13	5	ABW97699	Abp97699 Human pro	934	23	100.0	14	2	AAW16780	p185 bind
862	23	100.0	13	5	ABW97697	Abp97697 Human pro	935	23	100.0	14	2	AAW16709	p185 bind
863	23	100.0	13	5	ADG67226	Adg67226 Human 5G1	936	23	100.0	14	2	AAW16769	p185 bind
864	23	100.0	13	5	ADG66202	Adg66202 Human pro	937	23	100.0	14	2	AAW16773	p185 bind
865	23	100.0	13	5	ADG67227	Adg67227 Human 5G1	938	23	100.0	14	2	AAW16712	p185 bind
866	23	100.0	13	5	ADG66203	Adg66203 Human pro	939	23	100.0	14	2	AAW16775	p185 bind
867	23	100.0	13	5	ADG67228	Adg67228 Human 5G1	940	23	100.0	14	2	AAW16783	p185 bind
868	23	100.0	13	5	ADG66201	Adg66201 Human pro	941	23	100.0	14	2	AAW16713	p185 bind
869	23	100.0	13	5	ADG67229	Adg67229 Human 5G1	942	23	100.0	14	2	AAW16777	p185 bind
870	23	100.0	13	6	ABO10766	Abp10766 Murine E9	943	23	100.0	14	2	AAW16720	p185 bind
871	23	100.0	13	6	ABG75574	Abg75574 CDR3 pept	944	23	100.0	14	2	AAW16776	p185 bind
872	23	100.0	13	6	ADA03312	Ada03312 Angiotens	945	23	100.0	14	2	AAW16710	p185 bind
873	23	100.0	13	6	ADA03313	Ada03313 Angiotens	946	23	100.0	14	2	AAW16708	p185 bind
874	23	100.0	13	6	ADA03310	Ada03310 Angiotens	947	23	100.0	14	2	AAW16771	p185 bind
875	23	100.0	13	6	ADA03311	Ada03311 Angiotens	948	23	100.0	14	2	AAW16707	p185 bind
876	23	100.0	13	6	ADA03311	Ada03311 Angiotens	949	23	100.0	14	2	AAW16716	p185 bind
877	23	100.0	13	6	ABR56680	Abp56680 Angiotens	950	23	100.0	14	2	AAW16770	p185 bind
878	23	100.0	13	6	ABR56677	Abp56677 Angiotens	951	23	100.0	14	2	AAW16774	p185 bind
879	23	100.0	13	6	ABR56682	Abp56682 Angiotens	952	23	100.0	14	2	AAW16715	p185 bind
880	23	100.0	13	6	ABR56675	Abp56675 Angiotens	953	23	100.0	14	2	AAW16717	p185 bind
881	23	100.0	13	6	ABR56681	Abp56681 Angiotens	954	23	100.0	14	2	AAW16781	p185 bind
882	23	100.0	13	6	ABP72696	Abp72696 T cell ep	955	23	100.0	14	2	AAW16784	p185 bind
883	23	100.0	13	6	ABR44710	Abp44710 Murine E9	956	23	100.0	14	2	AAW16714	p185 bind
884	23	100.0	13	6	ABR64118	Abp64118 E. coli g	957	23	100.0	14	2	AAW16779	p185 bind
885	23	100.0	13	6	ABP98589	Abp98589 Beta-bar	958	23	100.0	14	2	AAW16719	p185 bind
886	23	100.0	13	6	ABP76124	Abp76124 Human GEN	959	23	100.0	14	2	AAW16706	p185 bind
887	23	100.0	13	6	ABP76126	Abp76126 Human GEN	960	23	100.0	14	2	AAW16711	p185 bind
888	23	100.0	13	6	ABP76127	Abp76127 Human GEN	961	23	100.0	14	2	AAW16772	p185 bind
889	23	100.0	13	6	ABP76125	Abp76125 Human GEN	962	23	100.0	14	2	AAW16782	p185 bind
890	23	100.0	13	6	AAO30456	Aao30456 Pan DR ep	963	23	100.0	14	2	AAW16721	p185 bind
891	23	100.0	13	6	AAO30463	Aao30463 Pan DR ep	964	23	100.0	14	2	AAW16778	p185 bind
892	23	100.0	13	7	ABR82484	Abp82484 Universal	965	23	100.0	14	2	AAW24020	Variable
893	23	100.0	13	7	ADC36627	Adc36627 Overlappi	966	23	100.0	14	2	AAW25683	Antimicro
894	23	100.0	13	7	ADC36629	Adc36629 Overlappi	967	23	100.0	14	2	AAW09827	UDP-gluc
895	23	100.0	13	7	ADC36628	Adc36628 Overlappi	968	23	100.0	14	2	AAW24946	C3/C4/C5-
896	23	100.0	13	7	ADC81611	Adc81611 Universal	969	23	100.0	14	2	AAW09477	Thrombopo
897	23	100.0	13	7	ABW00738	Abw00738 Human MMP	970	23	100.0	14	2	AAW16325	Murine AR
898	23	100.0	13	7	ABW00739	Abw00739 Human MMP	971	23	100.0	14	2	AAW01827	CD44 epit
899	23	100.0	13	7	ADE36941	Ade36941 Interfacci	972	23	100.0	14	2	AAW01828	CD44 epit
900	23	100.0	13	7	ADE36957	Ade36957 Interfacci	973	23	100.0	14	2	AAW36764	Thrombopo
901	23	100.0	13	7	ADE36943	Ade36943 Interfacci	974	23	100.0	14	2	AAW36628	Thrombopo

975 23 100.0 14 2 AAW50952 Somatosta
976 23 100.0 14 2 AAW52538 Cyclic pe
977 23 100.0 14 2 AAW52539 Cyclic pe
978 23 100.0 14 2 AAW53471 P2 predom
979 23 100.0 14 2 AAW37197 Human onc
980 23 100.0 14 2 AAY25550 Human MHC
981 23 100.0 14 2 AAY08740 TUMV Nla
982 23 100.0 14 2 AAY08736 TEV Nla p
983 23 100.0 14 2 AAY08735 TUMV Nla
984 23 100.0 14 2 AAY08737 PVY Nla p
985 23 100.0 14 2 AAY08733 WMV2 Nla
986 23 100.0 14 2 AAY08734 Plum pox
987 23 100.0 14 2 AAY08738 PFSV Nla
988 23 100.0 14 2 AAY17346 Antimicro
989 23 100.0 14 2 AAY17345 Antimicro
990 23 100.0 14 2 AAY42865 Vpr-bindl
991 23 100.0 14 2 AAY42864 Vpr-bindl
992 23 100.0 14 2 AAY42867 Vpr-bindl
993 23 100.0 14 3 AAY79175 Mouse ARP
994 23 100.0 14 3 AAB17012 TPO-mimic
995 23 100.0 14 3 AAB13866 L2/HNK1 c
996 23 100.0 14 3 AAY86562 Human gen
997 23 100.0 14 4 AAB97448 Peptide n
998 23 100.0 14 4 AAB20428 Anti-FIX/
999 23 100.0 14 4 AAM98830 Human pep
1000 23 100.0 14 4 AAM98837 Human pep

ALIGNMENTS

RESULT 1
AAR11090
ID AAR11090 standard; protein; 8 AA.
XX
AC AAR11090;
XX
DT 24-MAY-1991 (first entry)
XX
DE LHRH pseudopeptide analogue #2.
XX
KW Leutinizing hormone releasing hormone; pseudopeptide; agonist;
KW antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= (N-(alpha)-morpholinocarbonyl)-Phe
FT FT
FT Modified-site 5 /label= D-Trp
FT FT
FT Modified-site 8 /label= Pro-NH-Et
FT FT
XX EP417454-A.
XX
XX 20-MAR-1991.
XX
XX 01-AUG-1990; 90EP-00114752.
XX
XX 07-AUG-1989; 89US-00390269.
XX 10-JUL-1990; 90US-00548511.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Haviv F, Palabrica CA, Greer J, Fitzpatrick TD;
XX WPI; 1991-081768/12.
XX
XX Reduced size Pseudo peptide LHRH analogues - used as LHRH agonists or
XX antagonists e.g. in treatment of prostate cancer and benign prostatic
XX hypertrophy.

PS Claim 4; Page 86; 90pp; English.
XX
CC This is one of 57 specific examples of highly generic reduced size LHRH
CC analogues. It is based on amino acid residues 2 to 9 of natural LHRH. The
CC analogues can be used for treating diseases resulting from gonadal
CC hormone over- or under-production in either sex, controlling
CC reproduction, as fertility promoters when administered in pulses or for
CC reducing dihydrotestosterone levels. See also AAR11089 and AAR11091-4
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
Db 1 FWSYWLRP 8
RESULT 2
AAR35839
ID AAR35839 standard; protein; 8 AA.
XX
AC AAR35839;
XX
DT 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
DE Hepatitis C virus (HCV) epitope Epc.
XX
KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
PN WO9300365-A2.
XX
PD 07-JAN-1993.
XX
PF 24-JUN-1992; 92WO-US005388.
XX
PR 24-JUN-1991; 91US-00722489.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chien DY, Rutter W;
XX
DR WPI; 1993-036334/04.
XX
PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.
XX
PS Example A; Page 35; 80pp; English.
XX
CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In
CC the epitope mapping experiment three different samples of anti-sera were
CC reacted with the peptide octamer, and then incubated with HRP-labelled
CC goat anti-human Ig antisera, to enable detection of binding. This epitope
CC starts from amino acid 465 of the HCV polypeptide. This was found to be a
CC particularly strong epitope. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
Db 1 FDQGWGPI 8

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RESULT 3
AAW19954
ID AAW19954 standard; peptide; 8 AA.
XX
AC AAW19954;
XX
DT 10-NOV-1997 (first entry)
XX
DE Heat shock protein binding domain.
XX
KW Vaccine; immunotherapy; heat shock protein; BiP; cancer;
XX infectious disease.
XX
OS Synthetic.
XX
PN WO9706821-A1.
XX
PD 27-FEB-1997.
XX
PF 16-AUG-1996; 96WO-US013363.
XX
PR 18-AUG-1995; 95US-0002479P.
XX 18-AUG-1995; 95US-0002490P.
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Rothman JE, Hartl FU, Hoe MH, Houghton A, Takeuchi Y, Mayhew M;
XX WPI; 1997-165035/15.
XX
DR Compens. for inducing immune response contg. antigen and heat shock
XX protein - also new hybrid peptide and related nucleic acid, for treatment
XX of infectious diseases and tumours.
XX
PS Disclosure; Page 12; 58pp; English.
XX
CC A heat shock protein (HSP) binding domain (AAW19954) can be used as a
CC component of a hybrid target antigen that also comprises an immunogenic
CC domain. The hybrid antigen is combined in vitro with a HSP to form a
CC complex that, when administered to a subject, induces an immune response.
CC Target antigen-HSP complexes can be used to treat infectious diseases, or
CC to treat cancers by eliciting an immune response to a tumour antigen.
CC Alternatively, a nucleic acid encoding the HSP and the target antigen is
CC administered such that the HSP and target antigen bind in situ
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 1 FWGLWPWE 8

RESULT 4
AAW37211
ID AAW37211 standard; peptide; 8 AA.
XX
AC AAW37211;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human oncogenic protein MDM2 binding N-acylated peptide derivative 14.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection.
XX
OS Synthetic.
XX Homo sapiens.
XX

```

```

PH Key Location/Qualifiers
FT Modified-site 1
FT FT /note= "N-terminal acetyl"
FT Modified-site 3
FT FT /label= Aib
FT Modified-site 6
FT FT /note= "2-Aminoisobutyric acid"
FT FT /label= Aib
FT Modified-site 8
FT FT /note= "2-Aminoisobutyric acid"
FT FT /note= "C-terminal amide"
XX
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX Garcia-Echeverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Example 5; Page 25; 45pp; English.
XX
XX This is a MDM2 binding peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of
XX MDM2/p53 binding. They may also be used to purify binding partners
XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
XX cancer and leukaemia patients and for treatment or prevention of disease
XX involving p53/MDM2 interactions, especially tumours and viral infections.
XX The peptides can be administered nasally, rectally, orally or by
XX injection. By interfering with MDM2/p53 interaction, the peptides can
XX activate p53 function and accumulation in normal cells. The peptides
XX which mimic the MDM2 binding site in p53, have a significantly greater
XX blocking activity compared with wild-type p53
XX
XX Sequence 8 AA;
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
Db 1 FMXYWXXG 8

RESULT 5
AAW37218
ID AAW37218 standard; peptide; 8 AA.
XX
AC AAW37218;
XX
DT 20-JUL-1998 (first entry)
XX
XX Human oncogenic protein MDM2 binding peptide derivative 11.
XX

```

```

KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 3
FT /label= Aib
FT /note= "2-Aminoisobutyric acid"
FT Modified-site 8
FT /note= "C-terminal amide"
FT
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX Garcia-Scheverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Example 6; Page 26; 45pp; English.
XX
XX This is a MDM2 binding peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of
XX MDM2/p53 binding. They may also be used to purify binding partners
XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
XX cancer and leukaemia patients and for treatment or prevention of disease
XX involving p53/MDM2 interactions, especially tumours and viral infections.
XX The peptides can be administered nasally, rectally, orally or by
XX injection. By interfering with MDM2/p53 interaction, the peptides can
XX activate p53 function and accumulation in normal cells. The peptides
XX which mimic the MDM2 binding site in p53, have a significantly greater
XX blocking activity compared with wild-type p53
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 23; DB 2; Length 8;
XX Best Local Similarity 37.5%; Pred. NO. 1.8e+06;
XX Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FXXKXWXXX 8
XX |:|:|:|:|
XX 1 FMKYWEGL 8
XX
XX RESULT 6
XX AAW37174
XX ID AAW37174 standard; peptide; 8 AA.
XX AC AAW37174;
XX XX
XX 20-JUL-1998 (first entry)

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XX Human oncogenic protein MDM2 binding generic peptide sequence 2.
DE
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 2
FT /label= Met, Ile, Thr, Arg, Ala or Ser
FT /note= "preferentially Met"
FT Misc-difference 3
FT /label= Arg, His, Glu, Cys, Ser or Asp
FT /note= "preferentially Asp"
FT Misc-difference 4
FT /label= His, Phe or Tyr
FT Misc-difference 6
FT /label= Glu, Thr, Ala, Phe or Ser
FT /note= "preferentially Glu"
FT Misc-difference 7
FT /label= Gly, Glu, Thr, Ala or Asp
FT /note= "preferentially Gly"
FT Misc-difference 8
FT /label= Phe, Gln or Leu
FT
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS ) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX Garcia-Scheverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Claim 7; Page 42; 45pp; English.
XX
XX This represents a generic peptide that is capable of binding to an
XX oncogenic protein MDM2 (especially human DM2). The peptide and its
XX derivatives can specifically inhibit or block the binding of MDM2 to the
XX human p53 protein, in vitro or in vivo. Inhibiting the interaction
XX between the p53 and MDM2 can induce growth arrest or apoptosis in tumour
XX cells comprising a wild-type p53 and non-elevated levels of MDM2. The
XX peptide or its derivatives may be used to identify molecules that bind to
XX MDM2 and to identify and design inhibitors of MDM2/p53 binding. They may
XX also be used to purify binding partners especially MDM2, diagnose disease
XX by measuring levels of MDM2 in blood of cancer and leukaemia patients and
XX for treatment or prevention of disease involving p53/MDM2 interactions.
XX especially tumours and viral infections. The peptides can be administered
XX nasally, rectally, orally or by injection. By interfering with MDM2/p53
XX interaction, the peptides can activate p53 function and accumulation in
XX normal cells. The peptides which mimic the MDM2 binding site in p53, have
XX a significantly greater blocking activity compared with wild-type p53
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 23; DB 2; Length 8;
XX Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FXXKXWXXX 8

```


Db 1 FXXXXXXX 8

RESULT 7
AAW37217
ID AAW37217 standard; peptide; 8 AA.

AC AAW37217;

DT 20-JUL-1998 (first entry)

DE Human oncogenic protein MDM2 binding peptide derivative 10.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
tumour; diagnosis; binding; viral infection.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 9 /note= "C-terminal amide"

FT Modified-site 9 /note= "C-terminal amide"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -

XX useful in, e.g. diagnosis and treatment of cancer and viral infections

XX and identifying binding agents.

XX Example 6; Page 26; 45pp; English.

XX This is a MDM2 binding peptide derivative capable of binding to a human

XX oncogenic protein MDM2. The MDM2 binding peptides can specifically

XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro

XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can

XX induce growth arrest or apoptosis in tumour cells comprising a wild-type

XX p53 and non-elevated levels of MDM2. The peptides may be used to identify

XX molecules that bind to MDM2 and to identify and design inhibitors of

XX MDM2/p53 binding. They may also be used to purify binding partners

XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

XX cancer and leukaemia patients and for treatment or prevention of disease

XX involving p53/MDM2 interactions, especially tumours and viral infections.

XX The peptides can be administered nasally, rectally, orally or by

XX injection. By interfering with MDM2/p53 interaction, the peptides can

XX activate p53 function and accumulation in normal cells. The peptides

XX which mimic the MDM2 binding site in p53, have a significantly greater

XX blocking activity compared with wild-type p53

XX Sequence 8 AA;

XX Query Match 100.0%; Score 23; DB 2; Length 8;

XX Best Local Similarity 25.0%; Pred. No. 1.8e+06;

XX Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

XX 1 FXXXXXXX 8

QY

Db 1 FMDYWEGL 8

RESULT 8

AAW37215

ID AAW37215 standard; peptide; 8 AA.

XX AC AAW37215;

XX 20-JUL-1998 (first entry)

DT Human oncogenic protein MDM2 binding N-acylated peptide derivative 18.

DE MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;

XX tumour; diagnosis; binding; viral infection.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 3 /label= Aib

FT Modified-site 7 /note= "2-Aminoisobutyric acid"

FT Misc-difference 7 /label= OTHER

FT Modified-site 8 /note= "Ac3c (1-amino-cyclopropane-1-carboxylic acid)"

FT Modified-site 8 /note= "C-terminal amide"

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP003549.

XX 05-JUL-1996; 96GB-00014197.

XX 07-APR-1997; 97GB-00007041.

XX (NOVS) NOVARTIS AG.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;

XX Garcia-Echeverria C, Chene P, Furet P;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -

XX useful in, e.g. diagnosis and treatment of cancer and viral infections

XX and identifying binding agents.

XX Example 5; Page 25; 45pp; English.

XX This is a MDM2 binding peptide derivative capable of binding to a human

XX oncogenic protein MDM2. The MDM2 binding peptides can specifically

XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro

XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can

XX induce growth arrest or apoptosis in tumour cells comprising a wild-type

XX p53 and non-elevated levels of MDM2. The peptides may be used to identify

XX molecules that bind to MDM2 and to identify and design inhibitors of

XX MDM2/p53 binding. They may also be used to purify binding partners

XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of

XX cancer and leukaemia patients and for treatment or prevention of disease

XX involving p53/MDM2 interactions, especially tumours and viral infections.

XX The peptides can be administered nasally, rectally, orally or by

XX injection. By interfering with MDM2/p53 interaction, the peptides can

XX activate p53 function and accumulation in normal cells. The peptides

XX which mimic the MDM2 binding site in p53, have a significantly greater

XX blocking activity compared with wild-type p53

XX Sequence 8 AA;

XX Query Match 100.0%; Score 23; DB 2; Length 8;

XX Best Local Similarity 25.0%; Pred. No. 1.8e+06;

XX Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

XX 1 FXXXXXXX 8

QY

Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:|:|:|:
Db 1 FMXYWXXL 8

RESULT 9
AAW37214
ID AAW37214 standard; peptide; 8 AA.
XX
AC AAW37214;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human oncogenic protein MDM2 binding N-acylated peptide derivative 17.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 3 /note= "N-terminal acetyl"
FT Modified-site 3 /label= Aib
FT Modified-site 6 /note= "2-Aminoisobutyric acid"
FT Modified-site 6 /label= Aib
FT Misc-difference 7 /note= "2-Aminoisobutyric acid"
FT Modified-site 8 /label= OTHER
FT Modified-site 8 /note= "Ac3C (1-amino-cyclopropane-1-carboxylic acid)"
FT Modified-site 8 /note= "C-terminal amide"
XX
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX Garcia-Echeverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Example 5; Page 25; 45pp; English.
XX
XX This is a MDM2 binding peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of
XX MDM2/p53 binding. They may also be used to purify binding partners
XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
XX cancer and leukaemia patients and for treatment or prevention of disease
XX involving p53/MDM2 interactions, especially tumours and viral infections.
XX The peptides can be administered nasally, rectally, orally or by
XX injection. By interfering with MDM2/p53 interaction, the peptides can
XX activate p53 function and accumulation in normal cells. The peptides
XX which mimic the MDM2 binding site in p53, have a significantly greater

Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|:|:|:|:
Db 1 FMXYWXXL 8

RESULT 10
AAW37180
ID AAW37180 standard; peptide; 8 AA.
XX
AC AAW37180;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human oncogenic protein MDM2 binding peptide derivative 8.
XX
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Picksley S, Hochkeppel H;
XX Garcia-Echeverria C, Chene P, Furet P;
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Disclosure; Page 8; 45pp; English.
XX
XX This peptide is capable of binding to an oncogenic protein MDM2
XX (especially human DM2). The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of
XX MDM2/p53 binding. They may also be used to purify binding partners
XX especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
XX cancer and leukaemia patients and for treatment or prevention of disease
XX involving p53/MDM2 interactions, especially tumours and viral infections.
XX The peptides can be administered nasally, rectally, orally or by
XX injection. By interfering with MDM2/p53 interaction, the peptides can
XX activate p53 function and accumulation in normal cells. The peptides
XX which mimic the MDM2 binding site in p53, have a significantly greater

CC blocking activity compared with wild-type p53
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 23; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
 |:::|:::
 Db 1 FMDYWEGL 8

RESULT 11
 AAW37219
 ID AAW37219 standard; peptide; 8 AA.
 XX AAW37219;
 XX 20-JUL-1998 (first entry)
 XX Human oncogenic protein MDM2 binding peptide derivative 12.
 XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumour; diagnosis; binding; viral infection.
 XX Synthetic.
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /label= Aib
 FT Modified-site 8
 FT /note= "2-Aminoisobutyric acid"
 FT Modified-site 8
 FT /note= "C-terminal amide"
 XX WO9801467-A2.
 XX 15-JAN-1998.
 XX 04-JUL-1997; 97MO-EP003549.
 XX 05-JUL-1996; 96GB-00014197.
 PR 07-APR-1997; 97GB-00007041.
 XX (NOVS) NOVARTIS AG.
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 XX WPI; 1998-100996/09.
 XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT useful in, e.g. diagnosis and treatment of cancer and viral infections
 PT and identifying binding agents.
 XX Example 6; Page 26; 45pp; English.
 XX This is a MDM2 binding peptide derivative capable of binding to a human
 CC oncogenic protein MDM2. The MDM2 binding peptides can specifically
 CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 CC or in vivo. Inhibiting the interaction between the p53 and MDM2 can
 CC induce growth arrest or apoptosis in tumour cells comprising a wild-type
 CC p53 and non-elevated levels of MDM2. The peptides may be used to identify
 CC molecules that bind to MDM2 and to identify and design inhibitors of
 CC MDM2/p53 binding. They may also be used to purify binding partners
 CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC cancer and leukaemia patients and for treatment or prevention of disease
 CC involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by

CC injection. By interfering with MDM2/p53 interaction, the peptides can
 CC activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 23; DB 2; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.8e+06;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
 |:::|:::
 Db 1 FMDYWEGL 8

RESULT 12
 AAY40266
 ID AAY40266 standard; peptide; 8 AA.
 XX AAY40266;
 XX 17-OCT-2003 (revised)
 DT 19-NOV-1999 (first entry)
 XX Amino acid sequence of a HIV-1 epitope.
 XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
 KW vaccine; tumor; infection; immune response; cytokine profile;
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
 KW autoimmune disease.
 XX Human immunodeficiency virus 1.
 XX FR2774687-A1.
 XX 13-AUG-1999.
 XX 06-FEB-1998; 98FR-00001439.
 XX 06-FEB-1998; 98FR-00001439.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST PASTEUR LILLE.
 XX Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
 XX WPI; 1999-510734/43.
 XX New lipopeptide comprising C-terminal interferon-gamma fragment with
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating
 PT cancer or virus infection.
 XX Disclosure; Page 38; 53pp; French.
 XX AAY40123-Y40379 represent epitopes that are able to activate cytotoxic T
 CC lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or B
 CC epitopes recognized by corresponding antibodies. The epitopes may be used
 CC in the composition of the invention. The specification describes a
 CC lipopeptide that has a peptide part derived from mammalian interferon
 CC gamma (IFNG) and one or more lipophilic parts comprising a linear or
 CC branched (unsaturated 4-20C hydrocarbon) chain or a steroid. The
 CC lipopeptide mimics the activity of IFNG. Compositions comprising the
 CC lipopeptide are used to treat or prevent any condition that responds to
 CC IFNG, and as adjuvant for vaccines (particularly those directed against
 CC tumors, viral or parasitic infections), to stimulate or (re)orient the
 CC immune response between types 1 and 2 cytokine profiles. Particular
 CC applications are treatment of infections (particularly viral, e.g.
 CC acquired immune deficiency syndrome, papilloma (cancer) and hepatitis,
 CC but also bacterial, fungal, parasitic or helminth; cancers (particularly
 CC of kidney, cutaneous T cells or ovary, chronic myelogenous leukemia or
 CC mesothelioma), allergy; and autoimmune diseases. (Updated on 17-OCT-2003

CC to standardise OS field)

XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FSTWVVA 8

RESULT 13

AA25556
ID AAY25556 standard; peptide; 8 AA.

XX AC AAY25556;

XX DT 30-SEP-1999 (first entry)

XX DE Human MHC Class II hypothetical desensitising peptide #14.

XX KW Major histocompatibility complex; class II; desensitising; human;
allergen; grass; tree; weed; pollen; fungi; mould; food; insect; stinging;
chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX OS Synthetic.

XX PN WO9934826-A1.

XX PD 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-GB000080.

XX PR 09-JAN-1998; 98GB-00000445.

XX PR 21-SEP-1998; 98GB-00020474.

XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Larche M, Kay AB;

XX PR WPI; 1999-458255/38.

XX PT Desensitizing patients to polypeptide allergens.

XX PS Example 6; Fig 8; 117pp; English.

XX CC This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of teniprio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a hypothetical peptide which can be used to desensitize the human major histocompatibility complex (MHC) class II response to allergens

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 2; Length 8;

Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FSTWVVA 8

RESULT 14

AA53417
ID AAY53417 standard; protein; 8 AA.

XX AC AAY53417;

XX DT 18-JAN-2000 (first entry)

XX DE HIV-1 Gp120 protein (aa428-435) binds HLA-A2.

XX KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
human immunodeficiency virus; hepatitis B virus; papilloma virus;
melanoma; malaria; parasite.

XX OS Synthetic.

XX OS Human immunodeficiency virus 1.

XX PN FR2776926-A1.

XX PD 08-OCT-1999.

XX PF 07-APR-1998; 98PR-00004323.

XX PR 07-APR-1998; 98PR-00004323.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PA (INSP) INST PASTEUR LILLE.

XX PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;

XX PR WPI; 1999-583113/50.

XX PT New lipopeptide containing lipid regions and two epitopes, all separated by peptide spacers that impart hydrophilicity, useful in vaccines.

XX PS Disclosure; Page 20; 35pp; French.

XX CC The invention relates to the generation of a lipopeptide comprising at least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL) epitope and at least one lipid residue with (i) the epitopes and lipid portion and (ii) the epitopes, being separated independently by peptide spacers. These spacers comprise sequences of amino acids which carry an overall electrical charge in neutral media to ensure that the lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents examples of peptide epitopes used to generate the lipopeptides. These are used in therapeutic or prophylactic compositions and vaccines to induce specific immune responses against human immunodeficiency, hepatitis B or papilloma viruses; p53 of melanoma or the malaria parasite

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 2; Length 8;

Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FINWQEV 8

RESULT 15

AA26758
ID AAY26758 standard; peptide; 8 AA.

XX AAY26758;
 AC 14-SEP-1999 (first entry)
 DT HIV-derived lipopeptide epitope #28 for mixed micelles.
 DE
 XX Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
 KW melanoma; Plasmodium falciparum; malaria.
 XX Synthetic.
 OS Human immunodeficiency virus 1.
 XX FR2771640-A1.
 PN 04-JUN-1999.
 PD 03-DEC-1997; 97FR-00015246.
 XX 03-DEC-1997; 97FR-00015246.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (INSP) INST PASTEUR LILLE.
 XX Gras MH, Bossus M, Lippens G, Wieruszkeski JM, Tartar A;
 PI Guillet JG, Bourgault VI;
 XX WPI; 1999-349509/30.
 DR Immunogenic lipopeptide micelles - comprising lipopeptides containing
 XX cytotoxic and helper T-lymphocyte epitopes.
 PT Disclosure; Page 33; 60pp; French.
 XX The invention relates to the generation of mixed micelles or
 CC microaggregates for inducing an immune response comprise: (a) a first
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
 CC different from that of the first lipopeptide. This peptide represents an
 CC example of a lipopeptide epitope used in the invention and is derived
 CC from a human immunodeficiency virus type 1 (HIV-1) protein. The
 CC immunogenic lipopeptide micelles are used in vaccines, especially against
 CC HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma or
 CC Plasmodium falciparum malaria
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 23; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 |:::|:::
 Db 1 FINWQEV 8
 RESULT 16
 AAY16874
 ID AAY16874 standard; peptide; 8 AA.
 XX AAY16874;
 AC 20-JUL-1999 (first entry)
 DT Peptide Seq ID No: 144 of WO9922761.
 DE Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;

KW acquired immune deficiency; autoimmune disease.
 XX Synthetic.
 OS WO9922761-A1.
 PN 14-MAY-1999.
 PD 22-OCT-1998; 98WO-US022335.
 XX 31-OCT-1997; 97US-00961707.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Rothman JE, Mayhew M, Hoe MH, Houghton A, Hartl U, Ouerfelli O;
 PI Morol Y;
 XX WPI; 1999-313177/26.
 XX Identifying peptides which bind heat shock proteins.
 XX Example; Page 19; 155pp; English.
 XX The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzquinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 23; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 |:::|:::
 Db 1 FWGLWFE 8
 RESULT 17
 AAB09130
 ID AAB09130 standard; protein; 8 AA.
 XX AAB09130;
 AC 06-AUG-2003 (revised)
 DT 30-AUG-2000 (first entry)
 XX Hepatitis GB virus protein sequence SEQ ID NO:252.
 XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis.
 XX Hepatitis GB virus.
 OS US6051374-A.
 XX 18-APR-2000.
 PD 07-JUN-1995; 95US-00488445.
 XX 14-FEB-1994; 94US-00196030.
 PR

PR 13-MAY-1994; 94US-00242654.
 PR 29-JUL-1994; 94US-00283314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-00377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TV, Buijk SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX
 XX WPI; 2000-338307/29.
 XX
 PT Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the HGBV
 PT polynucleotide probe and detecting the complex that contains target HGBV.
 XX
 XX Example 9; Col 331-332; 369pp; English.
 XX
 CC The present invention describe a method for detecting target hepatitis GB
 CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
 CC containing HGBV. The method involves reacting (T) with a HGBV
 CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
 CC selectively hybridises to the HGBV genome or its full complement, and
 CC detecting the complex that contains THN, indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and
 CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 23; DB 3; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 |::|::|
 Db 1 FSHLWTS 8
 |::|::|
 RESULT 18
 AAG88890
 ID AAG88890 standard; peptide; 8 AA.
 XX
 AC AAG88890;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE HER2/neu epitope B7 supermotif peptide #50.
 XX
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200141787-A1.
 XX
 PD 14-JUN-2001.
 XX
 XX 11-DEC-2000; 2000WO-US033591.
 XX
 XX 10-DEC-1999; 99US-00458299.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;

XX WPI; 2001-374995/39.
 DR
 XX
 PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
 PT cellular immune responses for the prevention and treatment of cancer.
 XX
 XX Claim 1; Page 184; 199pp; English.
 XX
 CC The present invention describes isolated prepared HER2/neu epitopes (I).
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
 CC culture in vitro and binds to a complex of an epitope (I), bound to a
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
 CC and a second epitope and the peptide is less than 50 contiguous amino
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and
 CC (III) are useful for inducing cellular immune responses for the
 CC prevention and treatment of cancer. (I) and (II) are useful for
 CC monitoring or evaluating an immune response to a tumour-associated
 CC antigen when incubated with a T lymphocyte sample from a patient and
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
 CC based vaccines mean that immunosuppressive epitopes that may be present
 CC in whole antigens may be avoided. Selected epitopes may be combined to
 CC enhance immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigen is eliminated. The vaccine
 CC provides the ability to direct and focus an immune response to multiple
 CC selected antigens from the same pathogen. Epitope-based anti-tumour
 CC vaccines provides the opportunity to combine epitopes derived from
 CC multiple tumour-associated molecules addressing the problem of tumour-
 CC tumour variability and reducing the likelihood of tumour escape due to
 CC antigen loss. AAG88286 to AAG89121 represent amino acid sequences used in
 CC the exemplification of the present invention
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 |::|::|
 Db 1 FPIKWWAI 8
 |::|::|
 RESULT 19
 AAG88891
 ID AAG88891 standard; peptide; 8 AA.
 XX
 AC AAG88891;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE HER2/neu epitope B7 supermotif peptide #51.
 XX
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200141787-A1.
 XX
 PD 14-JUN-2001.
 XX
 XX 11-DEC-2000; 2000WO-US033591.
 XX
 XX 10-DEC-1999; 99US-00458299.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 DR WPI; 2001-374995/39.
 XX
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
 PT cellular immune responses for the prevention and treatment of cancer.
 XX
 XX Claim 1; Page 184; 199pp; English.
 XX
 CC The present invention describes isolated prepared HER2/neu epitopes (I).
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
 CC culture in vitro and binds to a complex of an epitope (I), bound to a
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
 CC and a second epitope and the peptide is less than 50 contiguous amino
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
 CC ; and (5) an isolated nucleic acid encoding (III). (I) has cytostatic and
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and
 CC (III) are useful for inducing cellular immune responses for the
 CC prevention and treatment of cancer. (I) and (II) are useful for
 CC monitoring or evaluating an immune response to a tumour-associated
 CC antigen when incubated with a T lymphocyte sample from a patient and
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
 CC based vaccines mean that immunosuppressive epitopes that may be present
 CC in whole antigens may be avoided. Selected epitopes may be combined to
 CC enhance immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigen is eliminated. The vaccine
 CC provides the ability to direct and focus an immune response to multiple
 CC selected antigens from the same pathogen. Epitope-based anti-tumour
 CC vaccines provides the opportunity to combine epitopes derived from
 CC multiple tumour-associated molecules addressing the problem of tumour-
 CC tumour variability and reducing the likelihood of tumour escape due to
 CC antigen loss. AAG89121 represent amino acid sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred.No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 Db 1 FPIKWWAL 8
 RESULT 20
 AAB59632
 ID AAB59632 standard; peptide; 8 AA.
 AC AAB59632;
 XX
 XX 23-MAR-2001 (first entry)
 DT
 XX Neuromedin B and somatostatin analogue #25.
 DE
 XX Neuromedin B; NMB; somatostatin; analogue; Helicobacter pylori; cancer;
 KW cyclic.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /label= OTHER
 FT /note= "modified by D-4-NO2"
 FT Modified-site 2 /label= OTHER
 FT /note= "3-pyridylalanine"
 FT Disulfide-bond 3. .7
 FT /note= "disulfide bond cyclises the peptide"
 FT Misc-difference 3

FT Modified-site 4 /note= "D-form residue"
 FT /label= OTHER
 FT /note= "modified by 4-O-Bzl"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 8 /label= OTHER
 FT /note= "C-terminal amide"
 XX
 XX WO200075186-A1.
 PN
 XX 14-DEC-2000.
 PD
 XX 05-JUN-2000; 2000WO-US015396.
 PF
 XX 04-JUN-1999; 99US-0137655P.
 PR
 XX (BIOM-) BIOMEASURE INC.
 PA
 XX Sadat-Aalae D, Morgan BA;
 PI
 XX WPI; 2001-146787/15.
 DR
 XX New polypeptide compounds are somatostatin and neuromedin B receptor
 PT agonists, for treating a wide range of disorders e.g. cancer,
 PT gastrointestinal disorders and inflammatory disorders.
 XX
 XX Claim 15; Page 72; 85pp; English.
 XX
 CC The present invention provides analogues of somatostatin and neuromedin B
 CC (NMB). These can be used in the treatment of various cancers, anorexia,
 CC hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation,
 CC acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and
 CC internal pancreatic pseudocysts and ascites, mesodiblastosis,
 CC hyperinsulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma,
 CC irritable bowel syndrome, pancreatitis, small bowel obstruction,
 CC gastroesophageal reflux, duodenogastric reflux, Cushing's syndrome,
 CC hyperparathyroidism, Graves' disease, diabetic neuropathy, Paget's
 CC disease, polycystic ovary disease, orthostatic hypotension, postprandial
 CC hypotension, panic attacks, diabetes mellitus, hyperlipidaemia, insulin
 CC insensitivity, syndrome X, peptic ulcers, arthritis, obesity, opioid
 CC overdose and gastrointestinal bleeding
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 37.5%; Pred.No. 1.8e+06;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 Db 1 FXCFWRCY 8
 RESULT 21
 AAU72016
 ID AAU72016 standard; peptide; 8 AA.
 XX
 XX AAU72016;
 XX
 XX 11-SEP-2003 (revised)
 DT 26-FEB-2002 (first entry)
 DT
 XX Melanoma antigen, javelin peptide #2.
 DE
 XX Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;
 KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYE01; GM2;
 KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
 KW javelin molecule; melanoma antigen recognised by T cells-1; human.
 XX
 OS Enterobacteria phage M13.
 XX

PN WO200178655-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US012449.
 XX
 PR 17-APR-2000; 2000US-0197462P.
 XX
 XX (HOUG/) HOUGHTON A.
 PA (LIVL/) LIVINGSTON P.
 PA (ALAW/) AL-AWQATI Q.
 PA (MAYH/) MAYHEW M.
 XX (HOEM/) HOE M.
 XX
 PI Houghton A, Livingston P, Al-Awqati Q, Mayhew M, Hoe M;
 XX
 XX WPI; 2001-663092/76.
 XX
 XX Anti cancer vaccine for the treatment of melanoma comprises a heat shock
 PT protein and a melanoma antigen i.e. tyrosinase.
 XX
 XX Disclosure; Page 14-15; 150pp; English.
 XX
 XX The invention relates to a method of induction of an immune response,
 CC comprising administration of an immunotherapeutic composition, comprising
 CC a heat shock protein, and a melanoma antigen, where the melanoma antigen
 CC is selected from tyrosinase, tyrosinase related protein 1, tyrosinase
 CC related protein 2, gp 100, MAGE antigens, BAGE antigens, NYES01, MART
 CC antigens, GM2, antigenic portions and combinations of these. The melanoma
 CC antigen is covalently bound to a javelin molecule, where the melanoma
 CC antigen bound to the javelin molecule is non-covalently bound to the heat
 CC shock protein. The composition is useful for inducing an immune response
 CC for the treatment of melanoma. AAU71980-AAU72481 represent melanoma
 CC antigen peptides of the invention. (Updated on 11-SEP-2003 to standardise
 CC OS field)
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 DB |:::|:::
 1 FWGLNPWE 8
 RESULT 22
 AAB76081
 ID AAB76081 standard; peptide; 8 AA.
 XX
 AC AAB76081;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE Tumour associated antigen Her2/neu immunogenic peptide.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
 KW HLA binding peptide; immune response; glycoprotein; cytostatic; virucide;
 KW hepatotropic; antiinflammatory; anti-HIV; vaccine;
 KW human immunodeficiency virus; protozoicide; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
 KW condyloma acuminatum.
 XX
 OS Homo sapiens.
 XX
 PN WO200100225-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 28-JUN-2000; 2000WO-US017842.
 XX
 PR 29-JUN-1999; 99US-0141422P.
 XX

PF 28-JUN-2000; 2000WO-US017842.
 XX
 PR 29-JUN-1999; 99US-0141422P.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 XX WPI; 2001-112389/12.
 DR
 XX
 XX Composition comprising human leukocyte antigen binding peptide which
 PT comprises isolated, prepared epitope useful for treating viral infections
 PT such as acquired immunodeficiency syndrome, and cancer.
 XX
 XX Claim 1; Page 47; 58pp; English.
 XX
 CC The present invention describes a composition (I) which comprises at
 CC least one human leukocyte antigen (HLA) binding peptide comprising an
 CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
 CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
 CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
 CC immunodeficiency virus) and protozoicide activities, which can be used in
 CC vaccine production and is an inducer of cytotoxic T-cell response. (I) is
 CC useful for inducing a cytotoxic T cell response against a preselected
 CC antigen in a patient expressing a specific major histocompatibility
 CC complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from
 CC the patient with (I). (I) is useful as a vaccine to treat and/or prevent
 CC viral infection and cancer such as prostate cancer, hepatitis B,
 CC hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus
 CC (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma,
 CC cervical carcinoma, lymphoma, malaria, and condyloma acuminatum
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 DB |:::|:::
 1 FPIKWMAI 8
 RESULT 23
 AAB76082
 ID AAB76082 standard; peptide; 8 AA.
 XX
 AC AAB76082;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE Tumour associated antigen Her2/neu immunogenic peptide.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
 KW HLA binding peptide; immune response; glycoprotein; cytostatic; virucide;
 KW hepatotropic; antiinflammatory; anti-HIV; vaccine;
 KW human immunodeficiency virus; protozoicide; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
 KW condyloma acuminatum.
 XX
 OS Homo sapiens.
 XX
 PN WO200100225-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 28-JUN-2000; 2000WO-US017842.
 XX
 PR 29-JUN-1999; 99US-0141422P.
 XX

PA (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S;
 XX WPI; 2001-112389/12.
 XX
 XX Composition comprising human leukocyte antigen binding peptide which
 PT comprises isolated, prepared epitope useful for treating viral infections
 PT such as acquired immunodeficiency syndrome, and cancer.
 XX
 XX Claim 1; Page 47; 58pp; English.
 XX
 XX The present invention describes a composition (I) which comprises at
 CC least one human leukocyte antigen (HLA) binding peptide comprising an
 CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
 CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
 CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
 CC immunodeficiency virus) and protozoacide activities, which can be used in
 CC vaccine production and is an inducer of cytotoxic T-cell response. (I) is
 CC useful for inducing a cytotoxic T cell response against a preselected
 CC antigen in a patient expressing a specific major histocompatibility
 CC complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from
 CC the patient with (I). (I) is useful as a vaccine to treat and/or prevent
 CC viral infection and cancer such as prostate cancer, hepatitis B,
 CC hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus
 CC (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma,
 CC cervical carcinoma, lymphoma, malaria, and condylooma acuminatum
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 Db |:::|:::
 1 FPIKWMAL 8
 RESULT 24
 AAU02206
 ID AAU02206 standard; peptide; 8 AA.
 AC
 XX AAU02206;
 XX
 XX 11-SEP-2003 (revised)
 DT 26-SEP-2001 (first entry)
 DT
 XX Trichoderma harzianum L-amino acid oxidase, peptide #1.
 DE
 XX L-amino acid oxidase; fungus; hydrogen peroxide; detergent; peroxidase;
 KW dye transfer inhibition; bleach; laundry; toothpaste; preservative;
 KW cosmetic; bread; dough improver; water treatment; pulp production;
 KW lignin; catalytic deamination; EC 1.4.3.2.
 XX
 XX Hypocrea lixii; CBS 223.93.
 OS
 XX US6248575-B1.
 PN
 XX 19-JUN-2001.
 PD
 XX 18-MAY-1999; 99US-00314242.
 PF
 XX 18-MAY-1998; 98US-00080428.
 PR
 XX (NOVO-) NOVOZYMES BIOFTECH INC.
 PA
 XX Golightly EJ;
 XX
 XX WPI; 2001-431859/46.
 DR
 XX
 XX Nucleic acids, useful for generating polypeptides with L-amino acid
 PT oxidase activity, which are useful as components of bread and dough,
 PT

PT toothpaste or cosmetics, or of detergent compositions having peroxidase
 PT systems.
 XX
 XX Example 4; Col 27; 28pp; English.
 XX
 XX The sequence represents the amino acid sequence of Trichoderma harzianum
 CC L-amino acid oxidase (EC 1.4.3.2), peptide #1. L-amino acid oxidase
 CC catalyses the deamination of an L-amino acid in the presence of water and
 CC oxygen to produce a 2-oxo acid, ammonia and hydrogen peroxide. The
 CC isolated nucleic acid sequence is useful for producing or generating in
 CC polypeptides with L-amino acid oxidase activity, which are useful in
 CC processes where in situ generation of hydrogen peroxide is desired, e.g.
 CC as component of detergent compositions having peroxidase systems. The
 CC polypeptides are particularly useful for dye transfer inhibition during
 CC laundering or for improved bleaching in laundry detergents. The
 CC polypeptides encoded by the nucleic acid may also be incorporated into
 CC toothpaste or used for preservation of cosmetics. The polypeptides may be
 CC used in bread and dough improving compositions. Furthermore, the
 CC polypeptides may be implemented in processes for treating wastewater from
 CC pulp production, and lignin modification. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXXXWXXX 8
 Db |:::|:::
 1 FSYPPWIK 8
 RESULT 25
 ABP20955
 ID ABP20955 standard; peptide; 8 AA.
 XX
 XX ABP20955;
 XX
 XX 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 DT
 XX HIV A03 motif nef peptide #105.
 DE
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX WO200124810-A1.
 PN
 XX 12-APR-2001.
 PD
 XX 05-OCT-2000; 2000WO-US027766.
 PF
 XX 05-OCT-1999; 99US-00412863.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 XX WPI; 2001-354887/37.
 DR
 XX
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT
 XX Claim 32; Page 299; 448pp; English.
 PS
 XX
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
 |::|::|
 Db 1 FFPDQWNY 8

RESULT 26

ABP23018
 ID ABP23018 standard; peptide; 8 AA.

AC ABP23018;

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A11 motif nef peptide #65.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

OS WO200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 340; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
 |::|::|

Db 1 FFPDQWNY 8

RESULT 27

ABP15754

ID ABP15754 standard; peptide; 8 AA.

AC ABP15754;

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A24 super motif nef peptide #16.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 191; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 8 AA;

Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXWXX 8
 |::|::|
 Db 1 FPDWQNY 8

RESULT 28

AAE12180
 ID AAE12180 standard; peptide; 8 AA.

XX AAE12180;

XX 18-DEC-2001 (first entry)

DE Polyglutamine repeat domain binding peptide #11.

XX Polyglutamine repeat domain; huntingtin; atrophin; ataxin;
 KW androgen receptor protein; neurodegenerative disease; anticonvulsant;
 KW Huntington's disease; dentatorubral pallidolysian atrophy; DRPLA;
 KW spinobulbar muscular atrophy; spinocerebellar ataxia; nontropic.

XX Unidentified.

XX WO200168678-A2.

XX 20-SEP-2001.

XX 14-MAR-2001; 2001WO-US008222.

XX 16-MAR-2000; 2000US-0189781P.

XX (UYDU-) UNIV DUKE.

XX Strittmatter WJ, Burke JR, Nagai Y;

XX WPI; 2001-616285/71.

XX New polypeptides which selectively bind to expanded polyglutamine repeat
 PT domains, useful for treating neurodegenerative diseases, e.g.
 PT Huntington's disease.

XX Disclosure; Page 14; 59pp; English.

XX The present sequence is a polyglutamine repeat domain binding peptide.
 CC The peptide is useful for treating a cell that contains and expresses a
 CC protein having an expanded polyglutamine region (e.g. huntingtin;
 CC atrophin 1, ataxin 1, 2, 6 or 7; or androgen receptor protein), or
 CC treating a neurodegenerative disease characterised by the presence of
 CC expanded polyglutamine repeats, e.g. Huntington's disease, dentatorubral
 CC pallidolysian atrophy (DRPLA), spinobulbar muscular atrophy, and
 CC spinocerebellar ataxia types 1, 2, 3, 6 and 7

SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXWXX 8
 |::|::|
 Db 1 FIGPWKW 8

RESULT 29

AAAM10739

ID AAAM10739 standard; peptide; 8 AA.

XX AAAM10739;

XX 09-OCT-2001 (first entry)

XX HLA-B8 octamer #369.

XX Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
 KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
 KW major histocompatibility complex; antigen presenting cell; melanoma;
 KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

XX Homo sapiens.

XX WO200135810-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US031513.

XX 15-NOV-1999; 99US-0165590P.

XX (DAND) DANA FARBER CANCER INST INC.

XX (UYBO-) UNIV BOSTON.

XX Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;

XX Von Bergwelt- Balldon M;

XX WPI; 2001-355537/37.

XX Treating a cancer patient involves administering to patient a cytotoxic T
 PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide
 PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX Disclosure; Page 78; 121pp; English.

XX The present invention describes a method for treating a patient having,
 CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
 CC which involves administering to the patient a cytotoxic T-lymphocyte
 CC (CTL) that kills the cell, an antigen presenting cell (APC) that
 CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
 CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
 CC peptide of CYP1B1. Also described are: (1) a method for assessing the
 CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
 CC binds to MHC complex molecule, involving measuring the level of CTL
 CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
 CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
 CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
 CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
 CC generated APC (III) that presents a peptide of a CYP1B1 in the context of
 CC a MHC complex molecule. The method is useful for treating a patient
 CC having or is at risk of having a cell that expresses CYP1B1. The method
 CC is useful for the prevention, treatment and diagnosis of cancer, e.g.
 CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
 CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
 CC brain cancer. AA06905 to AA013566 represent CYP1B1 peptides which can
 CC bind to human leukocyte antigens (HLAs), as well as other amino acid
 CC sequence used in the exemplification of the present invention

SQ Sequence 8 AA;		Query Match		100.0%; Score 23; DB 4; Length 8;	
		Best Local Similarity		25.0%; Pred. No. 1.8e+06;	
		Matches		2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FXXHWXXX 8				
DB	1 FVNQWSVN 8				
RESULT 30					
ID	AAU80566				
XX	AAU80566 standard; peptide; 8 AA.				
XX	AC AAU80566;				
XX	DT 26-MAR-2002 (first entry)				
XX	DE Heat shock binding peptide #2 useful as javelin peptide.				
XX	XX Immunogenic complex; non-pathogenic multi-component viral particle;				
KW	Javelin; heat shock protein; humoral immunity; cellular immunity;				
KW	anti-viral immune response; viral infection; hepatitis; influenza; mumps;				
KW	HIV infection; human immunodeficiency virus; polio;				
KW	tick-borne encephalitis; ebola virus infection;				
KW	heat shock binding peptide.				
XX	XX Homo sapiens.				
OS	WO200178772-A1.				
XX	PN 25-OCT-2001.				
XX	PD 17-APR-2001; 2001WO-US012568.				
XX	PF 17-APR-2000; 2000US-0197462P.				
XX	PR (MOJA-) MOJAVE THERAPEUTICS INC.				
XX	PA Hoe M, Landsberger F;				
PI	WPI; 2002-049177/06.				
XX	DR New heat shock protein-based viral vaccines, useful for enhancing anti-				
PT	viral immune response in an organism, particularly as a vaccine for				
PT	preventing or ameliorating viral infections, e.g. hepatitis, influenza or				
PT	HIV infection.				
XX	PS Disclosure; Page 9; 75pp; English.				
XX	CC The present invention relates to the use of an immunogenic complex,				
CC	comprising a non-pathogenic multi-component viral particle covalently				
CC	linked to a javelin molecule (preferably a peptide) that selectively				
CC	binds to a heat shock protein. The immunogenic complex is useful for				
CC	inducing both humoral and cellular immunity, especially for enhancing the				
CC	anti-viral immune response, in a human or non-human subject. The				
CC	immunogenic complex is particularly useful as a vaccine for preventing or				
CC	ameliorating viral infections, e.g. hepatitis, influenza, mumps, HIV				
CC	(human immunodeficiency virus) infection, polio, tick-borne encephalitis				
CC	or ebola virus infection. AAU80565-AAU80570 represent heat shock binding				
CC	peptides which may be used as javelins				
XX	XX Sequence 8 AA;				
		Query Match		100.0%; Score 23; DB 5; Length 8;	
		Best Local Similarity		25.0%; Pred. No. 1.8e+06;	
		Matches		2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FXXHWXXX 8				
DB	1 FWGLWPWE 8				

RESULT 31		ABJ08627		ABJ08627 standard; peptide; 8 AA.	
ID	ABJ08627				
XX	AC ABJ08627;				
XX	DT 14-NOV-2002 (first entry)				
XX	DE Hepatitis B virus epitope #2845.				
XX	XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;				
KW	virucide; hepatotropic; antiinflammatory.				
XX	OS Hepatitis B virus.				
XX	PN WO200219986-A1.				
XX	PD 14-MAR-2002.				
XX	PF 08-SEP-2000; 2000WO-US024802.				
XX	PR 08-SEP-2000; 2000WO-US024802.				
PA	(EPIM-) EPIMUNE INC.				
PA	(SETT/) SETTE A.				
XX	PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;				
PI	Cellis E, Kubo RT, Grey HM, Chesnut RW;				
XX	WPI; 2002-643192/69.				
XX	DR Vaccine composition for treating or preventing hepatitis B virus (HBV)				
PT	infection, and/or for stimulating an immune response to HBV, comprises a				
PT	HBV peptide epitope.				
XX	PS Disclosure; Page 174; 228pp; English.				
XX	CC The present invention relates to a composition comprising at least one				
CC	hepatitis B virus epitope. This can be used in the production of a				
CC	vaccine for use in preventing or treating hepatitis B virus infection.				
CC	The present sequence is a peptide described in the exemplification of the				
CC	invention				
XX	XX Sequence 8 AA;				
		Query Match		100.0%; Score 23; DB 5; Length 8;	
		Best Local Similarity		25.0%; Pred. No. 1.8e+06;	
		Matches		2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FXXHWXXX 8				
DB	1 FFCLWVYI 8				
RESULT 32					
ID	ABJ06552				
XX	ABJ06552 standard; peptide; 8 AA.				
XX	AC ABJ06552;				
XX	DT 14-NOV-2002 (first entry)				
XX	DE Hepatitis B virus epitope #770.				
XX	XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;				
KW	virucide; hepatotropic; antiinflammatory.				
XX	OS Hepatitis B virus.				
XX	PN WO200219986-A1.				
XX	PD 14-MAR-2002.				

CC can contribute to oncogenesis. FNfn10 includes an RGD sequence in the
CC loop connecting the F and G beta strands (FG loop) and can be expressed
CC in large scale in bacteria. The polypeptide monobody is useful for
CC inhibiting (antagonist) the activity of alphavbeta3 integrin. The
CC polypeptide monobody, or its conjugate comprising the polypeptide
CC monobody conjugated to a chemotherapeutic agent, a contrasting agent or
CC an organic chelating agent, is useful for treating, preventing or
CC assessing an alphavbeta3 integrin-mediated disease or disorder, such as
CC tumour metastasis, solid tumour growth, osteoporosis, Paget's disease,
CC humoral hypercalcaemia of malignancy, angiogenesis, retinopathy,
CC arthritis, periodontal disease, psoriasis, smooth muscle cell migration,
CC viral infection, fungal infection, bacterial infection and cancerous or
CC precancerous conditions. Administration is carried out by contacting one
CC or more cells expressing alphavbeta3 integrin with the polypeptide
CC monobody to inhibit the activity of alphavbeta3 integrin on the cells.
CC The sequence presented is the human FNfn10 FG loop, clone 3JCL15,
CC monobody
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FRGDWIEL 8

RESULT 35
ABP98084
ID ABP98084 standard; peptide; 8 AA.
AC ABP98084;
XX
XX
DT 11-AUG-2003 (first entry)
XX
DE Amino acid sequence of human apolipoprotein C-III epitope.
XX
XX Human; apolipoprotein C-III; ApocIII; epitope; atherosclerotic plaque;
KW atherosclerosis.
KW
XX Homo sapiens.
OS
XX
PN WO2003020765-A2.
XX
PD 13-MAR-2003.
XX
PF 29-AUG-2002; 2002WO-EP009650.
XX
PR 31-AUG-2001; 2001GB-00021171.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Fruchart J, Meykens R, Monteyne P;
XX WPI; 2003-290168/28.
DR
XX
PT Novel peptides comprising epitope of apolipoprotein C-III useful for
PT treatment or prophylaxis of atherosclerosis in an individual.
XX
PS Claim 3; Page 7; 37pp; English.
XX

The present sequence represents an epitope of human apolipoprotein C-III
CC (ApocIII). The specification describes ApocIII epitopes, derived from
CC within the region between amino acids 12-35, 12-21, 45-76 or 45-65.
CC ApocIII epitopes are potent in the prevention or reduction of
CC atherosclerotic plaque formation over prolonged period of time, thus
CC reducing the potential of atherosclerosis. ApocIII epitopes are useful in
CC the manufacture of a medicament for preventing or treating
CC atherosclerosis
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FRGDWIEL 8

RESULT 35
ABP98084
ID ABP98084 standard; peptide; 8 AA.
AC ABP98084;
XX
XX
DT 11-AUG-2003 (first entry)
XX
DE Amino acid sequence of human apolipoprotein C-III epitope.
XX
XX Human; apolipoprotein C-III; ApocIII; epitope; atherosclerotic plaque;
KW atherosclerosis.
KW
XX Homo sapiens.
OS
XX
PN WO2003020765-A2.
XX
PD 13-MAR-2003.
XX
PF 29-AUG-2002; 2002WO-EP009650.
XX
PR 31-AUG-2001; 2001GB-00021171.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Fruchart J, Meykens R, Monteyne P;
XX WPI; 2003-290168/28.
DR
XX
PT Novel peptides comprising epitope of apolipoprotein C-III useful for
PT treatment or prophylaxis of atherosclerosis in an individual.
XX
PS Claim 3; Page 7; 37pp; English.
XX

The present sequence represents an epitope of human apolipoprotein C-III
CC (ApocIII). The specification describes ApocIII epitopes, derived from
CC within the region between amino acids 12-35, 12-21, 45-76 or 45-65.
CC ApocIII epitopes are potent in the prevention or reduction of
CC atherosclerotic plaque formation over prolonged period of time, thus
CC reducing the potential of atherosclerosis. ApocIII epitopes are useful in
CC the manufacture of a medicament for preventing or treating
CC atherosclerosis
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FSEFWDLD 8

RESULT 36
ABP68156
ID ABP68156 standard; peptide; 8 AA.
AC ABP68156;
XX
XX
DT 08-JAN-2003 (first entry)
XX
DE Bacillus thuringiensis toxin Cry related peptide CryIaG.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN PR2822157-A1.
XX
PD 20-SEP-2002.
XX
PF 19-MAR-2001; 2001FR-00003691.
XX
PR 19-MAR-2001; 2001FR-00003691.
XX
PA (AVET) AVENTIS CROPS SCIENCE SA.
XX
PI Freyssinet G, Rang C, Frutos R;
XX WPI; 2003-002439/01.
DR
XX
PT New modified Cry protein, useful as insecticide, comprises at least one
PT additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS Example 4; Page 36; 134pp; French.
XX

The present invention describes a modified Cry protein (I) that is
CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (i); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry protein). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FGQRWGF 8

```
RESULT 37
ABP68179
ID ABP68179 standard; peptide; 8 AA.
XX
AC ABP68179;
XX
DT 08-JAN-2003 (first entry)
XX
DE Bacillus thuringiensis toxin Cry related peptide Cry1Ja.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN FR2822157-A1.
XX
PD 20-SEP-2002.
XX
PF 19-MAR-2001; 2001FR-00003691.
XX
PR 19-MAR-2001; 2001FR-00003691.
XX
PA (AVET ) AVENTIS CROPS SCIENCE SA.
XX
PI Freyssinet G, Rang C, Frutos R;
XX
DR WPI; 2003-002439/01.
XX
PT New modified Cry protein, useful as insecticide, comprises at least one
PT additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS Example 4; Page 37; 134pp; French.
XX
CC The present invention describes a modified Cry protein (I) that is
CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXHWXXX 8
DB 1 FGRWGGLT 8
|::|::|
RESULT 38
ABP68175
ID ABP68175 standard; peptide; 8 AA.
XX
AC ABP68175;
XX
DT 08-JAN-2003 (first entry)
XX
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```
DE Bacillus thuringiensis toxin Cry related peptide Cry1Ib.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN FR2822157-A1.
XX
PD 20-SEP-2002.
XX
PF 19-MAR-2001; 2001FR-00003691.
XX
PR 19-MAR-2001; 2001FR-00003691.
XX
PA (AVET ) AVENTIS CROPS SCIENCE SA.
XX
PI Freyssinet G, Rang C, Frutos R;
XX
DR WPI; 2003-002439/01.
XX
PT New modified Cry protein, useful as insecticide, comprises at least one
PT additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS Example 4; Page 37; 134pp; French.
XX
CC The present invention describes a modified Cry protein (I) that is
CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXHWXXX 8
DB 1 FGRWGGLS 8
|::|::|
RESULT 39
ABP68180
ID ABP68180 standard; peptide; 8 AA.
XX
AC ABP68180;
XX
DT 08-JAN-2003 (first entry)
XX
DE Bacillus thuringiensis toxin Cry related peptide Cry1Jb.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN FR2822157-A1.
```

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XX PD 20-SEP-2002.
XX PF 19-MAR-2001; 2001PR-00003691.
XX PR 19-MAR-2001; 2001PR-00003691.
XX PA (AVET ) AVENTIS CROPSCIENCE SA.
XX PI Freyssinet G, Rang C, Frutos R;
XX DR WPI; 2003-002439/01.
XX CC
XX CC The present invention describes a modified Cry protein (I) that is
XX CC sensitive to pepsin and comprises at least one additional pepsin cleavage
XX CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
XX CC proteins by incorporating at least one extra PCS; (b) polynucleotides
XX CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
XX CC (II) and terminator; (d) expression or transformation vector (III) that
XX CC contains CG; (e) host organism (IV) transformed with (III), also, where
XX CC the organism is a plant, its parts and seeds; (f) production of (I) by
XX CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
XX CC against (I). (I) has insecticide activity. (I) can be used as
XX CC insecticides, particularly where expressed in transgenic plants. (I) are
XX CC sensitive to enzymes in the digestive tract of mammals, so do not persist
XX CC in the tract (lack of persistence is required by regulatory authorities
XX CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
XX CC increase degradation in the digestive tract of insects, so have no effect
XX CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
XX CC represent sequences used in the exemplification of the present invention
XX CC
XX CC Sequence 8 AA;
SQ
Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXHWXXX 8
Db 1 FGERWGLT 8
|::|::|
|::|::|

RESULT 40
ABP68151
ID ABP68151 standard; peptide; 8 AA.
XX AC ABP68151;
XX DT 08-JAN-2003 (first entry)
XX DE Bacillus thuringiensis toxin Cry related peptide CryIab.
XX KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
XX OS pepsin; PCS.
XX OS Bacillus thuringiensis.
XX OS Synthetic.
XX PN FR2822157-A1.
XX PD 20-SEP-2002.
XX PF 19-MAR-2001; 2001PR-00003691.
XX PR 19-MAR-2001; 2001PR-00003691.
XX PA (AVET ) AVENTIS CROPSCIENCE SA.
XX

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PI Freyssinet G, Rang C, Frutos R;
XX WPI; 2003-002439/01.
XX New modified Cry protein, useful as insecticide, comprises at least one
XX additional pepsin cleavage site to reduce persistence in mammalian gut.
XX Example 4; Page 36; 134pp; French.
XX
XX The present invention describes a modified Cry protein (I) that is
XX sensitive to pepsin and comprises at least one additional pepsin cleavage
XX site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
XX proteins by incorporating at least one extra PCS; (b) polynucleotides
XX (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
XX (II) and terminator; (d) expression or transformation vector (III) that
XX contains CG; (e) host organism (IV) transformed with (III), also, where
XX the organism is a plant, its parts and seeds; (f) production of (I) by
XX growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
XX against (I). (I) has insecticide activity. (I) can be used as
XX insecticides, particularly where expressed in transgenic plants. (I) are
XX sensitive to enzymes in the digestive tract of mammals, so do not persist
XX in the tract (lack of persistence is required by regulatory authorities
XX for use, in foods, of seeds containing Cry proteins). Extra PCS do not
XX increase degradation in the digestive tract of insects, so have no effect
XX on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 23; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXHWXXX 8
Db 1 FGERWGLT 8
|::|::|
|::|::|

Search completed: October 19, 2005, 15:40:41
Job time : 115.647 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:41:05 ; Search time 27.7647 Seconds
(without alignments)
21.509 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*

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3: /cgn2_6/prodata/1/aaa/6A_COMB.pep:.*
4: /cgn2_6/prodata/1/aaa/6B_COMB.pep:.*
5: /cgn2_6/prodata/1/aaa/ECTUS_COMB.pep:.*
6: /cgn2_6/prodata/1/aaa/backfiles1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	8	1	US-08-221-580-9
2	23	100.0	8	2	US-08-466-103A-9
3	23	100.0	8	3	US-09-063-893A-8
4	23	100.0	8	3	US-08-444-818-323
5	23	100.0	8	3	US-09-314-242-4
6	23	100.0	8	3	US-08-981-392-83
7	23	100.0	8	4	US-08-469-260A-252
8	23	100.0	8	4	US-08-488-446-252
9	23	100.0	8	4	US-08-467-344A-252
10	23	100.0	8	4	US-09-780-070-13
11	23	100.0	8	4	US-09-794-529B-4
12	23	100.0	8	4	US-09-794-517A-4
13	23	100.0	8	4	US-09-011-645E-4
14	23	100.0	8	4	US-09-794-832-4
15	23	100.0	8	4	US-09-601-729-168
16	23	100.0	8	4	US-09-239-043D-700
17	23	100.0	8	4	US-09-680-806A-4
18	23	100.0	8	4	US-08-424-550B-252
19	23	100.0	8	4	US-09-552-868-4
20	23	100.0	8	4	US-09-636-295-4
21	23	100.0	8	4	US-09-908-322-83
22	23	100.0	8	5	PCT-US95-04018-71
23	23	100.0	9	1	US-08-350-884-5
24	23	100.0	9	1	US-08-350-884-8
25	23	100.0	9	1	US-08-350-884-11
26	23	100.0	9	1	US-08-350-884-14
27	23	100.0	9	1	US-08-709-173-5

28	23	100.0	9	1	US-08-709-173-8	Sequence 8, Appli
29	23	100.0	9	1	US-08-709-173-11	Sequence 11, Appl
30	23	100.0	9	1	US-08-709-173-14	Sequence 14, Appl
31	23	100.0	9	1	US-08-615-181-30	Sequence 30, Appl
32	23	100.0	9	1	US-08-638-911A-12	Sequence 12, Appl
33	23	100.0	9	1	US-08-638-911A-15	Sequence 15, Appl
34	23	100.0	9	1	US-08-638-911A-18	Sequence 18, Appl
35	23	100.0	9	1	US-08-638-911A-21	Sequence 21, Appl
36	23	100.0	9	2	US-08-709-177-5	Sequence 5, Appli
37	23	100.0	9	2	US-08-709-177-8	Sequence 8, Appli
38	23	100.0	9	2	US-08-709-177-11	Sequence 11, Appl
39	23	100.0	9	2	US-08-709-177-14	Sequence 14, Appl
40	23	100.0	9	3	US-08-159-339A-985	Sequence 985, App
41	23	100.0	9	3	US-09-249-272-3	Sequence 3, Appli
42	23	100.0	9	4	US-09-771-415-16	Sequence 16, Appl
43	23	100.0	9	4	US-09-239-043D-774	Sequence 774, App
44	23	100.0	9	4	US-09-239-043D-2028	Sequence 2028, App
45	23	100.0	9	4	US-09-870-089B-3	Sequence 3, Appli
46	23	100.0	9	4	US-09-870-089B-7	Sequence 7, Appli
47	23	100.0	9	4	US-09-870-089B-9	Sequence 9, Appli
48	23	100.0	10	1	US-08-221-580-2	Sequence 2, Appli
49	23	100.0	10	1	US-08-306-546C-24	Sequence 24, Appl
50	23	100.0	10	1	US-08-433-318A-134	Sequence 134, App
51	23	100.0	10	1	US-08-433-318A-135	Sequence 135, App
52	23	100.0	10	1	US-08-433-318A-136	Sequence 136, App
53	23	100.0	10	1	US-08-433-318A-137	Sequence 137, App
54	23	100.0	10	1	US-08-433-318A-138	Sequence 138, App
55	23	100.0	10	1	US-08-433-318A-139	Sequence 139, App
56	23	100.0	10	1	US-08-433-318A-140	Sequence 140, App
57	23	100.0	10	1	US-08-433-318A-141	Sequence 141, App
58	23	100.0	10	1	US-08-433-318A-142	Sequence 142, App
59	23	100.0	10	1	US-08-433-318A-143	Sequence 143, App
60	23	100.0	10	1	US-08-433-318A-144	Sequence 144, App
61	23	100.0	10	1	US-08-433-318A-145	Sequence 145, App
62	23	100.0	10	1	US-08-433-318A-146	Sequence 146, App
63	23	100.0	10	1	US-08-433-318A-147	Sequence 147, App
64	23	100.0	10	1	US-08-433-318A-148	Sequence 148, App
65	23	100.0	10	1	US-08-433-318A-149	Sequence 149, App
66	23	100.0	10	1	US-08-242-678D-5	Sequence 5, Appli
67	23	100.0	10	1	US-08-487-568-88	Sequence 88, Appl
68	23	100.0	10	2	US-08-530-524A-24	Sequence 24, Appl
69	23	100.0	10	2	US-08-370-909-17	Sequence 17, Appl
70	23	100.0	10	2	US-08-318-157B-25	Sequence 25, Appl
71	23	100.0	10	2	US-08-556-597-120	Sequence 120, App
72	23	100.0	10	2	US-08-922-048-134	Sequence 134, App
73	23	100.0	10	2	US-08-922-048-135	Sequence 135, App
74	23	100.0	10	2	US-08-922-048-136	Sequence 136, App
75	23	100.0	10	2	US-08-922-048-137	Sequence 137, App
76	23	100.0	10	2	US-08-922-048-138	Sequence 138, App
77	23	100.0	10	2	US-08-922-048-139	Sequence 139, App
78	23	100.0	10	2	US-08-922-048-140	Sequence 140, App
79	23	100.0	10	2	US-08-922-048-141	Sequence 141, App
80	23	100.0	10	2	US-08-922-048-142	Sequence 142, App
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82	23	100.0	10	2	US-08-922-048-144	Sequence 144, App
83	23	100.0	10	2	US-08-922-048-145	Sequence 145, App
84	23	100.0	10	2	US-08-922-048-146	Sequence 146, App
85	23	100.0	10	2	US-08-922-048-147	Sequence 147, App
86	23	100.0	10	2	US-08-922-048-148	Sequence 148, App
87	23	100.0	10	2	US-08-922-048-149	Sequence 149, App
88	23	100.0	10	2	US-08-806-378B-3	Sequence 3, Appli
89	23	100.0	10	3	US-08-485-324-16	Sequence 16, Appl
90	23	100.0	10	3	US-08-447-506-16	Sequence 16, Appl
91	23	100.0	10	3	US-08-235-437-16	Sequence 16, Appl
92	23	100.0	10	3	US-08-447-515-16	Sequence 16, Appl
93	23	100.0	10	3	US-09-186-958-11	Sequence 11, Appl
94	23	100.0	10	3	US-09-186-958-12	Sequence 12, Appl
95	23	100.0	10	3	US-09-333-441-3	Sequence 3, Appli
96	23	100.0	10	3	US-09-669-271A-11	Sequence 11, Appl
97	23	100.0	10	3	US-09-669-271A-12	Sequence 12, Appl
98	23	100.0	10	3	US-07-901-713A-4	Sequence 4, Appli
99	23	100.0	10	4	US-09-111-681C-150	Sequence 150, App
100	23	100.0	10	4	US-09-111-681C-151	Sequence 151, App

101	23	100.0	10	4	US-09-111-681C-152	Sequence 152, App	174	23	100.0	11	4	US-09-461-325-504	Sequence 504, App
102	23	100.0	10	4	US-09-111-681C-153	Sequence 153, App	175	23	100.0	11	4	US-09-881-276-4	Sequence 4, Appl
103	23	100.0	10	4	US-09-111-681C-154	Sequence 154, App	176	23	100.0	11	4	US-09-881-276-5	Sequence 5, Appl
104	23	100.0	10	4	US-09-111-681C-155	Sequence 155, App	177	23	100.0	11	4	US-09-881-276-6	Sequence 6, Appl
105	23	100.0	10	4	US-09-111-681C-156	Sequence 156, App	178	23	100.0	11	4	US-09-881-276-7	Sequence 7, Appl
106	23	100.0	10	4	US-09-111-681C-157	Sequence 157, App	179	23	100.0	11	4	US-09-881-276-8	Sequence 8, Appl
107	23	100.0	10	4	US-09-111-681C-158	Sequence 158, App	180	23	100.0	11	4	US-09-881-276-9	Sequence 9, Appl
108	23	100.0	10	4	US-09-111-681C-159	Sequence 159, App	181	23	100.0	11	4	US-09-881-276-10	Sequence 10, Appl
109	23	100.0	10	4	US-09-111-681C-160	Sequence 160, App	182	23	100.0	11	4	US-09-881-276-11	Sequence 11, Appl
110	23	100.0	10	4	US-09-111-681C-161	Sequence 161, App	183	23	100.0	11	4	US-09-881-276-12	Sequence 12, Appl
111	23	100.0	10	4	US-09-111-681C-162	Sequence 162, App	184	23	100.0	11	4	US-09-881-276-13	Sequence 13, Appl
112	23	100.0	10	4	US-09-111-681C-163	Sequence 163, App	185	23	100.0	11	4	US-09-881-276-14	Sequence 14, Appl
113	23	100.0	10	4	US-09-111-681C-164	Sequence 164, App	186	23	100.0	11	4	US-09-756-594-5	Sequence 5, Appl
114	23	100.0	10	4	US-09-111-681C-165	Sequence 165, App	187	23	100.0	11	4	US-10-158-847-104	Sequence 104, App
115	23	100.0	10	4	US-09-495-052-2	Sequence 2, Appl	188	23	100.0	11	4	US-09-069-827A-43	Sequence 43, Appl
116	23	100.0	10	4	US-09-881-276-11	Sequence 11, Appl	189	23	100.0	11	4	US-09-069-827A-44	Sequence 44, Appl
117	23	100.0	10	4	US-09-881-276-12	Sequence 12, Appl	190	23	100.0	11	4	US-09-069-827A-45	Sequence 45, Appl
118	23	100.0	10	4	US-09-428-082B-142	Sequence 142, App	191	23	100.0	11	4	US-09-069-827A-46	Sequence 46, Appl
119	23	100.0	10	4	US-09-253-794-25	Sequence 25, Appl	192	23	100.0	11	4	US-09-069-827A-47	Sequence 47, Appl
120	23	100.0	10	4	US-09-239-043D-396	Sequence 396, App	193	23	100.0	11	4	US-09-069-827A-172	Sequence 172, App
121	23	100.0	10	4	US-09-239-043D-907	Sequence 907, App	194	23	100.0	11	4	US-10-012-542-504	Sequence 504, App
122	23	100.0	10	4	US-09-239-043D-1654	Sequence 1654, App	195	23	100.0	11	4	US-09-428-082B-325	Sequence 325, App
123	23	100.0	10	4	US-09-498-557-8	Sequence 8, Appl	196	23	100.0	11	4	US-10-136-666-1	Sequence 1, Appl
124	23	100.0	10	4	US-09-620-091-46	Sequence 46, Appl	197	23	100.0	11	4	US-09-239-043D-1108	Sequence 1108, App
125	23	100.0	10	5	PCT-US95-04018-64	Sequence 64, Appl	198	23	100.0	11	4	US-09-239-043D-1626	Sequence 1626, App
126	23	100.0	10	5	PCT-US96-06270-134	Sequence 134, App	199	23	100.0	11	4	US-09-620-091-444	Sequence 444, App
127	23	100.0	10	5	PCT-US96-06270-135	Sequence 135, App	200	23	100.0	11	4	US-10-113-123-504	Sequence 504, App
128	23	100.0	10	5	PCT-US96-06270-136	Sequence 136, App	201	23	100.0	11	4	US-08-190-788A-200	Sequence 200, App
129	23	100.0	10	5	PCT-US96-06270-137	Sequence 137, App	202	23	100.0	12	1	US-08-200-011-5	Sequence 5, Appl
130	23	100.0	10	5	PCT-US96-06270-138	Sequence 138, App	203	23	100.0	12	1	US-08-383-474B-203	Sequence 203, App
131	23	100.0	10	5	PCT-US96-06270-139	Sequence 139, App	204	23	100.0	12	1	US-08-487-568-113	Sequence 113, App
132	23	100.0	10	5	PCT-US96-06270-140	Sequence 140, App	205	23	100.0	12	1	US-08-465-391A-200	Sequence 200, App
133	23	100.0	10	5	PCT-US96-06270-141	Sequence 141, App	206	23	100.0	12	2	US-08-406-330-32	Sequence 32, Appl
134	23	100.0	10	5	PCT-US96-06270-142	Sequence 142, App	207	23	100.0	12	2	US-08-406-330-33	Sequence 33, Appl
135	23	100.0	10	5	PCT-US96-06270-143	Sequence 143, App	208	23	100.0	12	2	US-08-464-538B-200	Sequence 200, App
136	23	100.0	10	5	PCT-US96-06270-144	Sequence 144, App	209	23	100.0	12	2	US-08-556-597-32	Sequence 32, Appl
137	23	100.0	10	5	PCT-US96-06270-145	Sequence 145, App	210	23	100.0	12	2	US-08-556-597-33	Sequence 33, Appl
138	23	100.0	10	5	PCT-US96-06270-146	Sequence 146, App	211	23	100.0	12	2	US-08-463-076E-254	Sequence 254, App
139	23	100.0	10	5	PCT-US96-06270-147	Sequence 147, App	212	23	100.0	12	3	US-09-188-579-45	Sequence 45, Appl
140	23	100.0	10	5	PCT-US96-06270-148	Sequence 148, App	213	23	100.0	12	3	US-09-315-444-45	Sequence 45, Appl
141	23	100.0	10	5	PCT-US96-06270-149	Sequence 149, App	214	23	100.0	12	3	US-09-186-958-2	Sequence 2, Appl
142	23	100.0	11	1	US-08-318-970B-10	Sequence 10, Appl	215	23	100.0	12	3	US-09-186-958-13	Sequence 13, Appl
143	23	100.0	11	2	US-08-486-839-9	Sequence 9, Appl	216	23	100.0	12	3	US-09-186-958-14	Sequence 14, Appl
144	23	100.0	11	3	US-08-485-324-14	Sequence 14, Appl	217	23	100.0	12	3	US-09-186-958-15	Sequence 15, Appl
145	23	100.0	11	3	US-09-151-011-9	Sequence 9, Appl	218	23	100.0	12	3	US-09-186-958-16	Sequence 16, Appl
146	23	100.0	11	3	US-08-447-506-14	Sequence 14, Appl	219	23	100.0	12	3	US-09-669-271A-2	Sequence 2, Appl
147	23	100.0	11	3	US-08-235-437-14	Sequence 14, Appl	220	23	100.0	12	3	US-09-669-271A-13	Sequence 13, Appl
148	23	100.0	11	3	US-08-447-515-14	Sequence 14, Appl	221	23	100.0	12	3	US-09-669-271A-14	Sequence 14, Appl
149	23	100.0	11	3	US-09-224-785-5	Sequence 5, Appl	222	23	100.0	12	3	US-09-669-271A-15	Sequence 15, Appl
150	23	100.0	11	3	US-09-186-958-4	Sequence 4, Appl	223	23	100.0	12	3	US-09-669-271A-16	Sequence 16, Appl
151	23	100.0	11	3	US-09-186-958-5	Sequence 5, Appl	224	23	100.0	12	4	US-09-721-362-45	Sequence 45, Appl
152	23	100.0	11	3	US-09-186-958-6	Sequence 6, Appl	225	23	100.0	12	4	US-09-099-631A-8	Sequence 8, Appl
153	23	100.0	11	3	US-09-186-958-7	Sequence 7, Appl	226	23	100.0	12	4	US-09-099-631A-10	Sequence 10, Appl
154	23	100.0	11	3	US-09-186-958-8	Sequence 8, Appl	227	23	100.0	12	4	US-09-752-165-65	Sequence 65, Appl
155	23	100.0	11	3	US-09-186-958-9	Sequence 9, Appl	228	23	100.0	12	4	US-09-881-276-2	Sequence 2, Appl
156	23	100.0	11	3	US-09-186-958-10	Sequence 10, Appl	229	23	100.0	12	4	US-09-881-276-13	Sequence 13, Appl
157	23	100.0	11	3	US-09-186-958-11	Sequence 11, Appl	230	23	100.0	12	4	US-09-881-276-14	Sequence 14, Appl
158	23	100.0	11	3	US-09-186-958-12	Sequence 12, Appl	231	23	100.0	12	4	US-09-881-276-15	Sequence 15, Appl
159	23	100.0	11	3	US-09-186-958-13	Sequence 13, Appl	232	23	100.0	12	4	US-09-881-276-16	Sequence 16, Appl
160	23	100.0	11	3	US-09-186-958-14	Sequence 14, Appl	233	23	100.0	12	4	US-08-634-332A-70	Sequence 70, Appl
161	23	100.0	11	3	US-09-669-271A-4	Sequence 4, Appl	234	23	100.0	12	4	US-09-428-082B-131	Sequence 131, App
162	23	100.0	11	3	US-09-669-271A-5	Sequence 5, Appl	235	23	100.0	12	4	US-09-428-082B-132	Sequence 132, App
163	23	100.0	11	3	US-09-669-271A-6	Sequence 6, Appl	236	23	100.0	12	4	US-09-428-082B-133	Sequence 133, App
164	23	100.0	11	3	US-09-669-271A-7	Sequence 7, Appl	237	23	100.0	12	4	US-09-428-082B-134	Sequence 134, App
165	23	100.0	11	3	US-09-669-271A-8	Sequence 8, Appl	238	23	100.0	12	4	US-09-428-082B-135	Sequence 135, App
166	23	100.0	11	3	US-09-669-271A-9	Sequence 9, Appl	239	23	100.0	12	4	US-09-428-082B-136	Sequence 136, App
167	23	100.0	11	3	US-09-669-271A-10	Sequence 10, Appl	240	23	100.0	12	4	US-09-428-082B-137	Sequence 137, App
168	23	100.0	11	3	US-09-669-271A-11	Sequence 11, Appl	241	23	100.0	12	4	US-09-428-082B-143	Sequence 143, App
169	23	100.0	11	3	US-09-669-271A-12	Sequence 12, Appl	242	23	100.0	12	4	US-09-428-082B-144	Sequence 144, App
170	23	100.0	11	3	US-09-669-271A-13	Sequence 13, Appl	243	23	100.0	12	4	US-09-428-082B-145	Sequence 145, App
171	23	100.0	11	3	US-09-669-271A-14	Sequence 14, Appl	244	23	100.0	12	4	US-09-428-082B-146	Sequence 146, App
172	23	100.0	11	3	US-09-343-623-9	Sequence 9, Appl	245	23	100.0	12	4	US-09-428-082B-816	Sequence 816, App
173	23	100.0	11	4	US-09-081-975-21	Sequence 21, Appl	246	23	100.0	13	1	US-08-305-871A-23	Sequence 23, Appl

247	23	100.0	13	1	US-08-487-568-87	Sequence 87, Appl	320	23	100.0	14	2	US-08-922-048-107	Sequence 107, App
248	23	100.0	13	2	US-08-480-190-26	Sequence 26, Appl	321	23	100.0	14	2	US-08-922-048-108	Sequence 108, App
249	23	100.0	13	2	US-08-488-379-26	Sequence 26, Appl	322	23	100.0	14	2	US-08-922-048-109	Sequence 109, App
250	23	100.0	13	2	US-08-806-378B-1	Sequence 1, Appli	323	23	100.0	14	2	US-08-922-048-110	Sequence 110, App
251	23	100.0	13	3	US-08-911-794-3	Sequence 3, Appli	324	23	100.0	14	2	US-08-922-048-111	Sequence 111, App
252	23	100.0	13	3	US-08-912-560-11	Sequence 11, Appl	325	23	100.0	14	2	US-08-922-048-112	Sequence 112, App
253	23	100.0	13	3	US-08-702-054B-35	Sequence 35, Appl	326	23	100.0	14	2	US-08-922-048-113	Sequence 113, App
254	23	100.0	13	3	US-09-333-441-1	Sequence 11, Appli	327	23	100.0	14	2	US-08-922-048-114	Sequence 114, App
255	23	100.0	13	3	US-09-085-072-7	Sequence 7, Appli	328	23	100.0	14	2	US-08-922-048-115	Sequence 115, App
256	23	100.0	13	3	US-09-236-415-5	Sequence 5, Appli	329	23	100.0	14	2	US-08-922-048-116	Sequence 116, App
257	23	100.0	13	4	US-08-788-822A-27	Sequence 27, Appl	330	23	100.0	14	2	US-08-922-048-117	Sequence 117, App
258	23	100.0	13	4	US-09-222-779-2	Sequence 2, Appli	331	23	100.0	14	2	US-08-922-048-118	Sequence 118, App
259	23	100.0	13	4	US-09-081-975-9	Sequence 9, Appli	332	23	100.0	14	2	US-08-922-048-119	Sequence 119, App
260	23	100.0	13	4	US-08-475-399A-26	Sequence 26, Appl	333	23	100.0	14	2	US-08-922-048-166	Sequence 166, App
261	23	100.0	13	4	US-10-158-847-103	Sequence 103, App	334	23	100.0	14	2	US-08-922-048-167	Sequence 167, App
262	23	100.0	13	4	US-10-158-847-105	Sequence 105, App	335	23	100.0	14	2	US-08-922-048-168	Sequence 168, App
263	23	100.0	13	4	US-10-158-847-108	Sequence 108, App	336	23	100.0	14	2	US-08-922-048-169	Sequence 169, App
264	23	100.0	13	4	US-10-158-847-109	Sequence 109, App	337	23	100.0	14	2	US-08-922-048-170	Sequence 170, App
265	23	100.0	13	4	US-10-158-847-110	Sequence 110, App	338	23	100.0	14	2	US-08-922-048-171	Sequence 171, App
266	23	100.0	13	4	US-09-543-608A-27	Sequence 27, Appl	339	23	100.0	14	2	US-08-922-048-172	Sequence 172, App
267	23	100.0	13	4	US-08-077-255A-26	Sequence 26, Appl	340	23	100.0	14	2	US-08-922-048-173	Sequence 173, App
268	23	100.0	13	4	US-09-556-818-65	Sequence 65, Appl	341	23	100.0	14	2	US-08-922-048-174	Sequence 174, App
269	23	100.0	13	4	US-09-695-437A-42	Sequence 42, Appl	342	23	100.0	14	2	US-08-922-048-176	Sequence 176, App
270	23	100.0	13	5	PCT-US93-07545-26	Sequence 26, Appl	343	23	100.0	14	2	US-08-922-048-177	Sequence 177, App
271	23	100.0	13	5	PCT-US94-01234-47	Sequence 47, Appl	344	23	100.0	14	2	US-08-922-048-178	Sequence 178, App
272	23	100.0	13	6	5185431-25	Patent No. 5185431	345	23	100.0	14	2	US-08-922-048-179	Sequence 179, App
273	23	100.0	13	6	5185431-25	Patent No. 5185431	346	23	100.0	14	2	US-08-922-048-180	Sequence 180, App
274	23	100.0	14	1	US-08-433-318A-102	Sequence 102, App	347	23	100.0	14	2	US-08-806-378B-2	Sequence 2, Appli
275	23	100.0	14	1	US-08-433-318A-103	Sequence 103, App	348	23	100.0	14	3	US-08-564-225-10	Sequence 10, Appl
276	23	100.0	14	1	US-08-433-318A-104	Sequence 104, App	349	23	100.0	14	3	US-09-129-855A-10	Sequence 10, Appl
277	23	100.0	14	1	US-08-433-318A-105	Sequence 105, App	350	23	100.0	14	3	US-08-973-225-33	Sequence 33, Appl
278	23	100.0	14	1	US-08-433-318A-106	Sequence 106, App	351	23	100.0	14	3	US-08-973-225-213	Sequence 213, App
279	23	100.0	14	1	US-08-433-318A-107	Sequence 107, App	352	23	100.0	14	3	US-09-244-298A-33	Sequence 33, Appl
280	23	100.0	14	1	US-08-433-318A-108	Sequence 108, App	353	23	100.0	14	3	US-09-247-154-10	Sequence 10, Appl
281	23	100.0	14	1	US-08-433-318A-109	Sequence 109, App	354	23	100.0	14	3	US-08-786-455B-4	Sequence 4, Appli
282	23	100.0	14	1	US-08-433-318A-110	Sequence 110, App	355	23	100.0	14	3	US-09-516-704-33	Sequence 33, Appl
283	23	100.0	14	1	US-08-433-318A-111	Sequence 111, App	356	23	100.0	14	3	US-09-516-704-33	Sequence 2, Appli
284	23	100.0	14	1	US-08-433-318A-112	Sequence 112, App	357	23	100.0	14	3	US-09-333-441-2	Sequence 10, Appl
285	23	100.0	14	1	US-08-433-318A-113	Sequence 113, App	358	23	100.0	14	4	US-09-480-718-10	Sequence 118, App
286	23	100.0	14	1	US-08-433-318A-114	Sequence 114, App	359	23	100.0	14	4	US-09-111-681C-118	Sequence 119, App
287	23	100.0	14	1	US-08-433-318A-115	Sequence 115, App	360	23	100.0	14	4	US-09-111-681C-119	Sequence 120, App
288	23	100.0	14	1	US-08-433-318A-116	Sequence 116, App	361	23	100.0	14	4	US-09-111-681C-120	Sequence 121, App
289	23	100.0	14	1	US-08-433-318A-117	Sequence 117, App	362	23	100.0	14	4	US-09-111-681C-121	Sequence 122, App
290	23	100.0	14	1	US-08-433-318A-118	Sequence 118, App	363	23	100.0	14	4	US-09-111-681C-122	Sequence 123, App
291	23	100.0	14	1	US-08-433-318A-119	Sequence 119, App	364	23	100.0	14	4	US-09-111-681C-123	Sequence 124, App
292	23	100.0	14	1	US-08-433-318A-166	Sequence 166, App	365	23	100.0	14	4	US-09-111-681C-124	Sequence 125, App
293	23	100.0	14	1	US-08-433-318A-167	Sequence 167, App	366	23	100.0	14	4	US-09-111-681C-125	Sequence 126, App
294	23	100.0	14	1	US-08-433-318A-168	Sequence 168, App	367	23	100.0	14	4	US-09-111-681C-126	Sequence 127, App
295	23	100.0	14	1	US-08-433-318A-169	Sequence 169, App	368	23	100.0	14	4	US-09-111-681C-127	Sequence 128, App
296	23	100.0	14	1	US-08-433-318A-170	Sequence 170, App	369	23	100.0	14	4	US-09-111-681C-128	Sequence 129, App
297	23	100.0	14	1	US-08-433-318A-171	Sequence 171, App	370	23	100.0	14	4	US-09-111-681C-129	Sequence 130, App
298	23	100.0	14	1	US-08-433-318A-172	Sequence 172, App	371	23	100.0	14	4	US-09-111-681C-130	Sequence 131, App
299	23	100.0	14	1	US-08-433-318A-173	Sequence 173, App	372	23	100.0	14	4	US-09-111-681C-131	Sequence 132, App
300	23	100.0	14	1	US-08-433-318A-174	Sequence 174, App	373	23	100.0	14	4	US-09-111-681C-132	Sequence 133, App
301	23	100.0	14	1	US-08-433-318A-175	Sequence 175, App	374	23	100.0	14	4	US-09-111-681C-133	Sequence 181, App
302	23	100.0	14	1	US-08-433-318A-176	Sequence 176, App	375	23	100.0	14	4	US-09-111-681C-181	Sequence 182, App
303	23	100.0	14	1	US-08-433-318A-177	Sequence 177, App	376	23	100.0	14	4	US-09-111-681C-182	Sequence 183, App
304	23	100.0	14	1	US-08-433-318A-178	Sequence 178, App	377	23	100.0	14	4	US-09-111-681C-183	Sequence 184, App
305	23	100.0	14	1	US-08-433-318A-179	Sequence 179, App	378	23	100.0	14	4	US-09-111-681C-184	Sequence 185, App
306	23	100.0	14	1	US-08-433-318A-180	Sequence 180, App	379	23	100.0	14	4	US-09-111-681C-185	Sequence 186, App
307	23	100.0	14	2	US-08-534-975-10	Sequence 10, Appl	380	23	100.0	14	4	US-09-111-681C-186	Sequence 187, App
308	23	100.0	14	2	US-08-449-933-11	Sequence 11, Appl	381	23	100.0	14	4	US-09-111-681C-187	Sequence 188, App
309	23	100.0	14	2	US-08-392-816-12	Sequence 12, Appl	382	23	100.0	14	4	US-09-111-681C-188	Sequence 189, App
310	23	100.0	14	2	US-08-764-640-33	Sequence 33, Appl	383	23	100.0	14	4	US-09-111-681C-189	Sequence 190, App
311	23	100.0	14	2	US-08-954-470-10	Sequence 10, Appl	384	23	100.0	14	4	US-09-111-681C-190	Sequence 191, App
312	23	100.0	14	2	US-08-750-359-3	Sequence 3, Appli	385	23	100.0	14	4	US-09-111-681C-191	Sequence 192, App
313	23	100.0	14	2	US-08-750-359-4	Sequence 4, Appli	386	23	100.0	14	4	US-09-111-681C-192	Sequence 193, App
314	23	100.0	14	2	US-08-685-589A-192	Sequence 192, App	387	23	100.0	14	4	US-09-111-681C-193	Sequence 194, App
315	23	100.0	14	2	US-08-685-589A-193	Sequence 193, App	388	23	100.0	14	4	US-09-111-681C-194	Sequence 195, App
316	23	100.0	14	2	US-08-922-048-102	Sequence 102, App	389	23	100.0	14	4	US-09-111-681C-195	Sequence 196, App
317	23	100.0	14	2	US-08-922-048-103	Sequence 103, App	390	23	100.0	14	4	US-09-111-681C-196	Sequence 33, Appl
318	23	100.0	14	2	US-08-922-048-104	Sequence 104, App	391	23	100.0	14	4	US-09-549-090-33	Sequence 213, App
319	23	100.0	14	2	US-08-922-048-105	Sequence 105, App	392	23	100.0	14	4	US-09-549-090-213	

393	23	100.0	14	4	US-09-461-325-508	Sequence 508, App	466	23	100.0	15	3	US-09-035-686-21	Sequence 21, Appl
394	23	100.0	14	4	US-09-610-833-10	Sequence 10, Appl	467	23	100.0	15	3	US-09-035-686-22	Sequence 22, Appl
395	23	100.0	14	4	US-09-832-230A-33	Sequence 33, Appl	468	23	100.0	15	3	US-09-224-480-51	Sequence 51, Appl
396	23	100.0	14	4	US-09-129-855A-10	Sequence 10, Appl	469	23	100.0	15	3	US-08-702-054B-21	Sequence 21, Appl
397	23	100.0	14	4	US-10-158-847-115	Sequence 115, App	470	23	100.0	15	3	US-09-217-352-9	Sequence 9, Appl
398	23	100.0	14	4	US-10-158-847-116	Sequence 116, App	471	23	100.0	15	3	US-09-063-733A-28	Sequence 28, Appl
399	23	100.0	14	4	US-10-158-847-119	Sequence 119, App	472	23	100.0	15	4	US-09-009-953-247	Sequence 247, App
400	23	100.0	14	4	US-10-012-542-508	Sequence 508, App	473	23	100.0	15	4	US-08-487-795A-2	Sequence 2, Appl
401	23	100.0	14	4	US-09-428-082B-68	Sequence 68, Appl	474	23	100.0	15	4	US-08-487-795A-3	Sequence 3, Appl
402	23	100.0	14	4	US-09-620-091-87	Sequence 87, Appl	475	23	100.0	15	4	US-08-487-795A-16	Sequence 16, Appl
403	23	100.0	14	4	US-10-115-123-508	Sequence 508, App	476	23	100.0	15	4	US-08-487-795A-17	Sequence 17, Appl
404	23	100.0	14	5	PCT-US96-06270-102	Sequence 102, App	477	23	100.0	15	4	US-08-487-795A-19	Sequence 19, Appl
405	23	100.0	14	5	PCT-US96-06270-103	Sequence 103, App	478	23	100.0	15	4	US-08-121-105B-2	Sequence 2, Appl
406	23	100.0	14	5	PCT-US96-06270-104	Sequence 104, App	479	23	100.0	15	4	US-08-121-105B-3	Sequence 3, Appl
407	23	100.0	14	5	PCT-US96-06270-105	Sequence 105, App	480	23	100.0	15	4	US-08-121-105B-16	Sequence 16, Appl
408	23	100.0	14	5	PCT-US96-06270-106	Sequence 106, App	481	23	100.0	15	4	US-08-121-105B-17	Sequence 17, Appl
409	23	100.0	14	5	PCT-US96-06270-107	Sequence 107, App	482	23	100.0	15	4	US-08-121-105B-19	Sequence 19, Appl
410	23	100.0	14	5	PCT-US96-06270-108	Sequence 108, App	483	23	100.0	15	4	US-09-081-975-24	Sequence 24, Appl
411	23	100.0	14	5	PCT-US96-06270-109	Sequence 109, App	484	23	100.0	15	4	US-09-461-325-295	Sequence 295, App
412	23	100.0	14	5	PCT-US96-06270-110	Sequence 110, App	485	23	100.0	15	4	US-09-914-293-165	Sequence 165, App
413	23	100.0	14	5	PCT-US96-06270-111	Sequence 111, App	486	23	100.0	15	4	US-08-634-332A-64	Sequence 64, Appl
414	23	100.0	14	5	PCT-US96-06270-112	Sequence 112, App	487	23	100.0	15	4	US-08-634-332A-65	Sequence 65, Appl
415	23	100.0	14	5	PCT-US96-06270-113	Sequence 113, App	488	23	100.0	15	4	US-08-634-332A-69	Sequence 69, Appl
416	23	100.0	14	5	PCT-US96-06270-114	Sequence 114, App	489	23	100.0	15	4	US-09-441-992-10	Sequence 10, Appl
417	23	100.0	14	5	PCT-US96-06270-115	Sequence 115, App	490	23	100.0	15	4	US-09-441-992-49	Sequence 49, Appl
418	23	100.0	14	5	PCT-US96-06270-116	Sequence 116, App	491	23	100.0	15	4	US-09-441-992-50	Sequence 50, Appl
419	23	100.0	14	5	PCT-US96-06270-117	Sequence 117, App	492	23	100.0	15	4	US-09-441-992-51	Sequence 51, Appl
420	23	100.0	14	5	PCT-US96-06270-165	Sequence 165, App	493	23	100.0	15	4	US-09-441-992-52	Sequence 52, Appl
421	23	100.0	14	5	PCT-US96-06270-166	Sequence 166, App	494	23	100.0	15	4	US-09-574-749B-54	Sequence 54, Appl
422	23	100.0	14	5	PCT-US96-06270-167	Sequence 167, App	495	23	100.0	15	4	US-09-644-442-7	Sequence 7, Appl
423	23	100.0	14	5	PCT-US96-06270-168	Sequence 168, App	496	23	100.0	15	4	US-09-157-689-51	Sequence 51, Appl
424	23	100.0	14	5	PCT-US96-06270-169	Sequence 169, App	497	23	100.0	15	4	US-09-157-689-52	Sequence 52, Appl
425	23	100.0	14	5	PCT-US96-06270-170	Sequence 170, App	498	23	100.0	15	4	US-10-013-542-295	Sequence 295, App
426	23	100.0	14	5	PCT-US96-06270-171	Sequence 171, App	499	23	100.0	15	4	US-09-428-082B-138	Sequence 138, App
427	23	100.0	14	5	PCT-US96-06270-172	Sequence 172, App	500	23	100.0	15	4	US-09-428-082B-139	Sequence 139, App
428	23	100.0	14	5	PCT-US96-06270-173	Sequence 173, App	501	23	100.0	15	4	US-09-428-082B-140	Sequence 140, App
429	23	100.0	14	5	PCT-US96-06270-174	Sequence 174, App	502	23	100.0	15	4	US-09-428-082B-141	Sequence 141, App
430	23	100.0	14	5	PCT-US96-06270-175	Sequence 175, App	503	23	100.0	15	4	US-09-689-097-53	Sequence 53, Appl
431	23	100.0	14	5	PCT-US96-06270-176	Sequence 176, App	504	23	100.0	15	4	US-09-239-043D-2142	Sequence 2142, Ap
432	23	100.0	14	5	PCT-US96-06270-177	Sequence 177, App	505	23	100.0	15	4	US-09-204-730B-10	Sequence 10, Appl
433	23	100.0	14	5	PCT-US96-06270-178	Sequence 178, App	506	23	100.0	15	4	US-09-142-524D-88	Sequence 88, Appl
434	23	100.0	14	5	PCT-US96-06270-179	Sequence 179, App	507	23	100.0	15	4	US-09-316-393-10	Sequence 10, Appl
435	23	100.0	14	5	PCT-US96-06270-180	Sequence 180, App	508	23	100.0	15	4	US-10-115-123-295	Sequence 295, App
436	23	100.0	15	1	US-08-311-611A-51	Sequence 51, Appl	509	23	100.0	15	4	US-09-953-510-51	Sequence 51, Appl
437	23	100.0	15	1	US-08-218-025A-139	Sequence 139, App	510	23	100.0	15	4	US-09-953-510-52	Sequence 52, Appl
438	23	100.0	15	1	US-08-372-783-51	Sequence 51, Appl	511	23	100.0	15	4	US-09-581-472B-4	Sequence 4, Appl
439	23	100.0	15	1	US-08-056-200-22	Sequence 22, Appl	512	23	100.0	15	4	US-09-732-384-6	Sequence 6, Appl
440	23	100.0	15	1	US-08-372-105-51	Sequence 51, Appl	513	23	100.0	15	5	PCT-US93-08699-1	Sequence 1, Appl
441	23	100.0	15	1	US-08-148-160-2	Sequence 2, Appl	514	23	100.0	15	5	PCT-US94-02465-51	Sequence 51, Appl
442	23	100.0	15	1	US-08-306-473A-51	Sequence 51, Appl	515	23	100.0	15	5	PCT-US94-10356-2	Sequence 2, Appl
443	23	100.0	15	1	US-08-277-660A-1	Sequence 1, Appl	516	23	100.0	15	5	PCT-US94-10356-3	Sequence 3, Appl
444	23	100.0	15	1	US-08-277-660A-5	Sequence 5, Appl	517	23	100.0	15	5	PCT-US94-10356-6	Sequence 6, Appl
445	23	100.0	15	1	US-08-277-660A-6	Sequence 6, Appl	518	23	100.0	15	5	PCT-US94-10356-7	Sequence 7, Appl
446	23	100.0	15	1	US-08-209-762-51	Sequence 51, Appl	519	23	100.0	15	5	PCT-US94-10356-20	Sequence 20, Appl
447	23	100.0	15	1	US-08-625-691-10	Sequence 10, Appl	520	23	100.0	15	5	PCT-US94-10356-22	Sequence 22, Appl
448	23	100.0	15	1	US-08-424-957-1	Sequence 1, Appl	521	23	100.0	15	5	PCT-US95-00498-51	Sequence 51, Appl
449	23	100.0	15	1	US-08-424-957-21	Sequence 21, Appl	522	23	100.0	15	5	PCT-US95-00656-51	Sequence 51, Appl
450	23	100.0	15	1	US-08-424-957-22	Sequence 22, Appl	523	23	100.0	16	1	US-07-959-946-5	Sequence 5, Appl
451	23	100.0	15	1	US-08-487-568-112	Sequence 112, App	524	23	100.0	16	1	US-08-079-051-2	Sequence 2, Appl
452	23	100.0	15	2	US-08-621-803-9	Sequence 9, Appl	525	23	100.0	16	1	US-08-077-797A-43	Sequence 43, Appl
453	23	100.0	15	2	US-08-485-445A-51	Sequence 51, Appl	526	23	100.0	16	1	US-08-473-344-51	Sequence 51, Appl
454	23	100.0	15	2	US-08-800-644-22	Sequence 22, Appl	527	23	100.0	16	1	US-08-333-577-5	Sequence 5, Appl
455	23	100.0	15	2	US-08-553-257A-10	Sequence 10, Appl	528	23	100.0	16	2	US-08-629-291A-19	Sequence 19, Appl
456	23	100.0	15	2	US-08-553-257A-49	Sequence 49, Appl	529	23	100.0	16	2	US-08-658-335B-19	Sequence 19, Appl
457	23	100.0	15	2	US-08-553-257A-50	Sequence 50, Appl	530	23	100.0	16	3	US-08-930-776-1	Sequence 1, Appl
458	23	100.0	15	2	US-08-553-257A-51	Sequence 51, Appl	531	23	100.0	16	3	US-09-149-303-1	Sequence 1, Appl
459	23	100.0	15	3	US-08-553-257A-52	Sequence 52, Appl	532	23	100.0	16	3	US-09-171-705-32	Sequence 32, Appl
460	23	100.0	15	3	US-08-292-345B-10	Sequence 10, Appl	533	23	100.0	16	3	US-09-093-539-51	Sequence 51, Appl
461	23	100.0	15	3	US-09-119-263-51	Sequence 51, Appl	534	23	100.0	16	4	US-09-009-953-39	Sequence 39, Appl
462	23	100.0	15	3	US-09-165-042-16	Sequence 16, Appl	535	23	100.0	16	4	US-09-009-953-230	Sequence 230, App
463	23	100.0	15	3	US-08-657-162-51	Sequence 51, Appl	536	23	100.0	16	4	US-09-458-745-1	Sequence 1, Appl
464	23	100.0	15	3	US-08-847-844A-22	Sequence 22, Appl	537	23	100.0	16	4	US-09-330-914A-11	Sequence 11, Appl
465	23	100.0	15	3	US-09-035-686-1	Sequence 1, Appl	538	23	100.0	16	4	US-09-406-640-19	Sequence 19, Appl

539	23	100.0	16	4	US-09-081-975-23	Sequence 23, Appl	612	23	100.0	17	2	US-08-746-257A-5	Sequence 5, Appl
540	23	100.0	16	4	US-09-790-230-51	Sequence 51, Appl	613	23	100.0	17	2	US-08-488-379-123	Sequence 123, App
541	23	100.0	16	4	US-08-413-233-3	Sequence 3, Appl	614	23	100.0	17	2	US-08-871-355A-238	Sequence 238, App
542	23	100.0	16	4	US-09-690-454-88	Sequence 88, Appl	615	23	100.0	17	3	US-08-990-823-88	Sequence 88, Appl
543	23	100.0	16	4	US-08-311-784B-308	Sequence 308, App	616	23	100.0	17	3	US-08-990-823-89	Sequence 89, Appl
544	23	100.0	16	4	US-09-170-496D-285	Sequence 285, App	617	23	100.0	17	3	US-09-082-279B-814	Sequence 814, App
545	23	100.0	16	4	US-09-546-013-72	Sequence 72, Appl	618	23	100.0	17	3	US-09-201-945-238	Sequence 238, App
546	23	100.0	16	4	US-09-620-091-89	Sequence 89, Appl	619	23	100.0	17	3	US-09-315-304B-814	Sequence 814, App
547	23	100.0	16	4	US-09-620-091-445	Sequence 445, App	620	23	100.0	17	4	US-08-487-795A-15	Sequence 15, Appl
548	23	100.0	16	4	US-09-854-133-587	Sequence 587, App	621	23	100.0	17	4	US-08-487-795A-18	Sequence 18, Appl
549	23	100.0	16	4	US-09-541-345-4	Sequence 4, Appl	622	23	100.0	17	4	US-08-121-105B-15	Sequence 15, Appl
550	23	100.0	16	4	US-09-541-345-20	Sequence 20, Appl	623	23	100.0	17	4	US-08-121-105B-18	Sequence 18, Appl
551	23	100.0	16	4	US-09-541-345-35	Sequence 35, Appl	624	23	100.0	17	4	US-08-475-399A-123	Sequence 123, App
552	23	100.0	16	4	US-09-541-345-37	Sequence 37, Appl	625	23	100.0	17	4	US-09-170-496D-286	Sequence 286, App
553	23	100.0	16	4	US-09-541-345-38	Sequence 38, Appl	626	23	100.0	17	4	US-09-834-784-814	Sequence 814, App
554	23	100.0	16	4	US-09-541-345-39	Sequence 39, Appl	627	23	100.0	17	4	US-09-477-135A-88	Sequence 88, Appl
555	23	100.0	16	4	US-09-541-345-40	Sequence 40, Appl	628	23	100.0	17	4	US-09-477-135A-89	Sequence 89, Appl
556	23	100.0	16	4	US-09-541-345-41	Sequence 41, Appl	629	23	100.0	17	4	US-09-515-965A-814	Sequence 814, App
557	23	100.0	16	4	US-09-541-345-42	Sequence 42, Appl	630	23	100.0	17	4	US-09-350-641C-814	Sequence 814, App
558	23	100.0	16	4	US-09-541-345-43	Sequence 43, Appl	631	23	100.0	17	4	US-09-428-082B-209	Sequence 209, App
559	23	100.0	16	4	US-09-541-345-44	Sequence 44, Appl	632	23	100.0	17	4	US-08-077-255A-123	Sequence 123, App
560	23	100.0	16	4	US-09-541-345-45	Sequence 45, Appl	633	23	100.0	17	4	US-09-350-841A-814	Sequence 814, App
561	23	100.0	16	4	US-09-541-345-46	Sequence 46, Appl	634	23	100.0	17	4	US-09-695-437A-40	Sequence 40, Appl
562	23	100.0	16	4	US-09-541-345-47	Sequence 47, Appl	635	23	100.0	17	5	PCT-US93-07545-123	Sequence 123, App
563	23	100.0	16	4	US-09-541-345-48	Sequence 48, Appl	636	23	100.0	17	5	PCT-US94-05684-7	Sequence 7, Appl
564	23	100.0	16	4	US-09-541-345-50	Sequence 50, Appl	637	23	100.0	17	5	PCT-US94-10356-19	Sequence 19, Appl
565	23	100.0	16	4	US-09-541-345-51	Sequence 51, Appl	638	23	100.0	17	5	PCT-US94-10356-21	Sequence 21, Appl
566	23	100.0	16	4	US-09-541-345-52	Sequence 52, Appl	639	23	100.0	18	1	US-08-218-025A-3	Sequence 3, Appl
567	23	100.0	16	4	US-09-541-345-53	Sequence 53, Appl	640	23	100.0	18	1	US-08-375-100-3	Sequence 3, Appl
568	23	100.0	16	4	US-09-541-345-55	Sequence 55, Appl	641	23	100.0	18	2	US-08-248-839C-166	Sequence 166, App
569	23	100.0	16	4	US-09-541-345-56	Sequence 56, Appl	642	23	100.0	18	2	US-08-448-603A-24	Sequence 24, Appl
570	23	100.0	16	4	US-09-541-345-57	Sequence 57, Appl	643	23	100.0	18	2	US-08-934-915-125	Sequence 125, App
571	23	100.0	16	4	US-09-541-345-58	Sequence 58, Appl	644	23	100.0	18	2	US-08-484-905-36	Sequence 36, Appl
572	23	100.0	16	4	US-09-541-345-59	Sequence 59, Appl	645	23	100.0	18	3	US-08-940-095-199	Sequence 199, App
573	23	100.0	16	4	US-09-541-345-61	Sequence 61, Appl	646	23	100.0	18	3	US-08-940-095-224	Sequence 224, App
574	23	100.0	16	4	US-09-541-345-62	Sequence 62, Appl	647	23	100.0	18	3	US-08-481-985B-39	Sequence 39, App
575	23	100.0	16	4	US-09-541-345-63	Sequence 63, Appl	648	23	100.0	18	3	US-08-940-093-199	Sequence 199, App
576	23	100.0	16	4	US-09-541-345-64	Sequence 64, Appl	649	23	100.0	18	3	US-08-940-093-224	Sequence 224, App
577	23	100.0	16	4	US-09-541-345-66	Sequence 66, Appl	650	23	100.0	18	3	US-09-134-075-24	Sequence 24, Appl
578	23	100.0	16	4	US-09-541-345-68	Sequence 68, Appl	651	23	100.0	18	3	US-08-940-096-199	Sequence 199, App
579	23	100.0	16	4	US-09-541-345-69	Sequence 69, Appl	652	23	100.0	18	3	US-08-940-096-224	Sequence 224, App
580	23	100.0	16	4	US-09-541-345-71	Sequence 71, Appl	653	23	100.0	18	3	US-08-513-968-40	Sequence 40, Appl
581	23	100.0	16	4	US-09-541-345-73	Sequence 73, Appl	654	23	100.0	18	3	US-08-370-476-36	Sequence 36, Appl
582	23	100.0	16	4	US-09-541-345-74	Sequence 74, Appl	655	23	100.0	18	3	US-09-082-279B-1147	Sequence 1147, Ap
583	23	100.0	16	4	US-09-541-345-75	Sequence 75, Appl	656	23	100.0	18	3	US-09-465-719-199	Sequence 199, App
584	23	100.0	16	4	US-09-541-345-76	Sequence 76, Appl	657	23	100.0	18	3	US-09-465-719-224	Sequence 224, App
585	23	100.0	16	4	US-09-541-345-77	Sequence 77, Appl	658	23	100.0	18	3	US-09-025-769B-249	Sequence 249, App
586	23	100.0	16	4	US-09-541-345-79	Sequence 79, Appl	659	23	100.0	18	3	US-09-453-605-199	Sequence 199, App
587	23	100.0	16	4	US-09-541-345-81	Sequence 81, Appl	660	23	100.0	18	3	US-09-453-605-224	Sequence 224, App
588	23	100.0	16	4	US-09-541-345-83	Sequence 83, Appl	661	23	100.0	18	3	US-09-492-739-24	Sequence 24, Appl
589	23	100.0	16	4	US-09-541-345-84	Sequence 84, Appl	662	23	100.0	18	3	US-08-992-877-16	Sequence 16, Appl
590	23	100.0	16	4	US-09-541-345-85	Sequence 85, Appl	663	23	100.0	18	3	US-09-315-304B-1147	Sequence 1147, Ap
591	23	100.0	16	4	US-09-541-345-86	Sequence 86, Appl	664	23	100.0	18	3	US-09-453-838-199	Sequence 199, App
592	23	100.0	16	4	US-09-541-345-89	Sequence 89, Appl	665	23	100.0	18	3	US-09-453-838-224	Sequence 224, App
593	23	100.0	16	4	US-09-541-345-91	Sequence 91, Appl	666	23	100.0	18	4	US-09-081-975-22	Sequence 22, Appl
594	23	100.0	16	4	US-09-541-345-92	Sequence 92, Appl	667	23	100.0	18	4	US-08-940-136-199	Sequence 199, App
595	23	100.0	16	4	US-09-541-345-96	Sequence 96, Appl	668	23	100.0	18	4	US-08-940-136-224	Sequence 224, App
596	23	100.0	16	4	US-09-541-345-98	Sequence 98, Appl	669	23	100.0	18	4	US-08-634-332A-8	Sequence 8, Appl
597	23	100.0	16	4	US-09-541-345-99	Sequence 99, Appl	670	23	100.0	18	4	US-08-634-332A-9	Sequence 9, Appl
598	23	100.0	16	4	US-09-541-345-100	Sequence 100, App	671	23	100.0	18	4	US-08-634-332A-11	Sequence 11, Appl
599	23	100.0	16	4	US-09-541-345-104	Sequence 104, App	672	23	100.0	18	4	US-08-634-332A-11	Sequence 11, Appl
600	23	100.0	16	4	US-09-541-345-105	Sequence 105, App	673	23	100.0	18	4	US-08-634-332A-12	Sequence 12, Appl
601	23	100.0	16	4	US-09-541-345-106	Sequence 106, App	674	23	100.0	18	4	US-08-634-332A-13	Sequence 13, Appl
602	23	100.0	16	4	US-09-269-703A-1	Sequence 1, Appl	675	23	100.0	18	4	US-08-634-332A-24	Sequence 24, Appl
603	23	100.0	16	5	PCT-US92-08634-5	Sequence 5, Appl	676	23	100.0	18	4	US-08-634-332A-25	Sequence 25, Appl
604	23	100.0	16	5	PCT-US94-01238-43	Sequence 43, Appl	677	23	100.0	18	4	US-08-634-332A-62	Sequence 62, Appl
605	23	100.0	16	5	PCT-US94-06994-2	Sequence 2, Appl	678	23	100.0	18	4	US-08-634-332A-63	Sequence 63, Appl
606	23	100.0	17	1	US-08-370-567-7	Sequence 7, Appl	679	23	100.0	18	4	US-09-834-784-1147	Sequence 1147, Ap
607	23	100.0	17	1	US-08-438-759-7	Sequence 7, Appl	680	23	100.0	18	4	US-09-453-841-199	Sequence 199, App
608	23	100.0	17	2	US-08-480-190-123	Sequence 123, App	681	23	100.0	18	4	US-09-453-841-224	Sequence 224, App
609	23	100.0	17	2	US-08-746-283-7	Sequence 7, Appl	682	23	100.0	18	4	US-10-158-847-78	Sequence 78, Appl
610	23	100.0	17	2	US-08-545-562A-64	Sequence 64, Appl	683	23	100.0	18	4	US-10-158-847-88	Sequence 88, Appl
611	23	100.0	17	2	US-08-637-759B-238	Sequence 238, App	684	23	100.0	18	4	US-10-158-847-120	Sequence 120, App

685	23	100.0	18	4	US-09-453-833-199	Sequence 199, App	758	23	100.0	20	1	US-08-372-105-151	Sequence 151, App
686	23	100.0	18	4	US-09-453-833-224	Sequence 224, App	759	23	100.0	20	1	US-08-372-105-152	Sequence 152, App
687	23	100.0	18	4	US-09-515-968A-1147	Sequence 1147, App	760	23	100.0	20	1	US-08-372-105-159	Sequence 159, App
688	23	100.0	18	4	US-09-453-826-199	Sequence 199, App	761	23	100.0	20	1	US-08-372-105-160	Sequence 160, App
689	23	100.0	18	4	US-09-453-826-224	Sequence 224, App	762	23	100.0	20	1	US-08-321-625-36	Sequence 36, Appl
690	23	100.0	18	4	US-09-350-641C-1147	Sequence 1147, App	763	23	100.0	20	1	US-08-306-473A-54	Sequence 54, Appl
691	23	100.0	18	4	US-09-490-070A-249	Sequence 249, App	764	23	100.0	20	1	US-08-306-473A-57	Sequence 57, Appl
692	23	100.0	18	4	US-09-490-153-249	Sequence 249, App	765	23	100.0	20	1	US-08-306-473A-58	Sequence 58, Appl
693	23	100.0	18	4	US-09-620-091-195	Sequence 195, App	766	23	100.0	20	1	US-08-306-473A-59	Sequence 59, Appl
694	23	100.0	18	4	US-09-453-840-199	Sequence 199, App	767	23	100.0	20	1	US-08-306-473A-101	Sequence 101, App
695	23	100.0	18	4	US-09-453-840-224	Sequence 224, App	768	23	100.0	20	1	US-08-306-473A-150	Sequence 150, App
696	23	100.0	18	4	US-09-865-989-199	Sequence 199, App	769	23	100.0	20	1	US-08-306-473A-151	Sequence 151, App
697	23	100.0	18	4	US-09-865-989-224	Sequence 224, App	770	23	100.0	20	1	US-08-306-473A-152	Sequence 152, App
698	23	100.0	18	4	US-09-350-841A-1147	Sequence 1147, App	771	23	100.0	20	1	US-08-306-473A-159	Sequence 159, App
699	23	100.0	18	4	US-09-453-834-199	Sequence 199, App	772	23	100.0	20	1	US-08-306-473A-160	Sequence 160, App
700	23	100.0	18	4	US-09-453-834-224	Sequence 224, App	773	23	100.0	20	1	US-08-209-762-54	Sequence 54, Appl
701	23	100.0	18	4	US-09-695-437A-64	Sequence 63, Appl	774	23	100.0	20	1	US-08-209-762-57	Sequence 57, Appl
702	23	100.0	18	4	US-09-695-437A-64	Sequence 64, Appl	775	23	100.0	20	1	US-08-209-762-58	Sequence 58, Appl
703	23	100.0	18	4	US-09-966-931A-24	Sequence 24, Appl	776	23	100.0	20	1	US-08-209-762-59	Sequence 59, Appl
704	23	100.0	18	4	US-09-774-639-236	Sequence 236, App	777	23	100.0	20	1	US-08-473-344-54	Sequence 54, Appl
705	23	100.0	18	4	US-09-490-324-249	Sequence 249, App	778	23	100.0	20	2	US-08-493-235-31	Sequence 31, Appl
706	23	100.0	19	2	US-08-537-400-35	Sequence 35, Appl	779	23	100.0	20	2	US-08-621-803-7	Sequence 7, Appl
707	23	100.0	19	3	US-08-974-549A-118	Sequence 118, App	780	23	100.0	20	2	US-08-621-803-47	Sequence 47, Appl
708	23	100.0	19	3	US-09-252-149B-8	Sequence 8, Appl	781	23	100.0	20	2	US-08-621-803-48	Sequence 48, Appl
709	23	100.0	19	4	US-09-081-975-13	Sequence 13, Appl	782	23	100.0	20	2	US-08-621-803-49	Sequence 49, Appl
710	23	100.0	19	4	US-09-461-325-291	Sequence 291, App	783	23	100.0	20	2	US-08-621-803-120	Sequence 120, App
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712	23	100.0	19	4	US-09-489-847-359	Sequence 359, App	785	23	100.0	20	2	US-08-485-445A-54	Sequence 54, Appl
713	23	100.0	19	4	US-09-489-847-360	Sequence 360, App	786	23	100.0	20	2	US-08-485-445A-57	Sequence 57, Appl
714	23	100.0	19	4	US-09-402-181B-118	Sequence 118, App	787	23	100.0	20	2	US-08-485-445A-58	Sequence 58, Appl
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718	23	100.0	19	4	US-09-794-529B-9	Sequence 9, Appl	791	23	100.0	20	2	US-08-485-445A-151	Sequence 151, App
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720	23	100.0	19	4	US-09-011-645E-9	Sequence 9, Appl	793	23	100.0	20	2	US-08-485-445A-159	Sequence 159, App
721	23	100.0	19	4	US-09-794-832-9	Sequence 9, Appl	794	23	100.0	20	2	US-08-485-445A-160	Sequence 160, App
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725	23	100.0	19	4	US-09-552-868-9	Sequence 9, Appl	798	23	100.0	20	2	US-08-714-677-17	Sequence 17, Appl
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729	23	100.0	19	4	US-09-774-639-342	Sequence 342, App	802	23	100.0	20	2	US-08-637-759B-458	Sequence 458, App
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738	23	100.0	20	1	US-08-311-611A-152	Sequence 152, App	811	23	100.0	20	3	US-08-871-355A-458	Sequence 458, App
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836	23	100.0	20	3	US-09-224-480-54	Sequence 54, Appl	909	23	100.0	20	4	US-09-794-832-13	Sequence 13, Appl
837	23	100.0	20	3	US-09-224-480-57	Sequence 57, Appl	910	23	100.0	20	4	US-09-794-832-15	Sequence 15, Appl
838	23	100.0	20	3	US-09-224-480-58	Sequence 58, Appl	911	23	100.0	20	4	US-09-794-832-17	Sequence 17, Appl
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897	23	100.0	20	4	US-09-794-517A-11	Sequence 11, Appl	970	23	100.0	20	5	PCT-US95-00656-151	Sequence 151, App
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901	23	100.0	20	4	US-09-794-517A-19	Sequence 19, Appl	974	23	100.0	20	5	PCT-US95-09307-11	Sequence 11, Appl
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977 22 95.7 7 1 US-08-277-660A-27 Sequence 27, Appl
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979 22 95.7 7 1 US-08-424-957-15 Sequence 15, Appl
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983 22 95.7 7 3 US-09-035-686-15 Sequence 71, Appl
984 22 95.7 7 3 US-09-433-043B-71 Sequence 36, Appl
985 22 95.7 7 4 US-09-638-202A-36 Sequence 36, Appl
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991 22 95.7 8 2 US-08-669-284B-31 Sequence 348, App
992 22 95.7 8 3 US-08-444-818-348 Sequence 386, App
993 22 95.7 8 3 US-08-444-818-386 Sequence 773, App
994 22 95.7 8 4 US-09-239-043D-773 Sequence 484, App
995 22 95.7 8 4 US-09-620-091-484 Patent No. 5514646
996 22 95.7 8 6 5514646-28 Patent No. 5514646
997 22 95.7 8 6 5514646-28 Sequence 77, Appl
998 22 95.7 9 2 US-08-417-174-77 Sequence 7, Appl
999 22 95.7 9 3 US-08-396-385-7 Sequence 29, Appl
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ALIGNMENTS

RESULT 1

US-08-221-580-9
; Sequence 9, Application US/08221580
; Patent No. 5519000
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 5519000ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: United States of America
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,580
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-221-580-9

Query Match 100.0%; Score 23; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;

Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXHWXX 8
DB 1 FSNHWNW 8
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|::|::|
RESULT 2
US-08-466-103A-9
; Sequence 9, Application US/08466103A
; Patent No. 5856124
; GENERAL INFORMATION:
; APPLICANT: Reppert, Steven M.
; APPLICANT: Ebisawa, Takashi
; TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,103A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/319,887
; FILING DATE: 07-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,857
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/250002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-103A-9

Query Match 100.0%; Score 23; DB 2; Length 8;

Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXX 8
DB 1 FAVCWAPL 8
|::|::|
|::|::|

RESULT 3

US-09-063-893A-8
; Sequence 8, Application US/09063893A
; Patent No. 6020464
; GENERAL INFORMATION:
; APPLICANT: Kenji OKAZAKI et al.
; TITLE OF INVENTION: A NOVEL SIGNAL TRANSDUCTION FACTOR AND A
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,893A
FILING DATE: April 22, 1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION/DOCKET NUMBER: 40,949
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note = "Xaa at position 7 is Ala, Pro,
Cys or Glu"
US-09-063-893A-8
Query Match 100.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.1e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
Db 1 FVKGWGXT 8
RESULT 4
US-08-444-818-323
; Sequence 323, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANEV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818

FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 323:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-323
Query Match 100.0%; Score 23; DB 3; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
Db 1 FDQGWGPI 8
RESULT 5
US-09-314-242-4
; Sequence 4, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Golightly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; FILE OF INVENTION: Having L-Amino Acid Oxidase Activity
; FILE REFERENCE: 5556.200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 09/080,428
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-314-242-4
Query Match 100.0%; Score 23; DB 3; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXWXXX 8
|::|::|
Db 1 PSYPWIK 8
RESULT 6
US-08-981-392-83
; Sequence 83, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94

```

CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-Dec-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9030
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRADNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-981-392-83

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Query Match 100.0%; Score 23; DB 3; Length 8;
Best Local Similarity 25.0%; Pred. NO. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels

Qy	1	FXXXWXXX	8
		:: :::	
Db	1	FGFTWPGT	8

```

RESULT 7
US-08-469-260A-352
; Sequence 252, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TYPE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-252

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Fred.No. 4.1e-05;
Matches 2; Conservative 6; Mismatches 0; Indels 0;

Qy 1 FXXKWXKX 8
   |::|:::
Db 1 FSHLWISG 8

RESULT 8
US-08-488-446-252
; Sequence 252, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365

```

TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-446-252

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXWXXX 8
|::|::|
DB 1 FSHLWTS 8

RESULT 9

US-08-467-344A-252
Sequence 252, Application US/08467344A
Patent No. 6586568

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUEHROFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,344A

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/424,550

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: FOREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 252:

US-08-467-344A-252

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;

Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXXXXWXXX 8
|::|::|
DB 1 FSHLWTS 8

RESULT 10

US-09-780-070-13

Sequence 13, Application US/09780070

Patent No. 6632616

GENERAL INFORMATION:

APPLICANT: Burke, James

APPLICANT: Strittmatter, Warren

APPLICANT: Nagai, Yoshitaka

TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT

TITLE OF INVENTION: AND METHODS OF USE THEREOF

FILE REFERENCE: 5405.242

CURRENT APPLICATION NUMBER: US/09/780,070

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/189,781

PRIOR FILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin version 3.0

SEQ ID NO 13

LENGTH: 8

TYPE: PRT

ORGANISM: synthetic construct

US-09-780-070-13

Query Match

Best Local Similarity 100.0%; Score 23; DB 4; Length 8;

Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXWXXX 8

|::|::|

DB 1 FIGPWWKW 8

RESULT 11

US-09-794-529B-4

Sequence 4, Application US/09794529B

Patent No. 6641812

GENERAL INFORMATION:

APPLICANT: Sloan-Kettering Instituté for Cancer Research

ROTHMAN, James E.

HARTL, F. Ulrich

HOB, Mee H.

HOUGHTON, Alan

TAKECHI, Yoshizumi

MAYHEW, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and

Immunotherapies

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: One Broadway

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/794,529B

FILING DATE: 09-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/002,479

FILING DATE: August 18, 1995

```

; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: heat shock protein binding motif
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-5298-4

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
Db 1 FWGLWPWE 8

RESULT 12
US-09-794-517A-4
; Sequence 4, Application US/09794517A
; Patent No. 6656679
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,517A
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995

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; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: heat shock protein binding motif
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-517A-4

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
Db 1 FWGLWPWE 8

RESULT 13
US-09-011-645E-4
; Sequence 4, Application US/09011645E
; Patent No. 6663868
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,645E
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995

```

APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: heat shock protein binding motif
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-011-645E-4

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FWGLWPWE 8

RESULT 14
US-09-794-832-4
; Sequence 4, Application US/09794832
; Patent No. 6673348
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Wee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,832
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,645
; FILING DATE: 13-Feb-1998
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995

APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: heat shock protein binding motif
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-832-4

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FWGLWPWE 8

RESULT 15
US-09-601-729-168
; Sequence 168, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-168

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8


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; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 1716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-252

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FSHLWTS 8

RESULT 19
US-09-552-868-4
; Sequence 4, Application US/09552868
; Patent No. 6761892
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS

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; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/552,868
; FILING DATE: 20-Apr-2000
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,479
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: 60/002,490
; FILING DATE: August 18, 1995
; APPLICATION NUMBER: PCT/US96/13363
; FILING DATE: August 16, 1996
; APPLICATION NUMBER: 09/011,645
; FILING DATE: February 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Delucia, Richard L.
; REGISTRATION NUMBER: 28,839
; REFERENCE/DOCKET NUMBER: 11746/8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; FEATURE:
; OTHER INFORMATION: heat shock protein binding motif
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-09-552-868-4

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FWGLWPWE 8

RESULT 20
US-09-636-295-4
; Sequence 4, Application US/09636295
; Patent No. 6773707
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.
; HOUGHTON, Alan
; TAKECHI, Yoshizumi
; MAYHEW, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
; Immunotherapies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS

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; APPLICATION NUMBER: US/09/908,322
; Filing Date: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; Filing Date: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
;
US-09-908-322-83

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.le+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXXXX 8
DB 1 FGFTWPGT 8

RESULT 22
PCT-US95-04018-71
; Sequence 71, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04018
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,580
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,583
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,581
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0232

```


TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
PCT-US95-04018-71

Query Match 100.0%; Score 23; DB 5; Length 8;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXXX 8
|::|::|
DB 1 FSNHWNW 8

RESULT 23
US-08-350-884-5
Sequence 5, Application US/08350884
Patent No. 5585258
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,884
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-884-5

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXXX 8
|::|::|
DB 1 FHTMHWHT 8

RESULT 24
US-08-350-884-8
Sequence 8, Application US/08350884
Patent No. 5585258
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,884
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-884-8

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXHWXXX 8
|::|::|
DB 1 FHTLWHTT 8

RESULT 25
US-08-350-884-11
Sequence 11, Application US/08350884
Patent No. 5585258
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/350,884
/ FILING DATE: 06-DEC-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/680,296
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CIOTTI, THOMAS E.
/ REGISTRATION NUMBER: 21,013
/ REFERENCE/DOCKET NUMBER: 22300-20100.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-350-884-11

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXWXXX 8
Db 1 FHTLWHTT 8

RESULT 26
US-08-350-884-14
/ Sequence 14, Application US/08350884
/ Patent No. 5585258
/ GENERAL INFORMATION:
/ APPLICANT: HOUGHTON, MICHAEL
/ APPLICANT: CHOO, QUI LIM
/ APPLICANT: KUO, GEORGE
/ TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 755 Page Mill Road
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/350,884
/ FILING DATE: 06-DEC-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/680,296
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CIOTTI, THOMAS E.
/ REGISTRATION NUMBER: 21,013
/ REFERENCE/DOCKET NUMBER: 22300-20100.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
```

```
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-350-884-14

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXWXXX 8
Db 1 FHTLWHTT 8

RESULT 27
US-08-709-173-5
/ Sequence 5, Application US/08709173
/ Patent No. 5712145
/ GENERAL INFORMATION:
/ APPLICANT: HOUGHTON, MICHAEL
/ APPLICANT: CHOO, QUI LIM
/ APPLICANT: KUO, GEORGE
/ TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 755 Page Mill Road
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/709,173
/ FILING DATE: 06-SEP-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/680,296
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CIOTTI, THOMAS E.
/ REGISTRATION NUMBER: 21,013
/ REFERENCE/DOCKET NUMBER: 22300-20100.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-709-173-5

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXXWXXX 8
Db 1 FHTLWHTT 8

RESULT 28
US-08-709-173-8
```

Sequence 8, Application US/08709173
Patent No. 5712145
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,173
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-173-8

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
DB 1 FHTLWHTT 8

RESULT 29
US-08-709-173-11
Sequence 11, Application US/08709173
Patent No. 5712145
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,173
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-173-11

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
DB 1 FHTLWHTT 8

RESULT 30
US-08-709-173-14
Sequence 14, Application US/08709173
Patent No. 5712145
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,173
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-709-173-14

Query Match      100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db 1 FHTLWHT 8

RESULT 31
US-08-615-181-30
; Sequence 30, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; RESPONSE: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: PCT/JP94/01756
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 261302/1993
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-30

Query Match      100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db 1 FPRPWLHS 8
```

```
RESULT 32
US-08-638-911A-12
; Sequence 12, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; APPLICANT: Chong, Susan M.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,911A
; FILING DATE: 04/24/96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Catalytic His region of Yellow Fever
; INDIVIDUAL ISOLATE: Virus NS3
US-08-638-911A-12

Query Match      100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
Db 1 FHTMWHVT 8

RESULT 33
US-08-638-911A-15
; Sequence 15, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; APPLICANT: Chong, Susan M.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,911A
FILING DATE: 04/24/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4600-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: catalytic His region of West Nile
INDIVIDUAL ISOLATE: Fever Virus NS3
US-08-638-911A-15

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FHTLWHTT 8

RESULT 34
US-08-638-911A-18
Sequence 18, Application US/08638911A
Patent No. 5766916
GENERAL INFORMATION:
APPLICANT: Belaevy, Alexander S.
APPLICANT: Chong, Susan M.
TITLE OF INVENTION: Hepatitis G Virus Protease
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,911A
FILING DATE: 04/24/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4600-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: catalytic His region of Murray
INDIVIDUAL ISOLATE: Valley Virus NS3
US-08-638-911A-18

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FHTLWHTT 8

RESULT 35
US-08-638-911A-21
Sequence 21, Application US/08638911A
Patent No. 5766916
GENERAL INFORMATION:
APPLICANT: Belaevy, Alexander S.
APPLICANT: Chong, Susan M.
TITLE OF INVENTION: Hepatitis G Virus Protease
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,911A
FILING DATE: 04/24/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4600-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: catalytic His region of Kunjin Virus
INDIVIDUAL ISOLATE: NS#
US-08-638-911A-21

Query Match 100.0%; Score 23; DB 1; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXWXXX 8
|::|::|
DB 1 FHTLWHTT 8

RESULT 36
US-08-709-177-5
Sequence 5, Application US/08709177
Patent No. 5885799
GENERAL INFORMATION:

;; APPLICANT: HOUGHTON, MICHAEL
;; APPLICANT: CHOO, QUI LIM
;; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 Page Mill Road
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/709,177
;; FILING DATE: 06-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/680,296
;; FILING DATE: 04-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CIOTTI, THOMAS E.
;; REGISTRATION NUMBER: 21,013
;; REFERENCE/DOCKET NUMBER: 22300-20100.20
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-709-177-5

Query Match 100.0%; Score 23; DB 2; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXKXXXX 8
|::|::|
DB 1 FHTMHWHT 8

RESULT 37
US-08-709-177-8
;; Sequence 8, Application US/08709177
;; Patent No. 5885799
;; GENERAL INFORMATION:
;; APPLICANT: HOUGHTON, MICHAEL
;; APPLICANT: CHOO, QUI LIM
;; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 Page Mill Road
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/709,177

;; FILING DATE: 06-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/680,296
;; FILING DATE: 04-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CIOTTI, THOMAS E.
;; REGISTRATION NUMBER: 21,013
;; REFERENCE/DOCKET NUMBER: 22300-20100.20
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-709-177-8

Query Match 100.0%; Score 23; DB 2; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXKXXXX 8
|::|::|
DB 1 FHTMHWHT 8

RESULT 38
US-08-709-177-11
;; Sequence 11, Application US/08709177
;; Patent No. 5885799
;; GENERAL INFORMATION:
;; APPLICANT: HOUGHTON, MICHAEL
;; APPLICANT: CHOO, QUI LIM
;; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 Page Mill Road
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/709,177
;; FILING DATE: 06-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/680,296
;; FILING DATE: 04-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CIOTTI, THOMAS E.
;; REGISTRATION NUMBER: 21,013
;; REFERENCE/DOCKET NUMBER: 22300-20100.20
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

US-08-709-177-11

Query Match 100.0%; Score 23; DB 2; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FHTLWHTT 8

RESULT 39

US-08-709-177-14
; Sequence 14, Application US/08709177
; Patent No. 5885799
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON, & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,177
; FILING DATE: 06-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-709-177-14

Query Match 100.0%; Score 23; DB 2; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 1 FHTLWHTT 8

RESULT 40

US-08-159-339A-985
; Sequence 985, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro

APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 985:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-985

Query Match 100.0%; Score 23; DB 3; Length 9;
Best Local Similarity 25.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXXWXXX 8
|::|::|
Db 2 FWLWKKAK 9

Search completed: October 19, 2005, 15:52:04
Job time : 28.7647 secs

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